## **SEARCH REQUEST FORM**

Reque Name			Serial Number:							
Date:			Phone:		Art Unit:					
Please	hat may have	a special meaning. G	ive examples or rele	event citations, authors	ne subject matter to be so keywords, etc., if know most relevent claim(s).	vn. ror sequences,				
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Copyright (c) 1993 - 2003 Compugen Ltd.
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-!- MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
-!- MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
-!- MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM A WYELOMA PROTEIN.
HSSP, PO1607; IREI.
InterPro; IPR00306; Ig_MHC.
InterPro; IPR003596; Ig_v.
Ffam; PF00047; ig_v.
SWART; SW00406; IGv; I.
Immunoglobulin V region.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
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FRAMEWORK-2.
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COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-V region MOPC 149.
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PAAH ECOLI
VP40 HSVSA
YSR2 CAEEL
KMIL CHICK
KRAF HUMAN
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MEDLINE-82057806; PubMed-6795447;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                               Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.; "Complete gnome sequence of the methanogenic archaeon, Methanococcus jannaschii."
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-!- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone phosphate + D-glyceraldehyde 3-phosphate.
-!- COFACTOR: ZINC (BY SIMILARITY).
-!- PATHWAY: Glycolysis; sixth step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                             Science 273:1058-1073(1996).
-!- SIMILARITY: STRONG, TO M.JANNASCHII MJ0748, AND LOW, TO
M.JANNASCHII MJ0534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
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393 AA; 45554 MW; CF01B59793BBA20F CRC64;
Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
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Pred. No. 11;
0; Mismatches
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01-NOV-1997 (Rel. 35, Last sequence update)
15-UND-2002 (Rel. 41, Last annotation update)
FAUTHORSPHIED (FOR MPNOSE) OR MP129.
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                                                                                       SEQUENCE FROM N.A.
STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE=96337999; Pubmed=8688087;
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Interpro, IPR001226; Flavodoxin.
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STRAIN=ATCC 29342 / M129;
MEDLINE=97105885; PubMed=8948633;
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Pfam; PF00753; lactamase_B; 1.
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HSSP; Q9F0J6; 1E5D.
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Best Local Similarity
Matches 6; Conserv
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                                         NCBI_TaxID=2190;
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P75089;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nt is in no way and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: OUTSIDE OF THE PERIPLASMIC MEMBRANE. MISCELLANEOUS: THE PI FORM CAN OXIDIZE ONLY D-GLUCOSE, WHILE THE P2 FORM CAN ALSO OXIDIZE MALTOSE. THE SEQUENCE OF P1 FORM IS SHOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLUCOSE DEHYDROGENASE [PYRROLOQUINOLINE-QUINONE].
                                                                                                                                                                                                                                                                                                                                                                               Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: D-glucose + acceptor = D-glucono-1,5-lactone reduced acceptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                           Cleton-Jansen A.-M., Dekker S., van de Putte P., Goosen N.; As single amino acid substitution changes the substrate specificity of quinoprotein glucose dehydrogenase in Gluconobacter oxydans."; Mol. Gen. Genet. 229:206-212(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE BACTERIAL POQ DEHYDROGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                Gluconobacter oxydans (Gluconobacter suboxydans).
Bacteria; Proteobacteria; alpha subdivision; Acetobacteraceae;
Gluconobacter.
    Glucose dehydrogenase [pyrrologuinoline-guinone] precursor (EC 1.1.99.17).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40; DB 1; Length 808;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRRDED, AND TO OPKEX.

INTERPRO, 1PR001479; Bac_PQQ.

INTERPRO, 1PR001479; Bac_PQQ.

INTERPRO, 1PR0011; Baccerial_PQQ; 7.

PROSITE; PS00364; BACTERIAL_PQQ_2; 1.

PROSITE; PS00364; BACTERIAL_PQQ_2; 1.

Oxidoreductase; PQQ; Transmembrane; Periplasmic; Signal.

33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0F4160DA78652445 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -> N (IN P2 FORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
Y732 METJA
ID Y73E METJA
AC 058142;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 40, Last annotation update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DF Hypotherical protein MJ0732.
GN MCTANOCOCUS jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X62710; CAA44594.1; ALT_SEQ.
PIR; S17716; QPKEX.
                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=92017653; PubMed=1833618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87567 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75.0%;
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470
788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   808 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                        REVISION TO 213
                                                                                                                                      NCBI_TaxID=442;
                                                                                                                                                                                                                                                                                                                                                                 Goosen N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
ACT SITE
VARTANT
SEQUENCE
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Length 393; 1; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
     -!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- DEVELOPMENTAL STAGE: IS INITIALLY EXPRESSED THROUGHOUT THE
PRESUMPTIVE MESODERM AND BECOMES RESTRICTED TO CARDIAC AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Hypothetical 83.7 kba protein in PRP5-TH12 intergenic region.
YBR238C OR YBR1608.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36; DB 1; Length 416;
Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aljinovic G., Pohl F.M., Pohl T.M.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77A6AE6F1EAA4FD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              731 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOMEOBOX.
POLY-GLN.
POLY-GLN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
Homeobox; DNA-binding; Developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -! - SIMILARITY: TO YEAST YGL107C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR01356; Homeobox.
Pfam; PF00046; homeobox; 1.
PRINTS; PR00024; HOMEOBOX.
ProDom; PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46124 MW;
                                                                                                                                                                                                                                                                                                                                                                  EMBL; X55192; CAA38978.1; -. EMBL; M77292; AAA28619.1; -. PIR; D33976; D33976. PIR; A43561; A43561.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.1%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z36107; CAA85201.1; -. PIR; S46115; S46115.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P23441; 1FTT.
TRANSFAC; T03612; -.
FlyBase; FBgn0004110; tin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 62.5
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 ОННИСИРН 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00389; HOX;
                                                                                       VISCERAL MUSCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QHHYGTPY 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     416 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=S288C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YB88 YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA BIND
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P38330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
YB88_YEAST
     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
SUBUNIT: HOMODIMER (BY SIMILARITY).
SIMILARITY: BELONGS TO CLASS II FRUCTOSE-BISPHOSPHATE ALDOLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91209226; PubMed=1982429;
Bodner R., Jan L.Y., Jan Y.N.;
A new homeobox-containing gene, msh-2, is transiently expressed early during mesoderm formation of Drosophila.";
Development 110:661-669(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37; DB 1; Length 288;
Pred. No. 12;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Muscle-specific homeobox protein tinman (Msh-2) (NK-4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174A7F2E4E215FD8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                 | DEST: F110-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 120-7, 
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MEDLINE=90046666; PubMed=2573058;
Kim Y., Nirenberg M.;
"Drosophila MK-homeobox genes.";
Proc. Natl. Acad. Sci. U.S.A. 86:7716-7720(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       416 AA
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                                                                                                                                                                                                                                                                                                                                        EMBL; AE000015; AAB95777.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 288 AA; 31069 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 QHHYAVPH 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QHHYGTPY 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                     HSSP; P11604; 1B57
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RESULT 5 HMTI\_DROME

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NCBI_TaxID=10116;
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MEDIINES-96044430, PubMed=7557990;

Tommerup N. Vissing H. Vissing H
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InterPro; IPR000822; Znf C2H2.
InterPro; IPR00096; zf-C2H2; 35.
PRINTS; PR00096; zNCFINGER.
SWART; SM00355; ZnF C2H2; 34.
PROSITE; PS00028; ZINC FINGER C2H2 1; 17.
PROSITE; PS50157; ZINC FINGER C2H2 2; 18.
Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Bone marrow;
MEDLINE=9719154; PubMed=9039502;
MEDLINE=9719154; PubMed=9039502;
Nagase T.. Seki N., Ishikawa K.-I., Ohira M., Kawarabayasi Y.,
Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;
Thediction of the coding sequences of unidentified human genes.
The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced lanalysis of cDNA clones from cell line KG-1 and brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                             ö
                                                                                                           Score 36; DB 1; Length 731;
Pred. No. 51;
2; Mismatches 2; Indels
SGD; S0000442; YBR238C.
Hypothetical protein.
SEQUENCE 731 AA; 83761 MW; 4A6800D8476F3DE2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                  2142 HUMAN STANDARD; PRT; 1687 AA. P52746; Q92510; 01-0CT-1996 (Rel. 34, Created) 15-UU-1998 (Rel. 36, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 2inc finger protein 142 (HA4654).
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C2H2-TYPE.
C2H2-TYPE.
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55.6%;
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Genew; HGNC:12927; ZNF142.
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44 EHNYAIPYT 52
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                                                                                   FINGER PROTEINS
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MEDLINE=55148647; PubMed=7846077;
Kakiuchi H., Watanabe M., Ushijima T., Toyota M., Imai K.,
Weisburger J.H., Sugimura T., Nagao M.;
"Specific 5'-GGGA-3'-->5'-GGA-3' mutation of the Apc gene in rat.colon tumors induced by 2-amino-1-methyl-6-phenylimidazo[4,5-b]pyridine.";
Proc. Natl. Acad. Sci. U.S.A. 92:910-914(1959).
!- FUNCTION: TUMOR SUPPRESSOR. ALLOWS THE RAPID TURNOVER OF BETA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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STRAIN=Fischer 344/N; TISSUE=Brain;
MEDLINE=56116966; PubMed=8563176;
Toyota M., Ushijima T., Kakiuchi H., Watanabe M., Imai K., Yachi A.,
Sugimura T., Magao M.;
McDIN cloning 6: The rat APC gene and assignment to chromosome 18.";
Mamm. Genome 6:746-748(1995).
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Pred. No. 1.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C2H2-TYPE.
TECG -> LKGS (IN REF. 2)
S -> A (IN REF. 2).
                   (ATYPICAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Adenomatous polyposis coli protein (APC protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 2842 AA
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                                      C242 - TYPE.
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85.7%;
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275
311
340
366
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451
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507
5567
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Best Local Similarity
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TISSUE=Fetal brain;
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   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
CATENIN. APC ACTIVITY CORRELATED WITH ITS PHOSPHORYLATION STATE ALLOWS THE DOWN-REGULATION OF CYTOPLASMIC BETA-CATENIN (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91335210; PubMed=1651562; Kinzler K.W., Nilbert M.C., Su L.-K., Vogelstein B., Bryan T.M., Levy D.B., Smith K.J., Preisinger A.C., Hedge P., McKechnie D., Finniear R., Markham A., Groffen J., Boguski M.S., Altschul S.F., Horii A., Ando H., Miyoshi Y., Miki Y., Nishisho I., Nakamura Y.; "Identification of FAP locus genes from chromosome 5q21."; Science 253:661-665(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                             SUBUNIT: FORMS HOMOOLIGOMERS AND ASSOCIATES WITH CATENINS (BY
                                                                                                                                                                                                                                                                                                                                                                           R: IN AN IQ-INDUCED COLON TUMOR. 3CBB2EA8A34E8F47 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                           Length 2842;
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0; Indels
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ARM 2.
ARM 3.
ARM 4.
ARM 6.
ARM 6.
ARM 6.
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ASP/GLU-RICH (ACIDIC).
                                               PTM: PHOSPHORYLATED BY GSK-3B (BY SIMILARITY) SIMILARITY: CONTAINS 7 ARM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1992 (Rel. 22, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Adenomatous polyposis coli protein (APC protein)
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SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
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0; Mismatches
                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                          Score 36;
Pred. No.
                                                                                                                                                                            InterPro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 6.
SMART; SM00185; ARM; 5.
PROSITE; PS50176; ARM REPEAT; 1.
Anti-oncogene; Phosphorylation; Coilec
DOMAIN 1 728
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P25054; Q15162; Q15163;
O1-MAY-1992 (Rell. 22, Created)
01-MAY-1992 (Rell. 22, Last sequ.
15-JUN-2002 (Rel. 41, Last anno
                                                                                                                                                             EMBL; D38629; BAA07609.1; -.
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                  SIMILARITY)
                                      SIMILARITY
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MEDINE=97094176; PubMed=8940264; Eccles D.M., van der Luijt R., Breukel C., Bullman H., Bunyan D., Fisher A., Barber J., du Boulay C., Primrose J., Burn J., Fodde R.; "Hereditary desmoid disease due to a frameshift mutation at codon 1924 of the APC gene.", Am. J. Hum. Genet. 59:1193-1201(1996).
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Nakatsuru S., Yanagisawa A., Ichii S., Tahara E., Kato Y.,
Nakamura Y., Horii A.;
"Somatic mutation of the APC gene in gastric cancer: frequent
mutations in very well differentiated adenocarcinoma and signet-ring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91335211; PubMed=1651563; Nishisho I., Nakamura Y., Miyoshi Y., Miki Y., Ando H., Horii A., Nishisho I., Nakamura Y., Miyoshi Y., Miki Y., Ando H., Horii A., Koyama K., Utsunomiya J., Baba S., Hedge P., Markham A., Krush A.J., Petersen G., Hamilton S.R., Nibert M.C., Levy D.B., Bryan T.M., Presisinger A.C., Smith K.J., Su L.-K., Kinzler K.W., Vogelstein B., "Mutations of chromosome 5q21 genes in FAP and colorectal cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20243021; PubMed=10782927; Couture J., Mitri A., Lagace R., Smits R., Berk T., Bouchard H.-L., Fodde R., Alman B., Bapat B.; "A germline mutation at the extreme 3-prime end of the APC gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hamilton S.R., Liu B., Parsons R.E., Papadopoulos N., Jen J., Powell S.M., Krush A.J., Berk T., Cohen Z., Tetu B., Burger P.C., Wood P.A., Taqi F., Booker S.V., Petersen G.M., Offerhaus G.J.A., Tersmette A.C., Gjardiello F.M., Vogelstein B., Kinzler K.W.; "The molecular basis of Turcot's syndrome.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94082295; PubMed=8259519; Su L.-K., Vogelstein B., Kinzler K.W.; Association of the APC tumor suppressor protein with catenins."; Science 262:1734-1137(11933).
MEDLIRE=91330307; PubMed=1678319;
Joslyn G., Carlson M., Thliveris A., Albertsen H., Gelbert L.,
Samowitz W., Groden J., Stevens J., Spirio L., Robertson M.,
Sargeant L., Krapcho K., Wolff E., Burt R., Hughes J.P.,
Warrington J., McPherson J.D., Wasmuth J., Le Paslier D.,
Abderrahm H., Cohen D., Leppert M., White R.;
"Identification of deletion mutations and three new genes at the familial polyposis locus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  results in a severe desmoid phenotype and is associated with overexpression of beta-catenin in the desmoid tumor."; clin. Genet. 57:205-212(2000).
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Nagase H., Nakamura Y.;
"Mutations of the APC (adenomatous polyposis coli) gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95174843; PubMed=7661930;
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                                                                                                                                                                                                                                                                                                                                                                                                [3] ASSOCIATION WITH CATENINS.
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Cell 66:601-613(1991)
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MEDLINE=99401091; PubMed=10470088; Lamlum H., Ilyas M., Rowan A., Clark S., Johnson V., Bell J.A., Frayling I.M., Efstathiou J., Pack K., Payne S., Roylance R., Gorman P., Sheer D., Neale K., Phillips R., Talbot I.C., Bodmer W.F., Tomlinson I.P.M.; "The type of somatic mutation at APC in familial adenomatous polypositis determined by the site of the germline mutation: a new facet to
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STRAIN=C57BL/6J, and CAST/R1; TISSUE=Brain;
MEDLINE=92263101; PubMed=1350108;
Su L.-K., Kinzler K.W., Vogelstein B., Preisinger A.C., Moser A.R.,
Luongo C., Gould K.A., Dove W.F.;
"Multiple intestinal neoplasia caused by a mutation in the murine
homolog of the APC gene."
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MEDLINE=98400259; PubMed=9731533; Woodage T., King S.M., Wacholder S., Hartge P., Struewing J.P., McAdams M., Laker S.J., Tucker M.A., Brody L.C.; "The APC 11307K allele and cancer risk in a community-based study Ashkenazi Jews.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                             Gryfe R., Di Nicola N., Lal G., Gallinger S., Redston M.; "Inherited colorectal polyposis and cancer risk of the APC 11307K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wallis Y.L., Morton D.G., McKeown C.M., Macdonald F., "Molecular analysis of the APC gene in 205 families: extended genotype-phonotype correlations in FAP and evidence for the role (APC amino acid changes in colorectal cancer predisposition."; Med. Genet. 36:14-20(1999).
                                                                                                                                                                                                                                                                                                                                                                                               JARIANTS FAP CYS-1171 AND THR-2738, AND VARIANTS GLY-1057 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36; DB 1; Length 2843;
Pred. No. 2.2e+02;
0; Mismatches 0; Indels
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Q61315; Q62044;

16-OCT-2001 (Rel. 40, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

Adenomatous polyposis coli protein (APC protein) (mAPC).
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STRAIN=BALB/c; TISSUE=Liver;
Dicker F., Lambertz S., Reitmair A., Ballhausen W.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                J. Hum. Genet. 64:378-384(1999).
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MEDLINE=99138651; PubMed=9973276;
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MEDLINE=99133859; PubMed=9950360;
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63.6%;
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Science 256:1114-1114(1992).
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Science 256:668-670(1992).
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Best Local Similarity 63.6
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                          polymorphism.";
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APC_MOUSE
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MEDLINE-95136430; PubMed=7833931;
Stella A., Montera M., Resta N., Marchese C., Susca F., Gentile M.,
Stella A., Montera W., Reste F., Mareni C., Guanti G.,
"Four novel mutations of the APC (adenomatous polyposis coli) gene in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANTS COLORECTAL CARCINOMA THR-880; ILE-890 AND VAL-1508.
MEDLINE-98080146; PubMed-9419979;
Miyaki M., Nishiko J., Konishi M., Kikuchi-Yanoshita R., Tanaka K.,
Miyaki M., Nagato M., Chong J.-M., Koike M., Terada T., Kawahara Y.,
Fukutome A., Tomiyama J., Chuganji Y., Momoi M., Utsunomiya J.;
"Drastic genetic instability of tumors and normal tissues in Turcot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98400248; PubMed=9731522;
Redetcon M., Nachanson K.L., Yuan Z.Q., Neuhausen S.L., Satagopan J.,
Wong N., Yang D., Nafa D., Abrahanson J., Ozcelik H.,
Antin-Ozerkis D., Andrulis I., Daly M., Pinsky L., Schrag D.,
Gallinger S., Kaback M., King M.-C., Woodage T., Brody L.C.,
Godwin A., Warner E., Weber B., Foulkes W., Offit K.;
"The APC 11307K allele and breast cancer risk.";
                                                                                                                                                                                        Baba S., Nakamura Y.;
"Screening for germ-line mutations in familial adenomatous polyposis
patients: 61 new patients and a summary of 150 unrelated patients.";
Hum. Mutat. 1:467-473(1992).
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                                                                                                                                                                                                                                                                                                                       VARIANT FAP TRP-99.

TISSUE=Peripheral blood lymphocytes;

MEDLINE=95134544; PubMed=7833149;

Dobbie Z., Spycher M., Huerliman R., Ammann R., Ammann T., Roth J.,

Mueller A., Mueller H., Scott R.J.;

"Mutational analysis of the first 14 exons of the adenomatous

polyposis coli (APC) gene.";
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MEDLINE=98393712; PubMed=9724771;
Frayling I.M., Beck N.E., Ilyas M., Dove-Edwin I., Goodman P.,
Pack K., Bell J.A., Williams C.B., Hodgson S.V., Thomas H.J.W.,
Talbot I.C., Bodmer W.F., Tomlinson I.P.M.;
"The APC variants Il307K and El317Q are associated with colorectal
tumors, but not always with a family history.";
Proc. Natl. Acad. Sci. U.S.A. 95:10722-10727(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Susca F., Gentile M.,
                                                                                     VARIANT FAP W-1348, AND VARIANTS D-1118; M-1292; V-1304 AND S-2502
                                                                                                        MEDLINE-93250848; PubMed-1338764;
Nagase H., Miyoshi Y., Horii A., Aoki T., Petersen G.M.,
Vogelstein B., Maher E., Ogawa M., Maruyama M., Utsunomiya J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stella A., Montera M., Resta N., Marchese C., Susca Romio L., Pilia S., Prete F., Mareni C., Guanti G.; Hum. Mol. Genet. 3:1918-1918(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Cancer 30A:1709-1713(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mol. Genet. 3:1687-1688(1994).
        carcinoma.";
Mol. Genet. 1:559-563(1992).
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ID HBB2 XE
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                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                     SIMILARITY).
-!- ALTERNATIVE PRODUCTS: 4 ISOFORMS; 1 (SHOWN HERE), 2, 3 AND 4; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: EXPRESSED IN LIVER, SPLEEN, KIDNEY, HEART, LUNG, BRAIN, STOMACH, INTESTINE, TESTIS AND OYARY.
-!- PTM: PHOSPHORYLATED BY GSK-3B (BY SIMILARITY).
-!- SIMILARITY: CONTAINS 7 ARM REPEATS.
                                            ALTERNATIVE SPLICING.
MEDLINE=94061824; PubMed=8242607;
MEDLINE=94061824; PubMed=8242607;
OSSHIMM M., Sugiyama H., Kitagawa K., Taketo M.;
"APC gene messenger RNs. novel isoforms that lack exon 7.";
Cancer Res. 53:5589-5591(1993).
-!- FUNCTION: TUMOR SUPPRESSOR. ALLOWS THE RAPID TURNOVER OF BETA-CATENIN. APC ACTIVITY CORRELATED WITH ITS PHOSPHORYLATION STATE
ALLOWS THE DOWN-REGULATION OF CYTOPLASMIC BETA-CATENIN (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISSING (IN ISOFORM 2 AND ISOFORM 4). MISSING (IN ISOFORM 3 AND ISOFORM 4).
                                                                                                                                                    SUBUNIT: FORMS HOMOOLIGOMERS AND ASSOCIATES WITH CATENINS (BY SIMILARITY).
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Pfam; PF00514; Armadillo_seg; 6.
SMART; SM00185; ARM; F.F.
PR051TE; PS50176; ARM REPEAT; 1.
Anti-oncogene; Phosphōrylation; Alternative splicing; Repeat;
'The murine APC gene: alternative splicing of 5' untranslated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.1%; Score 36; DB 1; Length 2845; 63.6%; Pred. No. 2.2e+02; live 0; Mismatches 0; Indels
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Y -> 7 (IN STRAIN CAST/EI).
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T -> 6 (IN STRAIN CAST/EI).
T -> 6 (IN STRAIN CAST/EI).
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              region segments.";
Submitted (OCT-1993) to the EMBL/GenBank/DDBJ databases.
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Best Local Similarity 63.0.
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MGD; MGI:88039; Apc.
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                                                                                                                                                                                                                                                                                                                                            Knoechel W., Korge E., Basner A., Meyerhof W.; "Globin evolution in the genus Xenopus: comparative analysis of cDNAs coding for adult globin polypeptides of Xenopus borealis and Xenopus tropicalis.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Mol. Evol. 23:211-223(1986).
-!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.
-!- SUBJUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
-!- TISSUE SPECIFICITY: RED BLOOD CELLS.
                                                                                                                                                                  Xenopus borealis (Kenyan clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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Pred. No. 14;
1; Mismatches 2; Indels
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IRON (HEME PROXIMAL LIGANI
4 4F108FC787F397A7 CRC64;
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INIT MET 0 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
                                                                       Last sequence update)
Last annotation update)
  145 AA.
                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
MEDLINE=87112760; PubMed=3100812;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; PO2118; 1A4F.
InterPro; IPR0002337; Beta_haem.
InterPro; IPR000971; Globin.
Pfam; PF00042; globin; 1.
                                                                                                                    Hemoglobin beta-2 chain (Minor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91 IR
15988 MW;
                                                01-APR-1988 (Rel. 07, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M32458; AAA49661.1; -.
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5; Conservative
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PROSITE; PS01033; GLOBIN;
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 HHFGEEYT 122
                                                                                                                                                                                                                                              Xenopodinae; Xenopus.
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145 AA;
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Best Local Similarity
Matches 5; Conserv
                                                                         (Rel.
                                                                                                                                                                                                                                                             NCBI_TaxID=8354;
                                                                    01-APR-1988
16-OCT-2001
XENBO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ar cress).

Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-92316202; PubMed-1618302; Imajuku Y., Hirayama T., Endoh H., Oka A.; "Exon-intron organization of the Arabidopsis thaliana protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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MEDLINE=92039027; PubMed=1937013;
Hirayama T., Imajuku Y., Anai T., Matsui M., Oka A.;
"Identification of two cell-cycle-controlling cdc2 gene homologs in
Arabidopsis thaliana.";
                                                                                        STRAINBMB4 / JCM 11007;

STRAINBMB4 / JCM 11007;

MEDLINE=2192816; PubMed=11997336;

Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,

Chen Y., Xue Y., Li W., Xu Y., Huang L., Dong X., Ma Y., Ling L.

Tan H., Chen R., Wang J., Yu J., Yang H.;

"A complete sequence of T. tengcongensis genome.";

"A complete sequence of T. tengcongensis genome.";

"ENGCTION: Essential for recycling GMP and indirectly, cGMP.

-! CATALITIC ACTIVITY: ATP + GMP. = ADP + GDP.

-! CATALITIC ACTIVITY: ATP + GMP. = ADP + GDP.

-! SUBCELLULAR LOCATION: CYCOPLasmic '(By similarity).

-! SIMILARITY: BELONGS TO THE GUANYLATE KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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P24100, Q9M301,
01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cell division control protein 2 homolog A (EC 2.7.1.-).
CDC2A OR CDC2 OR AT3G48750 OR T21J18_20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AE013108; AAM24729.1; -.
PROSITE; PS00856; GUANYLATE KINASE 1; 1.
PROSITE; PS50052; GUANYLATE KINASE 2; TANSFEASERSE, KINASE, KI
Thermoanaerobacteriaceae; Thermoanaerobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
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nes 5, Conservative
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81 HYYGTP 86
                        NCBI_TaxID=119072;
                                                                          FROM N.A.
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                                                                        SEQUENCE
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CC2A_ARATH
CCC2A_ARATH
CCC2A_ARATH
DT 01-MAR,
DT 01-MAR,
DT 01-MAR,
DT 01-MAR,
DT 01-MAR,
DT 01-MAR,
RESULIN,
RN 619
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                                                                                                                                                                                FUNCTION: PLAYS A KEY ROLE IN THE CONTROL OF THE EUKARYOTIC CELL CYCLE. COMPONENT OF THE KINASE COMPLEX THAT PHOSPHORYLATES THE REPETITIVE CARBOXYL-TERMINUS OF RNA POLYMERSES II. ENZYME REGILATION: PHOSPHORYLATION AT THR-14 OR TYR-15 INACTIVATES THE ENZYME, WHILE PHOSPHORYLATION AT THR-161 ACTIVATES IT (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. CDC2/CDKX SUBFAMILY.
-!- CAUTION: Ref.5 sequence differs from that shown due to erroneous gene model prediction.
                                                                                 Inze D., Ferreira P.C.G., Hemerly A.S., van Montagu M.;
"Control of cell division in plants.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thr pkinase.
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                                                                                                                             Biochem. Soc. Trans. 20:80-84(1992)
                                         SEQUENCE FROM N.A. MEDLINE=92339744; PubMed=1634002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000719; Euk pkinase.
InterPro; IPR002290; Ser thr pkir
Pfam; PF00069; pkinase; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; S45387; AAB23643.1; -.
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EBS Lett. 304:73-77(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 408:820-822(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X57839; CAA40971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR, A48984, A48984.
PIR, JQ0967, JQ0967.
PIR, JQ1337, JQ1337.
PIR, S23095, S23095.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P24941; 1HCL
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Gaps

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Indels

Mismatches

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5; Conservative
                                                                                        HRG_BOVIN
P33433;
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VARIANT
SEQUENCE
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                                                                    RESULT 15
HRG_BOVIN
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and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (See http://www.isb-sib.ch/announce/
        Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I., Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J., Bennett G.N., Koonin E.V., Smith D.R., "Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";
J. Bacteriol. 183:4822-4838(2001).
-!- CATALYTIC ACTIVITY: Succinyl-CoA + L-homoserine = CoA + O-
                                                                                                          PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY CAK) (BY SIMILARITY)
                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Homoserine O-succinyltransferase (EC 2.3.1.46) (Homoserine O-
                                                                                                                                                           Score 35; DB 1; Length 294;
Pred. No. 29;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as long as its content
removed. Usare
                                                                                                                                         BSFAESSFA9EC366E CRC64;
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Methionine biosynthesis; Transferase; Acyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ED40BA0DC247405D CRC64;
                                                                   PROTEIN KINASE.
ATP (BY SIMILARITY)
ATP (BY SIMILARITY)
                                                                                                                                                                                                                                                                         301 AA
                                                                                                BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=21359325; PubMed=11466286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as lor modified and this statement is not removentities requires a license agreement (for send an email to license@isb-sib.ch)
ProDom; PD000001; Euk_pkinase; 1.
                                                                            18 AT

33 AT

127 BY

14 PH

15 PH

161 PH

34030 MW;
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35123 MW;
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                                                                                                                                                            60.3%;
83.3%;
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                                                                                                                                                                                                                                                                                                                                                       Clostridium acetobutylicum
                                                                                                                                                                                5; Conservative
                                                                                                                                                                                                                                                                                                                                    transsuccinylase) (HTS).
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                                                                                                                                        294 AA;
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ACT SITE 142
SEQUENCE 301 AA;
                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                    2 HHYGTP 7
                                                                                                                                                                                                                                                                                                                                                                         Clostridium.
NCBI_TaxID=1488;
                                                                                                                                                                                                                                                                                                                                              META OR CAC1825
                                                                                                                                                                                                                                                                        META CLOAB
Q97129;
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MOD_RES
SEQUENCE
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BINDING
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Matches
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60.3%; Score 35; DB 1; Length 301; 83.3%; Pred. No. 30;

Best Local Similarity

Query Match

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MEDLINE=93351678; PubMed=8348977;
Socremsen C.B., Krogh-Pedersen H., Petersen T.E.;
Socremsen C.B., Krogh-Pedersen H., Petersen T.E.;
Locamination of the disulphide bridge arrangement of bovine histidine-rich glycoprotein.";
FEBS Lett. 328:285-290(1993).
-!- FUNCTION: THE PHYSIOLOGICAL FUNCTION IS NOT YET KNOWN. IT BINDS HEMS, DYES AND DIVALENT METAL IONS. IT CAN INHIBIT ROSETTE FORMATION AND IS KNOWN TO INTERACT WITH HEPARIN, THROMBOSPONDIN, AND THE LYSINE-BINDING SITE OF PLASMINGGEN. ON THE BASIS OF ITS HOWOLOGY WITH HWW KININGGEN, THE HERICH PROTEIN COAGULATION CASCABE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN: IN ADDITION TO HAVING A HIGH HIS AND PRO CONTENT, THIS PROTEIN HAS MANY INTERNAL REPEATS. 12 TANDEM REPETITIONS OF A 5-RESIDUE SEQUENCE (GHHPH, CONSENSUS) FORM A HISTIDINE-RICH REGION SIMILARITY: CONTAINS 2 CYSTATIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                               01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Histidine-rich glycoprotein (Histidine-proline rich glycoprotein)
(HPRG) (Fragments).
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S -> Q.
H -> Y.
: 128A8223499DE6FC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GLCNAC.
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CYSTATIN-LIKE 2.
PRO-RICH.
PRO/HIS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35; DB 1
Pred. No. 40;
1; Mismatches
                                                                                                                                                                      396 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ycoprotein; Heparin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44470 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60.3%;
illarity 62.5%;
Conservative
                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QHHYGTPY 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 322
396 AA;
                                        151 HHYGIP 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9913;
2 HHYGTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
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Firmicutes; Bacillales; Bacillaceae; Bacillus.

Bacillus subtilis. Bacteria; Firmicu NCBI\_TaxID=1423;

01-OCT-1994 (Rel. 30, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Hypothetical protein yaaO.

P37536; 01-0CT-1994 (Rel. 30, Created)

480 AA

PRT;

STANDARD;

BACSU

RESULT 17 YAAO BACSU YAAO

||| | |: 171 QHHLGRPF 178

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D. Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                               Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60.3%; Score 35; DB 1; Length 422; 83.3%; Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PATHWAY: Glycolysis.
SUBUNIT: HOMODIMER (BY SIMILARITY).
SUBCELLUAR LOCATION: CYCOPLASMIC (By similarity).
SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7FE6C766E2A3AC0D CRC64;
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PRINTS; PR00148; ENOLASE.
Probom; PD000902; Enclase; 1.
TIGRFAMs; TIGR01660; enc; 1.
PROSITE; PS00164; ENOLASE; 1.
Lyase; Glycolysis; Magnesium; Complete proteome.
ACT_SITE 153 153 BY SIMILARITY.
422 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20036896; PubMed=10567266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE002092; AAF12173.1; -.
HSSP; P56252; 1PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45541 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000941; Enolase.
                                                                                                                                                                                                                                                                                                                                        Deinococcaceae; Deinococcus.
NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 286:1571-1577(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 83.3
nes 5; Conservative
   STANDARD;
                                                                                                                                                                                                                                                                               Deinococcus radiodurans.
                                                                                                                                                                                                          glycerate hydro-lyase).
ENO OR DR2637.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THE DIMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rIGR; DR2637
   ENO DEIRA
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   SOLUTION DEPARTMENT OF THE PROPERTY OF THE PRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RA KEDINES-BU44031; Pubmed-31843/7;

RA Kunst F., Oggaswara N. G., Bessieres P., Bolotin A., Borchert S.,

Racevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

Racevedo V., Beruschi C.V., Caldwell B., Capuano V., Carter N.M.,

Brouilet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

Ra Brouilet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

Ra Brouilet S., Erington J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

Ra Britz C., Fujita M., Fujita Y., Funa S., Galizzi A., Galleron N.,

RA Fritz C., Fujita M., Fujita Y., Fuwa S., Galizzi A., Galleron N.,

RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,

RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Kurita K., Lapidus A., Lardhnois S., Lauber J., Lazarevic V.,

RA Kurita K., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,

RA Kurita K., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,

RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,

RA Rieger M., Rivolta C., Rocha E., Roche E., Ros M., Sadaie Y.,

Schowska A., Seros S.J., Schroeter R., Scoffone F.,

Sckyuchi J., Sckowska A., Seros S.J., Shin B.S., Soldo B.,

RA Sorokin A., Tanakoshi A., Tanaka T., Tarkanashi H., Takemaru K.,

Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarctti A.,

Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarctti A.,

Tosato V., Wambutt R., Wambutt R., Wedler H., Weitzenegger T.,

RA Visari A., Wambutter R., Wedler E., Wedler H., Weitzenegger T.,

Rh Frocomi E., Parkana H.F., Zumstein E., Yoshikawa H., Danchin A.;

Rh Frombellet Genome sequence of the Gram-positive bacterium Bacillus

RT "The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 390:249-256(1997).
-!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO FAMILY 1 OF ORNITHINE, LYSINE, AND ARGININE
DECARROXYLASES.
                                                                                                                                                                                                                                                                                                     Ogasawara N., Nakai S., Yoshikawa H.; "Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chromosome containing the replication origin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Decarbxylsel
                                                                                                                                                                                                                                                                                    MEDLINE=96051385; PubMed=7584024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D26185; BAA05263.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Z99104; CAB11803.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Subtilist, BG10091, yaaO.
InterPro, IPR000310, Decarb
Pfam, PF01276, OKR_DC_1; 1
                                                                                                                                                                                                                                                                                                                                                                                  NA Res. 1:1-14(1994)
                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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.; 0

Gaps

; 0

0; Indels

1; Mismatches

:||||| 354 RHHYGT 359

1 OHHYGT 6

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Matches

us-10-007-790-10.rsp

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ProDom; PD000066; SH3; 1.
                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                           PIXB RAT
                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                               RESULT 19
PIXB_RAT
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                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-98395067; Pubmed-9726964;
MEDLINE-98395067; Pubmed-9726964;
Magradia S., Taylor S.J., Jordon K.A., Van Aelst L., Cerione R.A.;
"A novel regulator of p21-activated kinases.";
J. Biol. Chem. 273:23633-23636(1998).
-! FUNCTION: Acts as a RAC1 guanine nucleotide exchange factor (GEF)
and can induce membrane ruffling (By similarity).
-! SUBUNIT: Interacts with PAK kinases through the SH3 domain.
-! ALTERNATIVE PRODUCTS: At least 2 isoforms are produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDILINE 56127530 PubMed=8590280;
Nagase T., Seki N., Tanaka A., Ishikawa K.-I., Nomura N.;
Nagase T. Seki N., Tanaka A., Ishikawa K.-I., Nomura N.;
"Prediction of the coding sequences of unidentified human genes. IV.
The coding sequences of 40 new genes (KIAA0121-KIAA0160) deduced by annalysis of cDNA clones from human cell line KG-I.";
                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
115-JUN-2002 (Rel. 41, Last annoctation update)
Rho quanine nuclectide exchange factor 7 (PAK-interacting exchange factor beta) (Beta-Pix) (COOL-1) (P85).
ARHGEF7 OR PAK3BP OR PIXB OR COOLI OR KIAA0142.
                                                     222 222 PYRIDOXAL PHOSPHATE (BY SIMILARITY). 480 AA; 53163 MW; 0166EE309B32AFB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Pfam; PF03711; OKR DC 1 C; 1.
PROSITE; PS00703; ÖKR DC 1; FALSE NEG.
Hypothetical protein; Lyase; Decarboxylase; Pyridoxal phosphate;
Complete proteome.
                                                                                           Match 60.3%; Score 35; DB 1; Length 480; Local Similarity 83.3%; Pred. No. 49; les 5; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alternative splicing.
-!- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY (DH) DOMAIN.
-!- SIMILARITY: CONTAINS 1 PH DOMAIN.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
                                                                                                                                                                                                                                             646 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIM; 605477; -...
InterPro; IPR001331; GDS_CDC24.
InterPro; IPR001849; PH.—
InterPro; IPR000219; RhoGEF.
InterPro; IPR001452; SH3.
Pfam; PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D63476; BAA09763.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HGNC:15607; ARHGEF7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF00621; RhoGEF; 1
                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                           182 HHYGIP 187
                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Bone marrow;
                                                                                                                                                  7
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                  2 HHYGTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P19174;
                                                                                                                                                                                                                                          PIXE HUMAN
Q14155;
                                                                   SEQUENCE
                                                                                            Query Match
                                                     BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genew;
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                                                                                                                     Matches
 RAMMES
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PRODOM; ELCCONTINE STATE STATE STATE SWART; SM00325; PH; 1.
SWART; SM00325; RhoGEF; 1.
SWART; SM00325; RhoGEF; 1.
PROSITE; PS0010; DH 2; 1.
PROSITE; PS50003; PH DOMAIN; 1.
PROSITE; PS50002; SH3; 1.
Guanine-nucleotide releasing factor; SH3 domain; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOL. Cell 1:183-192(1998).

-I- FUNCTION: Acts as a RAC1 guanine nucleotide exchange factor (GEF) and can induce membrane ruffling.

-I- SUBUNIT: Interacts with PAK kinases through the SH3 domain.

-I- SIMILARITY: CONTAINS I DBL-HOMOLOGY (DH) DOWAIN.

-I- SIMILARITY: CONTAINS I PH DOMAIN.

-I- SIMILARITY: CONTAINS I SH3 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Rho guanine nucleotide exchange factor 7 (PAK-interacting exchange factor beta) (Beta-Pix).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98324100; PubMed=9659915;
Manser E., Loo T.-H., Koh C.-G., Zhao Z.-S., Chen X.-Q., Tan L.,
Tan I., Leung T., Lim L.;
"PAR kinases are directly coupled to the PIX family of nucleotide
exchange factors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 60.3%; Score 35; DB 1; Length 646; Best Local Similarity 71.4%; Pred. No. 68; Matches 5; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                    400 PH.
73140 MW; B5B5A83F0EBC28D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     646 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P29355; 1SEM.
InterPro; IPR001331; GDS_CDC24.
InterPro; IPR001319; PH.
InterPro; IPR001219; RhoGEF.
InterPro; IPR00145; SH3.
Fam; PF00108; SH3; 1.
Pfam; PF00621; RhoGEF; 1.
Pfam; PF00621; RhoGEF; 1.
SMART; SM00233; PH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF044673; AAC39971.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARHGEF7 OR PAK3BP OR PIXB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00325; RhoGEF, SMART; SM00326; SH3; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              450 HHGTPHT 456
                                                                                                                                                                                                                                                                                                                                                                                  646 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 HYGTPYT 9
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Eactor beta) (Beta-Pix) (p85SPR)
                               ARHGEF7 OR PAK3BP
                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=88274327; PubMed=2839594; MGGOCD D.J., Dalan A., Frame M.C., MGGOCD D.J., Dalrymple M.A., Davison A.J., Dolan P.; Taylor P.; The complete DNA sequence of the long unique region in the genome of
                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Q9ES28; Q9ES27; O08757;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 44, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Rho guanine nucleotide exchange factor 7 (PAK-interacting exchange.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               herpes simplex virus type 1.";
J. Gen. Virol. 69:1531-1574(1988).
-!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL17,
HSV-6 ORF10R, EHV-1 45, HCMV UL93, EBV BGLF1, AND VZV 43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                       / Match 60.3%; Score 35; DB 1; Length 646; Local Similarity 71.4%; Pred. No. 68; or Indelense 5; Conservative 2; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X14112; CAA3229.1; -.
PIR; H30083; WMBET7.
SEQUENCE 703 AA; 74582 MW; 536DAF5421BD6B4E CRC64;
                                                                                                                                                                                                                                     73140 MW; 17CDE7DD96ADEA53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Herpes simplex virus (type 1 / strain 17).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
                                                                                                                     Guanine-nucleotide releasing factor; SH3 domain.
DOMAIN 6 65 813.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
Protein UL17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
PS00741; DH 1; FALSE NEG
PS50010; DH 2; 1.
PS50003; PH DOMAIN; 1.
PS50002; SH3; 1.
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Best Local Similarity 83...
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                           646 AA;
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RHHYGT 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 20
117 HSV11
AC P10201;
DT O1-MAR-1989
DT 01-MAR-1989
DT 01-DEC-1992
DE Protein UL17
GS UL17
OC VIRUGES; dSD
OC VIRUGES

                                                          PROSITE;
PROSITE;
   PROSITE;
PROSITE;
                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                DOMAIN
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PIXB_MOUSE
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      RESERVES
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SEYDSTWTAHSYRMGSASR -> S (IN ISOFORM A).

KT -> PH (IN REF. 1).

PPS -> AWG (IN REF. 1).

RP -> WT (IN REF. 1).

RP -> WT (IN REF. 1).
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DOMAIN 6 6 65
                                                                                                                                                                                                                                    -i- FUNCTION: Acts as a RACI guanine nucleotide exchange factor (GEF) and can induce membrane ruffling (By similarity).
-i- SUBUNIT: Interacts with PAK kinases through the SH3 domain (By
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS B AND C).
STRAIN=C57BL/6; TISSUE=Brain;
MEDLINE=2018134; PubMed=10860822;
Kim S., Kim T., Lee D., Park S.H., Kim H., Park D.;
Mindecular cloning of neuronally expressed mouse betaPix isoforms.";
Biochem. Biophys. Res. Commun. 272:721-725(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
-!- ALTENATUVE PRODUCTS: 3 isoforms; a, b (shown here) and c; are
produced by alternative splicing.
-!- TISSUE SPECIFICITY: Seems to be expressed in the central nervous
                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY (DH) DOMAIN.
-!- SIMILARITY: CONTAINS 1 PH DOMAIN.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                        Biochem. Biophys. Res. Commun. 235:794-798(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00741; DH_1; FALSE_NEG. PROSITE; PS50010, DH_2; 1. PROSITE; PS50003; PH_DOMAIN; 1. PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:1860493; Arhgef7.
InterPro; IPR001331; GDS_CDC24.
InterPro; IPR001331; BH.
InterPro; IPR000219; RhGGF.
InterPro; IPR001452; SH3.
Pfam; PF00169; BH; 1.
Pfam; PF00161; RhGEF; 1.
Pfam; PF00621; RhGEF; 1.
Pfam; PF00621; RhGEF; 1.
Probom; PR006452; SH310MAIN.
                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM A).
TISSUE=Thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF247654; AAG18017.1; -. AF247655; AAG18018.1; -.
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SMART; SM00325; RhoGEF; 1.
SMART; SM00326; SH3; 1.
Mus musculus (Mouse).
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PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolaes; Metalloprotease; Aminopeptidase; Zinc
Hydrolaes; Metalloprotease; Signal-anchor.
Sulfation; Transmembrane; Repeat; Signal-anchor.
INIT MET 0 0 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                 64
3383
384
387
387
172
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325 NHYNTPY 331
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592
965 AA;
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Matches 5; Conserv
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                                  Sulfation;
INIT MET
DOMAIN
TRANSMEM
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A MEDLINE-90092508; PubMed-2574692;
A MEDLINE-90092508; PubMed-2574692;
A Mansen G.H.;
Hansen G.H.;
"Onset of transcription of the aminopeptidase N (leukemia antigen CD 13) gene at the crypt/villus transition zone during rabbit enterocyte differentiation."; PEBS Lett. 259:107-112(1989).

C -! - CATALYTIC ACTIVITY: Release of an N-terminal amino acid, preferably a neutral or hydrophobic one, from a polypeptide.

A Minoacyl-arylandses are poor substrates.

C -! - COPGATOR: BINDS 1 ZINC ION.

-! - SUBCELLULAR LOCATION: Type II membrane protein.

-! - STM: SULFATED (BY SIMILARITY).

-! - SIMILARITY: BELONGS TO PEPTIDASE FAMILY MI.
                                                    Gaps
                                                                                                                                                                                                                       01-APR-1990 (Rel. 14, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Aminopeptidase N (EC 3.4.11.2) (Microsomal aminopeptidase) (Leukemia antigen CD13).
                                                                                                                                                                                                                                                                                                                   Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-82113673; PubMed=6120002;
Feracci H., Maroux S., Bonicel J., Desnuelle P.,
"The amino acid sequence of the hydrophobic anchor of rabbit
intestinal brush border aminopeptidase N.";
Biochim. Biophys. Acta 684:133-136(1982).
                   Length 705;
                                                    0; Indels
                     DB 1;
                                                                                                                                                                                              965 AA
                                                  2; Mismatches
                   Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Kidney;
MEDLINE=94099942; PubMed=7903857;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001930; Ala peptase.
InterPro; IPR000130; Zn MTpeptdse.
Pfan, PF01433; Peptidase M1; 1.
PRINTS; PR00756; ALADIPTASE.
                60.3%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; S68687; AAB29534.1; -. EMBL; X51508; CAA35873.1; -.
Query Match
Best Local Similarity 71...,
Sines 5; Conservative
                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR, B25985, B25985.
PIR, S07099, S07099.
MEROPS, M01:001; -.
                                                                                                               HHGTPHT 456
                                                                                  σ
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 5-18.
                                                                                  3 HYGTPYT
                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9986;
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                                                                                                              450
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CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "identification of three gene regions associated with virulence in
Dichelobacter nodosus, the causative agent of ovine footrot.";
J. Gen. Microbiol. 137:2117-2124(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
Dichelobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=A198;
MEDLINE=92085031; PubMed=1748867;
Katz M.E., Howarth P.M., Yong W.K., Riffkin G.G., Depiazzi L.J.,
Rood J.I.;
                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
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Katz M.E., Rood J.I., Strugnell R.A.,
"Molecular characterization of a genomic region associated with
virulence in Dichelobacter nodosus.",
Zinc; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
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0
                                                                                                                                        METALLOPROTEASE.
ZINC (CATALYTIC) (BY SIMILARITY)
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ZINC (CATALYTIC) (BY SIMILARITY)
ZINC (CATALYTIC) (BY SIMILARITY)
                                                                                                   (POTENTIAL).
CYTOSOLIC SER/THR-RICH JUNCTION
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SULFATION (POTENTIAL).
SULFATION (POTENTIAL).
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SULFATION (POTENTIAL)
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4 -> S (IN REF. 2).
9 -> L (IN REF. 2).
E -> QQ (IN REF. 2
                                                                                                                                                                                                                                                                                                                                                       (GLCNAC.
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15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last cannotation update)
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Pred. No. 13;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                   MEDLINE=76004342; PubMed=50995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A01903; K4HULN.
HSSP; P01607; IREI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
83.3%;
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SMART; SM00406; IGv; 1.
Immunoglobulin V region;
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                5; Conservative
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Les 5; Conserv
Local Similarity
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                                               3 HYGTPY
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TYRT STRLN
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                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                            MEDLINE=94222846; PubMed=8169216;
Katz M.B., Wright C.L., Gartside T.S., Cheetham B.F., Doidge C.V.,
Moses E.K., Rood J.I.;
"Genetic organization of the duplicated vap region of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95362676; PubMed=7543479;
Galli D.M., Leblanc D.J.;
"Transcriptional analysis of rolling circle replicating plasmid
transcriptional evidence for replication control by antisense RNA.";
J. Bacteriol. 177:4474-4480(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                  15112582A678D9B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Virulence-associated protein D homolog. Actinobacillus actinomycetemcomitans (Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34; DB 1;
Pred. No. 13;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-UUL-1999 (Rel. 38, Created)
15-UUL-1999 (Rel. 38, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95 AA.
                                                                                                                             Dichelobacter nodosus genome.";
J. Bacteriol. 176:2663-2669(1994).
-!- SIMILARITY: BELONGS TO THE VAPD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO THE VAPD FAMILY
                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch)
   Infect. Immun. 60:4586-4592(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                  10590 MW;
                                                                                                                                                                                                                                                                                                                       EMBL; L31763; AAB00950.1; ~.
                                                                                                                                                                                                                                                                                                                                                                                                                                               58.6%;
83.3%;
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Best Local Similarity 83.3.,
Local Similarity 63.2.,
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                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                      L22308;
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Salomon A.;
Submitted (AUG-1996) to the SWISS-PROT data bank.
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
-!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleosiomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schneider M., Hilschmann N.; "The primary structure of a monoclonic immunoglobulin-L-chain of subgroup IV of the kappa type (Bence-Jones protein Len)."; Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
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COMPLEMENTARITY-DETERMINING-2.
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FRAMEWORK-4.
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                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 kappa chain V-IV region Len.
Homo sapiens (Human).
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
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or send an email to license@isb-sib.ch)
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66.7%;
                                               HSSP, P80362; 1WTL.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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                         EMBL; J00561; AAA38776.1;
                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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644
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129
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148
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                                       PIR; A01916; KVMS11.
                                                                                                                                                                                                                                                                                          149 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fraser C.M.;
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SEQUENCE
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Q9RS38;
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DEIRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            myeloma MPC 11.";
Biochem. J. 171:337-347(1978).
-!- MISCELLANEOUS: THE MATURE CHAIN HAS 12 ADDITIONAL RESIDUES AT ITS
-- AMINO END, DUE TO A TANDEM DUPLICATION OF 36 NUCLECTIDES AFFER THE
CODON FOR RESIDUE 36. RESIDUE 42 CORRESPONDS TO THE AMINO-TERMINAL
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-80176554; PubMed-6245773;
Rabbitts T.H., Hamlyn P.H., Matthyssens G., Roe B.A.;
"The variability, arrangement, and rearrangement of immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith G.P.; "Sequence of the full-length immunoglobulin kappa-chain of mouse
                                                                                                                                                                                                                                                                                          ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=83001944; PubMed=6288267; Kelley D.E., Coleclough C., Perry R.P.; "Functional significance and evolutionary development of the 5'-terminal regions of immunoglobulin variable-region genes.";
                     STRAIN=78-11;
Zhang H.Z., Piepersberg W.;
Zhang H.Z., Piepersberg W.;
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: THIS PROTEIN MAY FUNCTION TO DELIVER COPPER TO TYROSINASE.
                                                                                                                                                                                                                                                             58.6%; Score 34; DB 1; Length 140; 71.4%; Pred. No. 20;
                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                       Melanin biosynthesis, Copper.
SEQUENCE 140 AA; 14189 MW; 8752156617FD15A6 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-V region MPC11 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                             149 AA
                                                                                                                                                                                                                                                                                         1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Can. J. Biochem. 58:176-187 (1980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=78186617; PubMed=418775;
                                                                                                                                                                                                            EMBL; X95703; CAA64999.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 41-149 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-71 FROM N.A.
                                                                                                                                                                                                                                                                                         5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell 29:681-689(1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Mouse)
                                                                                                                                                                                                                                                                                                                                           80 HHHGTGY 86
                                                                                                                                                                                                                                                                                                                   2 HHYGTPY 8
                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 30-149
             FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                             KV5A MOUSE
            SEQUENCE
                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genes.
                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Azavind L., Daly M.J., Minton K.W., Fleischmann R.D. Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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                                                                                                                                       KAPPA CHAIN V-V REGION MPC11.
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                                                                                                                                IG KAPPA CHAIN V-V REGION MPCI:
PRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
                                                                                                                                                                                                                                                                                                                                              COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                                                                                                                              COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34; DB 1; Length 149;
Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           radiodurans R1 ";
Science 286:1571-1577(1999).
-!- FUNCTION: ESSENTIAL FOR RECYCLING GMP AND INDIRECTLY,
-!- CATALYTIC ACTIVITY: ATP + GMP = ADP + GDP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16434 MW; B0480C87B682AC3E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
GMK OR DR2289.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                              FRAMEWORK-4
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MEDLINE=20036896; PubMed=10567266;
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CYACA
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                                                                                                                                                                                                                                                                                        P48873;
                                                                                                                                                                                                                          RESULT 30
COX3 CYACA
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPEB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXP. ZOO1. 285:41-49(1999).
FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS (BY
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99259633; PubMed=10327649; Sneal E.J., Scemana J.L., Stellwag E.J.; Semenic organization of the Hoxa4-Hoxa10 region from Morone gaxatilis: implications for Hox gene evolution among vertebrates.";
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PROSITE; PS50071; HOMEOBOX 2; 1.
Homeobox; DNA-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                                                                                 58.6%; Score 34; DB 1; Length 239; 83.3%; Pred. No. 35;
                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                        930AE5040D622722 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOMEOBOX.

BD49DCE0597D2A4C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Nuclear (By similarity). SIMILARITY: BELONGS TO THE ABD-B HOMEOBOX FAMILY.
                                                         Pfam; Draces; IRR00619; Guanylate kin.
Pfam; PF00625; Guanylate kin; I.
SMART; SM00072; GuKc; 1.
PROSITE; PS00856; GUANYLATE KINASE 1; 1.
Transferase; Kinase; ATP-binding; Complete proteome.
NP_BIND
26
33 ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See hor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269 AA
                                                                                                                                                                                                                                                                                                             1; Mismatches
    AAF11836.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P02833; 9ANT.
InterPro; IPR000047; HTH repressr.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Morone saxatilis (Striped bass).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29600 MW;
                                                                                                                                                                                                                        239 AA; 26528 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00024; HOMEOBOX.
PRINTS; PR00031; HTHREPRESSR.
ProDOM: PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF089743; AAD46396.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcription regulation.
DNA BIND 202 261
SEQUENCE 269 AA; 29600
                                                                                                                                                                                                                                                                                           Local Similarity 83.3
nes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homeobox protein Hox-A9.
                         P15454; 1GKY.
                                                                                                                                                                                                                                                                                                                                                                                  :|||||
NHYGTP 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Moronidae; Morone.
                                                                                                                                                                                                                                                                                                                                                         2 HHYGTP 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=34816;
    AE002061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY)
EMBL; AE00206
HSSP; P15454;
TIGR; DR2289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HXA9 MORSA
                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                  92
                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9PWD5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the enzyme complex. 
 -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Rhodophyta; Bangiophyceae; Porphyridiales; Porphyridiaceae;
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE SUBUNIT 3 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces clavuligerus.
Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thesis (1995), Justus Liebig University / Frankfurt, Germany.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P37819; P72400; 01-0CT-1994 (Rel. 30, Created) 01-0CT-1994 (Rel. 30, Last sequence update) 01-0CT-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) Possible agmatinase (EC 3.5.3.11) (Agmatine ureohydrolase) (AUH) (Proclavaminic acid amidino hydrolase).
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Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58.6%; Score 34; DB 1; Length 270; 100.0%; Pred. No. 40;
                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31564 MW; 52917FBDCAE953C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                       01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Cytochrome Coxidase polypeptide III (EC 1.9.3.1).
COX3 OR COXIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
        DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     313 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Preα. ...
... 0; Mismatches
                                                        0; Mismatches
     Score 34;
Pred. No.
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PROSITE; PS50253; COX3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000298; CytC_oxdse_III. Pfam; PF00510; COX3; 1.
  58.6%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z48930; CAA88770.1;
                                                           5; Conservative
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                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cyanidium caldarium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           270 AA;
  Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                    82 HHYGHP 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 QHHYG 242
                                                                                                              2 HHYGTP 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=2771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=RK-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viehmann S.;
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expressed Arabidopsis GBF bZIP proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thaliana.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GBF1 ARATH STANDARD; PRT; 315 AA.

P42774; Q96263;
01-NOV-1995 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
6-box binding factor 1.
GBF1 OR AT4G36730 OR C710 630.
Arabidopsis thaliama (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids 11; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-cv. Columbia; TISSUE-Leaf, and Stem;
MEDLINE=92224864; PubMed=1373374;
Schindler U., Menkens A.E., Beckmann H., Ecker J.R., Cashmore A.R.;
"Heterodimerization between light-regulated and ubiquitously
                                                         Aidoo K.A., Wong A., Alexander D.C., Rittammer R.A.R., Jensen S.E.; "Cloning, sequencing and disruption of a gene from Streptomyces clavuligerus involved in clavulanic acid biosynthesis.";
                                                                                                               SEQUENCE FROM N.A.
Hodgson J.E., Fosberry A., Rawlinson N.S.; Ross H.N.M., Neal R.J.,
Arnell J.C., Earl A.J., Lawlor E.J.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: POSSIBLY INVOLVED IN CLAVULANIC ACID BIOSYNTHESIS.
-!- CATALYTIC ACTIVITY: Agmatine + H(2)O = putrescine + urea.
-!- COFACTOR: MANGANESE (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE ARGINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                 MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 1 (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AND 2 (BY SIMILARITY)
2 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34; DB 1; Length 313; Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        759E9B5644B8BD5E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                 STRAIN=ATCC 27064 / DSM 738 / NRRL 3585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MANGANESE 1
                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000287; Arginase.
Pfam; PF00491; arginase; 1.
TIGRAMS; TIGR01230; agmatinase; 1.
PROSITE; PS00147; ARGINASE 1; 1.
PROSITE; PS01053; ARGINASE 2; 1.
PROSITE; PS01053; ARGINASE 3; 1.
                                               MEDLINE=94374706; Pubmed=8088547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4
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                                                                                                                                                                                                                                                                                                                        EMBL; U87786; AAA62451.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58.6%;
                                                                                                                                                                                                                                                                                                                                     EMBL; X84101; CAA58904.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         146
148
235
237
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                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase; Manganese
                                                                                              Gene 147:41-46(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QHHYGTPY 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       313 AA;
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                     SEQUENCE FROM N.A.
 NCBI_TaxID=1901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METAL
SEQUENCE
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METAL
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8
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RAM MEDUREAL 2008 1981 Purphed TO C., Wanbutt R., Murphy G., Volckaert G., RM MEDUREAL 2008 1981 Purphed TO, Grivell L.A., Rieger M., Parish P. Brandt P. Grivell L.A., Rieger M., Harris B., Ansorge W., Brandt P. Grivell L.A., Rieger M., Metheler M., de Simone V., Obermaier B., Mache R., Mueller M., Rieder M., Schmidtheini T., Radis M., Delseny M., Pulgdomenech P., Matson M., Schmidtheini T., Radis M., Delseny M., Elablam L., Robben J., Langham S.-A., McCullagh B., Bllham L., Robben J., Vorden B., Bastisens I., Aert R., Defoor E., Radeken M., Welt J., Vorden M., Bastisens I., Aert R., Defoor E., Radeken M., Welt J., Vorden B., Bastisens I., Aert R., Defoor E., Radeken M., Welt J., Vorden B., Santisens I., Hampel S., You Robber J., Vorden Landhorst R., Vorden M., Lanberth S., Von den Daele H., Bernets S., Yous S., Vollarroel R., De Clercq R., Bernetser S., Hampel S., Feldpausch M., Lanberth S., Von den Daele H., De Keyser A., Buyssheart C., Gielen J., Villarroel R., De Chmann S., Androgeu M., Scopers J., Cronin A., Quail M., Enchert S., Androgeu M., Scopers J., Clonin A., Lothner D., Herzl A., Doogget J., Hall S., Kay M., Lennard N., Meller R., A., Doogget J., Hall S., Kay M., Lennard N., Meller R., Schmet S., Gelber G., Schaefer M., Meller R., Perler R., Schmeth S., Argiriou A., Vittale D., Liguori R., Paravandi E., Schmeth S., Argiriou A., Vittale D., Liguori R., Paravandi E., Schmeth S., Hiller R., Schmidt W., Lecharry A., Abubourg S., Radisham D., Haase D., Liguori R., Paravandi E., Schmet S., Schmeth S., Pracace P., Bielke C., Frishman D., Haase D., Liguori R., Melson D., Berger C., Monfort A., Schce S., Pracace P., Bielke C., Frishman D., Haase D., Lemcke K., Mewes H., W., Stocker S., Schmeth D., Couring V., Melson D., Marsie D., Schwet S., Schwet 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its concent is in no way
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                                                                                                                      STRAIN=cv. Columbia;
Terryn N., Villarroel R., Neyt P., de Clercq R., Ardiles W.,
de Keyser A., van den Daele H., Rouze P., Gielen J., van Montagu M.;
"Nucleotide sequence of the Arabidopsis thaliana gene encoding the G-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBUNIT: DNA-BINDING HETERODIMER.
-!- SUBCELLUIAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: FOUND IN BOTH LIGHT AND DARK GROWN LEAVES.
-!- SIMILARITY: BELONGS TO THE BZIP FAMILY.
                                                                                                                                                                                                                                                                                                                                                         In) Plant Gene Register PGR96-111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=cv. Columbia;
MEDLINE=20083488; PubMed=10617198;
                                                                                                                                                                                                                                                                                                               box-binding factor 1 (GBF1)."
EMBO J. 11:1261-1273(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 402:769-777(1999)
                                                                                SEQUENCE FROM N.A.
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P04408;
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KITH_HSVSM
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LGI_MAIZE
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96379.751; PubMed=8787764; Henyey E.L., Holland L.Z.; Holland N.D., Panganiban G.E., Henyey E.L., Holland L.Z.; Sequence and developmental expression of Amphibll, an amphioxus blotal-less gene transcribed in the ectoderm, epidermis and nervous system: insights into evolution of craniate forebrain and neural
                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. DLL homolog.
Branchiostoma floridae (Florida lancelet) (Amphioxus).
Eukaryota, Metazoa, Chordata; Cephalochordata; Branchiostoma.
                                                                                                                                                                                                                                                                             4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- SUBCELLULAR LOCATION: Nuclear (Potential).
                                          EMBL; X63894; CAA45356.1; --
EMBL; X99941; CAA68197.1; --
EMBL; AD9708; CAB16806.1; --
EMBL; AL161589; CAB80339.1; --
HSSP; P03069; 1YSA.
TRANSPAC; T01078; --
INTEAPERC; IPPO04827; TF_DZIP.
Pfam; PF00170; bZIP; 1.
SMART; SM00338; BZIZ; 1.
PROSITE; PS00035; BZIP BASIC; 1.
Transcription regulation; DNA-binding; Nuclear protein.
                                                                                                                                                                                                                                                   Score 34; DB 1; Length 315;
Pred. No. 48;
0; Mismatches 0; Indels
                                                                                                                                                                                                                 43 43 T -> S (IN REF. 1).
315 AA; 33932 MW; 8585EF0249C91C21 CRC64;
                                                                                                                                                                                         BASIC MOTIF.
LEUCINE-ZIPPER.
                                                                                                                                                                                                                                                                                                                                                                                    321 AA.
                                                                                                                                                                               PRO-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001047; HTH repressr.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0024; HOMEOBOX.
PRINTS; PRO0031; HTHREPRESSR.
Prodom; PD00010; Homeobox; 1.
SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Development 122:2911-2920(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U47058; AAB36860.1; -.
                                                                                                                                                                                                                                                     58.6%;
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                                                                                                                                                                                                                                                                  63.6%;
                                                                                                                                                                                                                                                                Local Similarity 63.0
                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                          OHHMMPPYCTP 75
                                                                                                                                                                                           243
                                                                                                                                                                                                                                                                                                   1 QHH----YGTP 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=7739;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                   HMDL BRAFL
P53772;
                                                                                                                                                                                                                 CONFLICT
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                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phosphate.
-!- SIMILARITY: BELONGS TO THE HERPESVIRUSES THYMIDINE KINASE FAMILY.
                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Otsuka H., Kit S.;
"Nucleotide sequence of the marmoset herpesvirus thymidine kinase
gene and predicted amino acid sequence of thymidine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  · .;
                                                                                                                                                                              .;
0
PROSITE; PS50071; HOMEOBOX_2; 1.
Homeobox; DNA-binding; Developmental protein; Nuclear protein.
DNA_BIND 116 175 HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kit S.;
Submitted (JUN-1989) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + thymidine = ADP + thymidine 5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Herpesvirus saimiri (type 1 / strain MV-5-4-PSL) (Marmoset
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58.6%; Score 34; DB 1; Length 361; 75.0%; Pred. No. 55; tive 0; Mismatches 2; Indels
                                                                                                                            Length 321
                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 24 ATP (PROBABLE).
361 AA; 39458 MW; B2E322DBID5542DB CRC64;
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Alphaherpesvirinae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P03176; 2KI5.
InterPro; IPR001889; TK_herpes.
Pfam; PF00693; TK_herpes; 1.
ProDom; PD001519; TK_herpes; 1.
Transferase; Kinase; DNA synthesis; ATP-binding.
NP BIN ATP
                                                                       321 AA; 35436 MW; F4408D46FE1443C7
                                                                                                                         Score 34; DB 1;
Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-AUG-1987 (Rel. 05, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Thymidine kinase (EC 2.7.1.21).
                                                                                                                                                                                                                                                                                                                                                                                                              361 AA
                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=84251697; PubMed=6330976;
                                                                                                                            58.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; K02122; AAA67102.1; -. PIR; A00614; KIBETM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /irology 135:316-330(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 75.00,
Best Local 6; Conservative
                                                                                                                                                                              5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                             62 HPYGNPYS 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88 OLHMGTPY 95
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                                                                                                                                                                                                                                2 HHYGTPYT 9
                                                                                                                         Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       herpesvirus)
                                                                                                                                                                                                                                                                                                                                                                                                           KITH HSVSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REVISIONS.
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SEQUENCE
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                           "Catabolism of phemylacetic acid in Escherichia coli. Characterization of a new aerobic hybrid pathway.";
J. Biol. Chem. 273:25974-25986(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20229831; PubMed=10766858;
Ferrandez A., Garcia J.L., Diaz E.;
"Transcriptional regulation of the divergent paa catabolic operons for phenylacetic acid degradation in Escherichia coli.";
J. Biol. Chem. 275:12214-12222(2000).
-!- CATALYTIC ACTIVITY: (S)-3-hydroxybutanoyl-COA + NADP(+) = 3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acetoacetyl-CoA + NADPH.
-!- PATHWAY: BUTYRATE/BUTANOL-PRODUCING PATHWAY.
-!- PATHWAY: Phenylacetic acid aerobic catabolism.
-!- INDUCTION: ACTIVATED BY CAMP RECEPTOR PROTEIN (CRP) AND
-!- INTEGRATION HOST PACTOR (IHF). INHIBITED BY PAAX.
-!- SIMILARITY: BELONGS TO THE 3-HYDROXYACYL-COA DEHYDROGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDILNE=9721317; VLUDMGGE=9097039;
Abba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Makaito K., Miki T., Misobuchi K., Mori H., Mori T., Motomura K., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto Y., Takeuchi Y., Wada C., Yamanoto Y., Horiuchi T., Saito N., Takeuchi Y., Wada C., Yamanoto Y., Horiuchi T., Saito N., A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map.";
                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE=97426617, PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 475; 74;
                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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BHBD 2.
I -> V (IN STRAIN W).
I -> V (IN STRAIN W).
W, DEB6190F08D527C6 CRC64;
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Pfam; PF02737; 3HCDH; N; 1.
PROSTIE: PS00067; 3HCDH; FALSE NEG.
Oxidoreductase; NADP; Fatty acid metabolism; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58.6%; Scor.
100.0%; Pred. No. ...
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EMBL; D90778; BAA15006.1; ALT_INIT.
EMBL; D90777; BAA15001.1; ALT_INIT.
HSSP; P00348; 3HDH.
ECGENE; EG13742; paaH.
InterPro; IPR002135; 3HCDH.
InterPro; IPR002055; NAD_binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97251357; PubMed=9097039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51732 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X97452; CAA66097.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRANSCRIPTIONAL REGULATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Res. 3:363-377(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     284
475
132
344
          Garcia J.L., Diaz E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  475 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome.
                                                                                                                                                                                                                                                                                                                                  Gregor J., Davis
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT
VARIANT
SEQUENCE
          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=cv. W22; TISSUE=Leaf;
MEDLINE=97230364; PubMed=9119226;
Moreno M.A., Harper L.C., Krueger R.W., Dellaporta S.L., Freeling M.;
Liguleless encodes a nuclear-localized protein required for induction of ligules and auricles during maize leaf organogenesis.";
Genes Dev. 11:616-628(1997).
--- FUNCTION: INVOLVED IN THE FORMATION OF LIGULES AND AURICLES DURING
                                                                                                                                                                                                                      Zea mays (Maize).
Eukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta, Liliopsida; Poales; Poaceae; PACC clade;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLUAR LOCATION: Nuclear.
TISSUE SPECIFICITY: LEAF LIGULAR REGION, BLADE AND SHEATH.
TISSUE SPECIFICITY: LEAF LIGULAR REGION, BLADE AND SHEATH.
BUSUELOPMENTAL STAGE: DEVELOPING LEAVES. PRESENT AT HIGHEST
LEVELS IN VERY YOUNG LIGULES AND AURICLES. PRESENT PRE- AND POST-
LIGULE AND AURICLE DEVELOPMENT.
SIMILARITY: CONTAINS 1 SBP DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF0311U; SDF; 1.
Nuclear protein; Developmental protein.
10.11.1. 259 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAAH ECOLI STANDARD; PRT; 475 AA.
7976031, 7978089; 053016;
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
FOCT-2001 (Rel. 40, Last annotation update)
Probable 3-hydroxybutyryl-COA dehydrogenase (EC 1.1.1.157) (Beta-hydroxybutyryl-COA dehydrogenase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ferrandez A., Minambres B., Garcia B., Olivera E.R., Luengo J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1E89F304232D7B8C CRC64;
                                                         15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
LIGULELESS1 protein.
   399 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR004333; SBP_plant_prot.
Pfam; PF03110; SBP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=W / ATCC 11105;
MEDLINE=98421522; PubMed=9748275;
                                                                                                                                                                                                                                                                                                                            Panicoideae; Andropogoneae; Zea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      399 AA; 43367 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U89496; AAB51071.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 62.9
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEAF ORGANOGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QOHYGFPF 342
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                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4577;
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Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                   Eukaryota; Merazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Erythroblast;
MEDLINE=88217299; PubMed=3285296;
MEDLINE=88217299; PubMed=3285296;
MEDLINE=88217299; PubMed=3285296;
"Primary structure of the chicken c-mil protein:identification of domains shared with or absent from the retroviral v-mil protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oncogene 2:179-185(1988).
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
MIL/RAF SUBFAMILY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
16-OCT-2011 (Rel. 40, Last annotation update)
MIL proto-oncogene serine/threonine-protein kinase (EC 2.7.1.37)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG BINDING DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 482; 75;
                                                                                                                                                                                                                                                                                                                                                                                                            Lloyd C.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                              01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 54.6 kDa protein F59B10.2 in chromosome II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POLY-ARG.
1BD7D31E9DDAA74B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       647 AA.
482 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 34;
Pred. No. 7
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POLY-SER.
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ARG-RICH.
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                                                      01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54641 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.6%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z48716; CAA88601.1; -. WormPep; F59B10.2; CE01591.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 62.5
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken)
                                                                                                                                                                                                    Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            482 AA;
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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P05625;
CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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KMIL_CHICK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Primary structure of the herpesvirus saimiri genome.";
J. Virol. 66:5047-5058(1992).
-!- FUNCTION: VP22A IS A COMPONENT OF THE CAPSID CORE INVOLVED IN PROCESSING AND PACKAGING OF PROGENY DNA. VP24 IS A PROTEASE WHICH CAN PROTEOLYTICALLY CLEAVE ITSELF AND VP22A AT THE CTERMINUS (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: Cleaves -Ala-|-Ser- and -Ala-|-Ala-bonds in the scaffold protein.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S21.
-!- SIMILARITY: TO OTHER HERPESVIRUSES CAPSID PROTEIN VP40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92333688; PubMed=1321287; Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Biesinger B., Newman C., Wittmann S., Craxton M.A., Coleman H., Fleckenstein B., Honess R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | Processon | Proc
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                                                                                                                                                                                                                                                        01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Capsid protein P40 (Contains: Capsid protein VP24 (Assemblin)
(Protease) (EC 3.4.21.97); Capsid protein VP22A].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58.6%; Score 34; DB 1; Length 475; 50.0%; Pred. No. 74; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    Herpesvirus saimiri (strain 11).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
                                                                                                                                                                                                       475 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro, IPR001847; Assemblin.
Pfam; PF00716; Peptidase S21; 1.
PRINTS; PR00236; HSVCAPSIDP40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X64346; CAA45641.1; -. PIR; H36807; WZBEM4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 50.0
اتاء 4; Conservative
                                                                                                                                                                                                       STANDARD;
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MEROPS; S21.006; -.
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                                                      449 QHHYG 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10383;
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                                                                                                                                                                                                    HSVSA
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ACT_SITE
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SEQUENCE
                                                                                                                                                                      VP40_HSVSA
ID VP40_HSV.
AC Q01002;
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RESULT 38 YSR2\_CAEEL

8

CHAIN

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Gaps

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2; Indels

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PROSITE; PS00479; DAG_PE_BIND_DOM_2; 1.
PROSITE; PSS00107; PROTEIN_KINASE_AP; 1.
PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.
PROSITE; PSS00108; PROTEIN_KINASE_ST, 1.
Transferase; Serine/threonine-protein kinase; Proto-oncogene; Zinc; ATP-binding; Phorbol-ester binding.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=86120351; PubMed=3003687;

Bonner T.I., Oppermann H., Seeburg P., Kerby S.B., Gunnell M.A., Young A.C., Rapp U.R.;

Troung A.C., Rapp U.R.;

"The complete coding sequence of the human raf oncogene and the corresponding structure of the c-raf-1 gene.";

Nucleic Acids Res. 14:1009-1015(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1986 (Rel. 03, Created)
01-NOV-1986 (Rel. 03, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
RAF proto-oncogene serine/threonine-protein kinase (BC 2.7.1.-)
(RAF-1) (C-RAF).
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY).
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                                                                                                                                                                        InterPro; IPR002219; DAG PE-bind.
InterPro; IPR000719; ENK_pkinase.
InterPro; IPR004040; STY pkinase.
InterPro; IPR004040; STY pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
Fram; PF00069; pkinase; I.
Pfam; PF00130; DAG_PE-bind; I.
Pfam; PP02196; RBD; I.
                                                                                                                                                                                                                                                                                                       PRINTS; PRO0008; DACPEDOMAIN.
ProDom; PD000001; Euk pkinase; 1.
SMART; SM00109; C1; 1.
SMART; SM00455; RBD; 1.
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HSSP; P04049; 1FAR.
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647 AA;
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Strausberg R.;
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NP_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRUCTURE BY NMR OF 55-132.
MEDIATRE=5554022; PubMed=7765599;
MEDIATRE=5554022; PubMed=7765599;
Emerson S.D., Madison V.S., Palermo R.E., Waugh D.S., Scheffler J.E.,
Tsao K.L., Kiefer S.E., Liu S.P., Fry D.C.;
"Solution structure of the Ras-binding domain of c-Raf-1 and
identification of its Ras interaction surface.";
Biochemistry 34:6911-6918(1995).
                                                                     King A.J., Sun H., Diaz B., Barnard D., Miao W., Bagrodia S.,
Marshall M.S.,
"The protein kinase Pak3 positively regulates Raf-1 activity through
phosphorylation of serine 338.";
Nature 396:180-183(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ras and phospholipid binding site.";
Proc. Natl. Acad. Soi. U.S.A. 93:8312-8317(1996).
-!- FUNCTION: INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS FROM
THE CELL MEMBRANE TO THE NUCLEUS. PART OF THE RAS-DEPENDENT
SIGNALING PATHARY FROM RECEPTORS TO THE NUCLEUS.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
MIL/RAF SUBFAMILY.
-!- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
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Nat. Struct. Biol. 3:723-729(1996).
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                                                                                                                                                                                                             King A.J., Sun H., Diaz B., Barnard D., Miao W., Bagrodia Marshall M.S.;
Nature 406:439-439(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRUCTURE BY NMR OF 136-187.
MEDLINE-96323218; PubMed=8710867;
MOTH H.R., Carpenter J.W., Zhong S., Ghosh S., Bell R.M.,
Campbell S.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nassar N., Horn G., Herrmann C., Block C., Janknecht R., Wittinghofer A.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 51-131.
MEDLINE=95312074; Pubmed=7791872;
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InterPro; IPR000719; Euk_pkinase.
                                                        MEDLINE=99039505; PubMed=9823899;
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EMBL; BC018119; AAH18119.1;
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MIM; 164760; -.
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PDB; 1GUA; 11-JAN-97
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DR InterPro; IPR003116; RBD.

DR InterPro; IPR004040; STY_pkinase.

DR Pfam; PF000180; DSar_thr_pkinase.

DR Pfam; PF00110; DAG_PE-bind; 1.

DR Pfam; PF00110; DAG_PE-bind; 1.

DR PF01110; DAG_PE-bind; 1.

DR PROSTE; SM00109; C1; 1.

DR SMART; SM00109; C1; 1.

DR SMART; SM00109; C1; 1.

DR PROSTE; PS00101; PROTEIN KINASE ATP; 1.

DR PROSTE; PS00107; PROTEIN KINASE DOM; 1.

DR PROSTE; PS00107; PROTEIN KINASE DOM; 1.

DR PROSTE; PS00107; PROTEIN KINASE DOM; 1.

DR PROSTE; PS00101; PROTEIN KINASE DOM; 1.

DR PROSTE; PS00101; PROTEIN KINASE DOM; 1.

DR PROSTE; PS00100; PROTEIN KINASE DOM; 1.

DR PROSTE; PS00100; PROTEIN KINASE DOM; 1.

PROMAIN 349 609 PROTEIN KINASE.

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FT DOMAIN 349 609 PROTEIN KINASE.

FT ND BIND 355 363 ATP (BY SIMILARITY).

FT ND BIND 355 363 ATP (BY SIMILARITY).

FT ND BIND 355 363 ATP (BY SIMILARITY).

FT MOD RES 338 338 338 PHOSPHORYLATION (BY PAKZ AND PAK3).

SQ SEQÜENCE 648 AA; 73051 MW; EF8128349711BC3 CRC64;

ACLT SITE 468 609 PROTEIN KINASE.

FT MOD RES 338 378 375 PROSTEIN MOD RES 2; Indels 0; Gaps 0;

MATCHES S; CORDERVATION NO. 14+02;
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Search completed: July 18, 2003, 15:07:20 Job time : 6.58 secs

1 QHHYGTPY 8 || | ||: 229 QHRYSTPH 236

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2003 Compugen Ltd.
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58
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score distribution.	Description	O8wz18 homo sapien	O9xwk6 caenorhabdi		Q8qrv8 chimpanzee	Q9klp1 neisseria m	O92ne3 rhizobium m	Q9sdb1 arabidopsis	Q8s8t6 arabidopsis	Q8w010 arabidopsis	OBVCD0 mus musculu	O9n8n5 trypanosoma	Q9erz9 musculu	027992 archaeoglob	P95466 pantoea cit	09svz7 arabidopsis	
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20111111

OSXWK6; 01-NOV-1999 (TrEMBLrel. 12, Created) 01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

PRT; 332 AA.

PRELIMINARY;

RESULT 2 Q9XWK6 ID Q9XWK6 AC Q9XWK6 DT 01-NOV-DT 01-NOV-DT 01-NOV-

38 65.5 1168 10 08 38 65.5 1392 10 09 37 63.8 1392 10 09 37 63.8 139 16 09 37 63.8 439 17 08 37 63.8 439 17 08 37 63.8 451 17 09 37 63.8 451 17 09 37 63.8 575 5 09 37 63.8 575 5 09 37 63.8 575 5 09 38 62.1 293 16 09 36 62.1 293 16 09 36 62.1 293 16 09 36 62.1 293 16 09 36 62.1 293 16 09 36 62.1 293 16 09 36 62.1 293 16 09 36 62.1 298 17 09 36 62.1 298 17 09 36 62.1 298 16 09 36 62.1 298 17 09 37 09 38 09 38 09 38 09 38 09 39 09 30 09 30 09 30 00	Q887C7 oryza sativ Q9sdg9 oryza sativ Q9cit2 lactococcus Q9thQ2 arabidopsis Q8tb97 thermoaner Q8ulv4 pyrococcus Q9v076 pyrococcus Q9v076 pyrococcus Q9v076 pyrococcus Q9v076 pyrococcus Q9v076 pyrococcus Q9v076 encephalito Q9y11 caenorhabdi Q9y12 encephalita Q9y12 caenorhabdi Q9y12 caenorhabdi Q9y13 caenorhabdi Q9y13 caenorhabdi Q9y14 meisseria m	09086; 091vf 091vf 094ea; 094bu; 00682;	ate) pdate) brata; Bute inidae; Hom inidae; Ac din W.X., Z din M.X., Z	DB 4; Length 235; 4.1; ches 1; Indels 0; Gaps 0;
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Pfam; PF00702; Hydrolase; 1.
Complete proteome.
SEQUENCE 237 AA; 26836 MW; E905994
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TIGR; NMB0040; -.
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                       RESULT 4
                                                                                                      Q8QRV8
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                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                              "Genome sequence of the nematode C.elegans: A platform for investigating biology.";
Science 282:2012-2013-2014.
Rembi, ALO32642; CAA21653.1; -. Rembi, ALO32642; CAA21653.1; -. Rembi, ALO32642; CAA21653.1; -. Remover, IPR001842; Znf C2H2.
Remi, PF00096; zf-C2H2; Znf C2H2.
Remi, PF00096; zf-C2H2; Znf C2H2.
Remover, SMART; SM0035; Znf C2H2; 1.
Remover PROSITE; PS01078; ZiNC FINGER C2H2.1; UNKNOWN.1.
Remover prosition of the property of the prope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72.4%; Score 42; DB 5; Length 461; 85.7%; Pred. No. 19; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72.4%; Score 42; DB 5; Length 332;
85.7%; Pred. No. 14;
iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                           Gardner A.E.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53033 MW; 310B2510C869AF57 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00028; ZINC FINGER C2H2 1; UNKNOWN 2.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     461 AA.
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                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            investigating biology.";
Science 282:2012-2018(1998).
EMBL; AL032642; CAA21651.2; -.
Interpro; IPR000822; Znf C2H2.
Pfam; PF000056; Zf-C2H2; ZnsAART; SM00355; ZnF C2H2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1999 (TrEMBLrel. 12, 01-DEC-2001 (TrEMBLrel. 19, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA-binding; Zinc-finger.
SEQUENCE 461 AA; 53033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 85.7
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                               Caenorhabditis elegans
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Best Local Similarity
Matches 6; Conserv
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 Y48A6C.3 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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STRAIN=MCS8 / SEROGROUP B;
MEDLINE=20175755; PubMed=10710307;
Tettelin H., Saunders N.J., Headelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Melson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Mason T., Ciecko A., Parkesy D.S., Blair B., Cittone H., Clark B.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Cotton M.D., Jerser C.M., Massignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon B.R., Rappuoli R., Venter J.C.; "Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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                                                                                                                                                                                                                                                                                                                   Alcendor A.J., Akter P., Dolan A., Wright K.M., Addison C., Alcendor D.J., Hayward G.S., McGeoch D.J.;
"The human cytomegalovirus genome revisited.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AF480884, AAM00780.1; -
SEQUENCE 228 AA, 25902 MW; 42D8D01531D6939D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                          chimpanzee cytomegalovirus.
Viruses; d8DNA viruses, no RNA stage; Herpesviridae;
Betaharpesvirinae; Cytomegalovirus.
NCBI_TaxID=188763;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                     Last annotation update)
Last sequence update)
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Pred. No. 20;
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ATP-binding cassette transporter ABCAI.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCH_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA;
Rounsley S.D., Lin. K., Ketchum K.A., Crosby M.L., Brandon R.C.,
Sykes S.M., Kaul.S., Mason T.M., Kerlavage A.R., Adams M.D.,
Somerville C.R., Venter J.C.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1222;
                                                                                                                                                                                                                                                                                  Score 40; DB 10; Length 750;
Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                       Indels
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STRAIN=CV. COLUMBIA;
Town C.D., Kaul S.;
Submitted (FBA-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AC002510; AAM14842.1; -.
                                        Town C.D., Kaul S.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AC002339; AAC02761.3; -.
Hypothetical protein.
NON TER 750 750
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                                                                                                                                                                           750 750 750 750 750 AA; 83833 MW; 23A0361A36398CAE CRC64;
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01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Putative ABC transporter (Fragment).
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Pred. No. 1.2e+02;
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                                                                                                                                                                                                                                                                              Match 69.0%;
Local Similarity 66.7%;
les 6; Conservative
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66.7%;
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STRAIN=CV. COLUMBIA;
   COLUMBIA;
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01-MAR-2002 (
01-MAR-2002 (
   STRAIN=CV.
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SEQUENCE
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Q8W010
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   CCC SETTING
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STRAIN
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STRAIN=1021;

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STRAIN=CV. COLUMBIA;
Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C.,
Spriggs T.A., Mason T.M., Kerlavage A.R., Adams M.D., Somerville C.R.,
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MR-2002 (TrEMBLrel. 20, Last annotation update)
Putative ABC transporter protein.
R02264 OR SMC01652.
Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria: Proteobacteria: alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
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0
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Last annotation update)
                                                                                                                                                                                                                                                 386 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        750 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 21, Last sequence 01-JUN-2002 (TrEMBLrel. 21, Last annotatio Hypothetical 83.8 kDa protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.
                                                                                                                                                                                                                                                 PRELIMINARY;
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                                    220 QNHYNTPY 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUL-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
1 QHHYGTPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome
SEQUENCE 386 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 HYGTPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9SDB1
                                                                                                                                                                                                                                             Q92NE3
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                                                                                                                                                                RESULT 6
092NB3
092NB3
AC 092NB3
DD 01-D
DT 01
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(958B)

OOSD
AC 095B
D 01-0
DT 01-0
DT 01-1
DT 01-0
DE HYPO
OC EUKA
OC SPER
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Gaps

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Gaps

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SEQUENCE FROM N.A.

Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;

"Cloning and sequencing of the light chain fragment of variable region genes of an anti-hTNF-a monoclonal antibody.";
J. Cell. Mol. Immunol. 12:21-26(1996).
                                     Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5691;
                                                                                                                                         Hall N., Bowman S., Quail M., Ivens A.C., Kay M.P., Bray-Allen S., Lennard N.J., Clark L.N., Harris B.R., Melville S., Lawson D., Gerrard C., Rajandream M.A., Barrell B.G.; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AL359782, CAB95508.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Chen P., Mang Z.L., Han H., Yao L.B., Su C.Z.; Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.; Construction and sequencing of the single-chain antibody gene of human TNF-alpha specific monoclonal antibody.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Anti human TNF-alpha light chain variable region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 66.7%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                   67.2%; Score 39; DB 5; Length 713; 100.0%; Pred. No. 1e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF262753; AAG23804.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107 AA; 11784 MW; 2B15EEA6604A26C3 CRC64;
                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEOUENCE 713 AA; 75955 MW; 5D9F2057727E79EA CRC64;
                                                                                                                                                                                                                                             Interpro; IPR000194; ATPASE a/bcentre.
PROSITE; PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 AA
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InterPro; IPR003599; IG.
InterPro; IPR003006; IG_MHC.
InterPro; IPR003596; IG_V.
                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
nes 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig; 1.
SMART; SM00409; IG; 1.
SMART; SM00406; IGv; 1.
NON TER 107 107
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92 QQHYRTPFT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QHHYGTPYT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  612 QHHYGT 617
                 Prypanosoma brucei
                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                  SEQUENCE FROM N.A. STRAIN=TREU927;
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 OHHYGT
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SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                                                                                                                                                                                                                                   69.0%; Score 40; DB 10; Length 1884; 66.7%; Pred. No. 1.9e+02; ive 1; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 39; DB 11; Length 234;
Pred. No. 32;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                              1884 AA; 209477 MW; 93CA7AB44D65D588 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25702 MW; 102551C58AC2FA9F CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 76.0 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UJN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 25.7 kDa protein.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                       PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (DEC-2001) to the EV
EMBL; BC019474; AAH19444.1;
InterPro; IPR003599; IG.
InterPro; IPR003597; Ig.
InterPro; IPR00306; Ig_MHC.
InterPro; IPR003596; Ig_V.
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66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 60.7.,
6; Conservative
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Les 6, Conservative
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SMART; SM00409; 1G; 2.
SMART; SM00407; 1Gc1; 1.
SMART; SM00406; 1Gv; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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QHHSGIPFT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             734 KHHYGVGYT 742
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QHHYGTPYT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein SEQUENCE 234 AA;
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                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
NCBI_TaxID=3702
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                                                                                                                                                                                                                                                                                           ATP-binding
                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                          Query Match
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Q9N8NS
ID Q9N8N
AC Q9N8N
DT 01-OC
DT 01-OC
DT 01-AC
DT HYDOL
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CONCPO
DO ON CONCPO
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Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
SEQUENCE FROM N.A.
Bevan M., Peters S.A., van Staveren M., Dirkse W., Stiekema W., Hoheisel J., Mawes H.W., Mayer K.F.X., Schueller C., Stiekema W., Submitted (MAR.1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. Peters S.A., van Staveren M., Dirkse W., Stiekema W., Mewes Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.5%; Score 38; DB 2; Length 786; 75.0%; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ALO49480; CAB39609-1; -.
EMBL; ALI61564; CAB79443.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EU Arabidopsis sequencing project;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                     372402AAD8B067CC CRC64;
                                                                                                                                                              POTENTIAL.
PERIPLASMIC (POTENTIAL).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 20, Last annotation update)
Pumilio-like protein.
F14M19.160 OR AT4G25880.
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                                                                                                                                                                                                                                                                                                                                                                                     PQQ-BINDING.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                            POTENTIAL.
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Pfam; PF00806; PUF; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                      86038 MW;
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Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                     786 AA;
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TRANSMEM
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SEQUENCE
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Q9SVZ7
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                                                                                                                                                                                                                                                                 MEDLINE-98049343; PubMed-9308475; Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Klenk M.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glucose dehydrogenase that is essential for causing pink disease of pineapple.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Appl. Environ. Microbiol. 63:71-76(1997).
-!- CATALYTIC ACTIVITY: D-GLUCOSE + ACCEPTOR = D-GLUCONO-1,5-LACTONE REDUCED ACCEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- COFACTOR: PQQ.
-!- SUBCELLULAR LOCATION: PERIPLASMIC (BY SIMILARITY).
-!- MISCELLANEOUS: RESPONSIBLE FOR PINK TO BROWN DISCOLORATIONS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Glucose dehydrogenase [pyrroloquinoline-quinone] (EC 1.1.99.17).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.5%; Score 38; DB 17; Length 287; 62.5%; Pred. No. 59; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cha J.-S., Pujol C., Kado C.I.; "Identification and characterization of a Pantoea citrea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 protein; Complete proteome.
287 AA; 33541 MW; 8DA315595CE2AC58 CRC64;
                                                                                                                                            Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
NCBI_TaxID=2234;
                                                                                               Last sequence update)
Last annotation update)
                                                 287 AA
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=VC-16 / DSM 4304 / ATCC 49558;
                                                                                 Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97133947; PubMed=8979341;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE000946; AAB88967.1; -.
                                                                             01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-MAR-2002 (TrEMBLrel. 20, Hypothetical protein AF2292.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1997 (TrEMBLrel. 03, 01-MAY-1997 (TrEMBLrel. 03, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||:|| |:
212 QHYYGAPF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QHHYGTPY 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=53336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGR; AF2292; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pantoea citrea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=1056R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pantoea.
                                               027992
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                RESULT 13
027992
ID 02799
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P95466
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Gaps

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H.W.,

Gaps

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Length 1168;

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Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales; Streptococcaceae; Lactococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similar to putative polyprotein.
Oryza sativa (Rice).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
Salzberg S.L., White O., Fraser C.M.;
"Oryza satuva chromosome 10 BAC OSJNBA0057L21 genomic sequence.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AC087599; AAL79695.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Anaerobic ribonucleoside-triphosphate reductase activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AP000836; BAA88175.1; -. InterPro; IPR001584; Rve. InterPro; IPR001878; Znf_CCHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1392 AA; 154506 MW; 7188F034FDA07AAE CRC64;
                                                                                                                                                                        1168 AA; 128502 MW; B3ED6E5C79954CAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                  Score 38; DB 10;
Pred. No. 2.6e+02;
1; Mismatches · 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1392 AA.
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                                                                                                                                                                                                                                  Similarity 66.7%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00665; rve; 1.
Pfam; PF00098; zf-CCHC; 1.
SMART; SMO0343; ZnF_C2HC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.5%;
66.7%;
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Best Local Similarity 66..
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | || |||:
| 588 QRHYTTPYS 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                         455 ORHYTTPYS 463
                                                                                                                                                                                                                                                                                                                                                                                     1 QHHYGTPYT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QHHYGTPYT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone:P0038F12."
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                                                                                                                                           Polyprotein.
SEQUENCE 1
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SEQUENCE 1
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STRAIN=CV. NIPPONBARE;
Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N.,
Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M.,
Tsitrin T., Riggs F., Hsiao J., Zismann V., Blunt S., Pai G.,
VanAken S.E., Utterback T.R., Feldblyum T.V., Kalb E., Quackenbush J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L., Carninci P., Cheu H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J. Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Skinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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0
                                                                                                    65.5%; Score 38; DB 10; Length 849; 75.0%; Pred. No. 1.9e+02; Live 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Theologis A.;
"Full Length cDNA of gene AT4g25880 (GI:7269439).";
"Full Length cDNA of gene AT4g25880 (GI:7269439).";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF360298, AAX260081;
InterPro; IPR001313; Pumilio/Puf.
Pfam: PF00806; PUF; 8.
SMART; SM00025; Pumilio; 8.
SEQUENCE 861 AA; 96105 MW; 44555848AAFCDE5A CRC64;
                                   74EFC4593EB7B498 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative gag-pol polyprotein.
OSJNBA0057121.25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                861 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
   SMART; SM00025; Pumilio; 8.
SEQUENCE 849 AA; 94894 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Putative pumilio protein.
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nes 6; Conservative
                                                                                                                                    Local Similarity 75.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                267 ÓFHYĞQPY 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QHHYGTPY 8
                                                                                                                                                                                                                                                1 QHHYGTPY 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4530;
                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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10 0857C7
AC 0857C
DT 01-JU
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Tan H., Chen R., Wang J., Yu J., Yang H.;
"A complete sequence of T. tengcongensis genome.";
Genome Res. 12:689-700(2002).
EMBL, AE013058, AAM24181.1; -.
Carboxypeptidase; Complete proteome.
SEQUENCE 416 AA; 46794 MW; 586681D1A33FC870 CRC64;
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Weissenbach J., Ehrlich S.D., Sorokin A.; "The complete genome sequence of the lactic acid bacterium Lactococcus lactis IL1403."; Genome Res. 11:731-753(2001).
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NCBI_TaxID=119072;
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Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,
Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome 1 BAC F13E17 genomic sequence.";
Submitted (SER-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, ACO74284; AAG12615.1;
Hypothetical protein.
SEQUENCE 279 AA; 32364 MW; E4698FAC34C61COC CRC64;
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MEDLINE=21992816; PubMed=11997336;
Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Hypothetical 32.4 kDa protein.
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                                                                                                                                                       EMBL, AE006264, AAK04372.1; -.
InterPro, IPR001989, Radical activat.
Pfam; PF02143; Radical_activat, 1.
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
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192 HHFGTP 197
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Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
Masuchi Y., Shizuya H., Kikuchi H.,
"Complete sequence and gene organization of the genome of a hyperthermophilic archaebacterium, Pyrococcus horikoshii OT3.",
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Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
"The complete sequence of the Pyrococcus furiosus genome.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AE010220; AAL81225.1;
Hypothetical protein; Complete proteome.
SEQUENCE 439 AA; 49079 MW; B3ABA93A7F06CE68 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypochetical protein PF1101.
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100.0%; Pred. No. 1.4e+02;
tive 0; Mismatches 0;
63.8%; Score 37; DB 16; 62.5%; Pred. No. 1.3e+02;
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nes 5; Conservative
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STRAIN=JCM 10545 / 7;
Pubbled=11572479;
Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
Yoshixawa T., Tanawa T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
Oshima T., Kikuchi H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea, Crenarchaeota, Thermoprotei, Sulfolobales, Sulfolobaceae,
Sulfolobus.
                                                                                                                                                                                                                    Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F., Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker P. Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M., Weissenbach J., Vivares C.P.;
                                                                                                                                                                                                                                                                                                                           "Genome sequence and gene compaction of the eukaryote parasite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 37; DB 5; Length 517; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodaii strain7.";
DNA Res. 8:123-140(2001).
EMBL; AP000984; BAB66629.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                         Genoscope;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                  Encephalitozoon cuniculi.";
Nature 414:450-453(2001).
BEBL; AL590442; CAD25114.1; -
SEQUENCE 517 AA; 59068 MW; 87CB15737957BE3B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein, Complete proteome.
SEQUENCE 547 AA; 63567 MW; A888D7EAD99CEDCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 19, Last sequence update) (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.8%; Score 37; DB 17; L
100.0%; Pred. No. 1.8e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            547 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                     STRAIN=GB-M1;
MEDLINE=21576510; PubMed=11719806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.8%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein ST1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 85...
6. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 407 HLGTPYT 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sulfolobus tokodaii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162 YGTPYT 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 HYGTPYT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=111955;
                                                                                                                        [2]
SEQUENCE FROM N.A.
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                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9GYL1
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Q972Y4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9GYL1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAGE
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                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                   63.8%; Score 37; DB 17; Length 450; 100.0%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Encephalitozoon cuniculi.
Eukaryota, Microsporidia, Unikaryonidae, Encephalitozoon.
NCBI_TaxID=6035,
                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    structure and evolution.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ248285; CAB49829.1;
InterPro; IPR001279; Blactmase-like.
InterPro; IPR004613; MG423.
InterPro; IPR001587; UPF0036.
                                                                                                                                                                     TIGRFAMS; TIGRO0649; MG423; 1.
PROSITE; PS01222; UPF0036; UNKNOWN 1.
HYPOCHELICAL protein; Complete profeome.
SEQUENCE 450 AA; 50341 MW; 4F8833725B966DFB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGRFAMS; TIGRO0649; MG423; 1.
PROSTIE; PS01292; UPP0036; UNKNOWN 1.
Hypothetical protein; Complete proteome.
SEQUENCE 451 AA; 50517 MW; AA689437804BC24E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ol-MAY-2000 (TrEMBLrel. 13, Created)
01-JUN-2002 (TrEMBLrel. 13, Last sequence update)
Hypothetical protein PAB1751.
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Last annotation update)
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Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.8%; Scc...
100.0%; Pred. No....
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    451 AA
                                                                                                                                                                                                                                                                                                                   100.0%; Preα, ...
                  EMBL, AP000004, BAA30170.1, -.
InterPro, IPR001279; Blactmase-like.
InterPro, IPR004613, MG423.
InterPro, IPR001587; UPF0036.
Pfam; PF00753; lactamase B; 1.
Pfam; PF02147; UPF0036; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2002 (TrEMBLrel. 21, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00753; lactamase B; 1.
Pfam; PF02147; UPF0036; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 21, (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein disulfide isomerase.
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Best Local Similarity luv.
                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      110 YGTPYT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 YGTPYT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Pyrococcus abyssi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                       4 YGTPYT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pyrococcus abyssi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=29292;
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01-JUN-2002
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                                                                                                                                                                                                                                                                                                      Query Match
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QBSSFS;
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08SSF
AC 08SSF
AC 08SSF
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DE Prote
GN ECU02
OS Encep
OC Enkar
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Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R., Nyakatura G., Mewes H.W., Mannhaupt G., Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36; DB 3; Length 211;
Pred. No. 96;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36; DB 4; Length 90;
Pred. No. 39;
2; Mismatches 1; Indels
                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        German Neurospora genome project;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL451021; CAC18294.2; -.
Hypothetical protein
SEQUENCE 211 AA; 23425 MW; B75964FD26EC5C4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Phillimore B.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 AA; 9894 MW; 2A2466BC91A1F556 CRC64;
                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-OCT-2001 (TrEMBLrel. 18, Last annotation update) DJ908M14.1.3 (ribosomal protein S21, isoform 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 23.4 kDa protein.
    Pred. No. 3.7e+02;
                                                                                                                                                                                                90 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            211 AA
                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pram; PF01249; Ribosomal_S21e; 1.
ProDom; PD006584; Ribosomal_S21E; 1.
PROSITE; PS00996; RIBOSOMAL_S21E; 1.
                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AL121832; CAC29248.1; -. InterPro; IPR001931; Ribosomal_S21E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01249; Ribosomal S21e;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 62.1%;
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 62.1%;
Similarity 62.5%;
5; Conservative
  85.7%;
                        6; Conservative
                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                              566 QHHAGTP 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 HHYGTPYT 9
  Best Local Similarity
Matches 6; Conserv
                                                            1 QHHYGTP 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ribosomal protein.
SEQUENCE 90 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                      NCBI TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O9HEF6
                                                                                                                                                                                              Q9BYK1
                                                                                                                                                                                                                                                                                                              RPS21.
                                                                                                                                                      RESULT 29
Q9BYK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                          Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leishmania major.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                    investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98146435; PubMed-9477341;
IVens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
Smith D.F.;
                                                                                                                                                                                                                                  'Genome sequence of the nematode C. elegans: a platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.8%; Score 37; DB 5; Length 1086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.8%; Score 37; DB 5; Length 575; 62.5%; Pred. No. 1.9e+02; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A physical map of the Leishmania major Friedlin genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1086 AA; 116056 MW; 19C4A930165C3415 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Waterston R.;
"Direct Submission.";
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; U41538; AAGO0007.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Masuy D., Purnelle B., Goffeau A., Ivens A.C., Quail M., Rajandream M.A., Barrell B.G., Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                "The sequence of C. elegans cosmid R04E5.";
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro, IPR001664; IF.
Pfam, PR00038, filament; 1.
Hypochetical profain.
SEQUENCE 575 AA, 66699 MW, DCD9581BECC52C01 CRC64;
01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Hypothetical 66.7 kDa protein.
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Last annotation update)
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                                                                                                                                                                        STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
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P1295.12.
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EMBL; AL359773; CAB95220.1; -.
Hypothetical protein.
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                                                        Caenorhabditis elegans.
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427 HHYGSSYS 434
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Matches 5; Conserv
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                                        R04E5.10
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Probom, PD000039; Response_reg; 1.
Probom, PD0000329; Trans_reg_C; 1.
SMART; SM00448; REC; 1.
DNA-binding; Phosphorylation; Sensory transduction;
     Pfam; PF00072; response_reg; 1.
Pfam; PF00486; trans_reg_C; 1.
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CN 8.
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Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron. B.
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Brouillet S., Brischi C.V., Connerton I.F., Cummings N.J., Daniel R.A.,
Denizof F., Devine K.M., Dusterhoft A., Erhilch S.D., Emmerson P.T.,
Brian K.D., Errington J., Fuma S., Galizzi A., Galleron N.,
Britz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
Guiseppi G., Guy B.J., Haga K., Haich W.F., Itaya M., Jones L.,
Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
M. Guiseppi G., Guy B.J., Haga K., Haich J., Lazarevic V.,
A., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
M. Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
Mone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
Mone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
None D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
Rieger M., Rivolta C., Roche B., Roche B., Rose M., Sadaie Y.,
A sekguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
Sato T., Scanlan E., Schleich S., Schroeter R., Shin B.S., Soldo B.,
Sorokin A., Tanaka T., Tanaka T., Taraka B., Tarandot T.,
Takeuchi M., Tamakoshi A., Tanaka T., Taraka B., Wadler E., Wedler E., Wedler E., Wedler E., Weller B., Waller B., Tosanoto K., Yasumoto M., Woollius Bacillus
Witters P., Wipat A., Yamamoto Of the gram-positive bacterium Bacillus
Willish W. Wallerin B., Wedler E., Wedle
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"Sequence analysis of the 70kb region between 17 and 23 degree of th
Bacillus subtilis chromosome."
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER
REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.
-!- SIMILARITY: TO BACTERIAL REGULATORY PROTEINS INVOLVED IN SIGNAL
TRANSDUCTION.
                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales; Bacillacee; Bacillus.
NCBI_TaxID=1423;
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                    Created)
Last sequence update)
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                                                                                                                                                                     223 AA.
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InterPro; IPR001789; Response_reg.
InterPro; IPR001867; Trans_reg_C.
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                                                                                                                                                                  PRELIMINARY;
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ENHYGTP 35
                                                                                                                                                                                                                                                                                                                                                          Bacillus subtilis.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
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                                                                            Query Match 62.1%; Score 36; DB 16; Length 223; Best Local Similarity 83.3%; Pred. No. 1e+02; Matches 5; Conservative 1; Mismatches 0; Indels
franscription regulation; Complete proteome.
SEQUENCE 223 AA; 26173 MW; 9DB646AD90675A86 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AP0033002; BAB50599 1; -.
InterPro; IPR001264; GT_51.
Pfam; PF00912; Transglycosyl; 1.
ProDom; PD001895; GT_51; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptidoglycan transglycosylase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 71.4 tes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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Cho Y., Ramer J., Rivailler P., Quink C., Garber R.L., Beier D.R., Wang F.;

"An Epstein-Barr-related herpesvirus from marmoset lymphomas.";

Proc. Natl. Acad. Sci. U.S.A. 98:1224-1229(2001).

EMBL; AF19782; AAK88249.1; -

SEQUENCE 303 AA; 34855 MW; D6BFB90656294623 CRC64;
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Lymphocryptovirus.
NCBI_TaxID=106331;
                                                                               MEDLINE=21107697; PubMed=11158621;
                                                                                                                                                                                                                                                                89 HHYSDPY 95
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                                                       SEQUENCE FROM N.A. STRAIN=CJ0149;
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MEDLINE-21470413; PubMed=115.0, Pach Dougan G, Pellwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Genome sequence of Yersinia pestis, the causative agent of plague.";
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                      MEDLINE=20183931; Pubmde=10706631;
Shinohara N., Demura T., Fukuda H.;
"Isolation of a vascular cell wall-specific monoclonal antibody
recognizing a cell polarity by using a phage display subtraction
method.";
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                                                                                         Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).

EMBL; AB036341; BAA88633.1; -.

HSSP, PO1607; IRRI.

InterPro; IPR003006; Ig MHC.

InterPro; IPR003596; Ig_V.

FFam; PP00047; ig; 2.

SMART; SM00406; IGV; 2.

SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AJ44158; CAC33086.1; -. Hypothetical protein; Complete proteome. SEQUENCE 299 AA; 33184 MW; DFD537C9C5DE4C86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, C;
01-JUN-2001 (TrEMBLrel. 17, L;
01-JUN-2001 (TrEMBLrel. 17, L;
0RF41.
                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein YPO3617.
                 STRAIN=BALB/C; TISSUE=SPLEEN;
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Best Local Similarity 83.5
Enc. The S; Conservative
                                                                                                                                                                                                                           Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 413:523-527(2001
                                                                                                                                                                                                                                                                                          261 OHFWITPYT 269
                                                                                                                                                                                                                                                                  1 QHHYGTPYT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |:||||
HFGTPY 103
    FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yersinia pestis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98
                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yersinia
                                                                                                                                                                                                                                                                                                                                                                       Q8ZB12;
                                                                                                                                                                                                                                                                                                                                                        Q8ZB12
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Q8ZB12
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Q993G9
ID Q993G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Oin H., Vamathevan J., Smith H.O., Fraser C.M., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon B.R., Rappuoli R., Venter J.C., "Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis (serogroup B).
Bacteria, Proteobacteria, beta subdivision, Neisseriaceae, Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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0
   Length 303;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00044; HTH LYSR FAMILY; UNKNOWN 1.
DNA-binding; Transcription regulation; Complete proteome.
SEQUENCE 309 AA; 34831 MW; 7086861A2DE26637 CRC64;
                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                01-077-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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62.1%; Score 36; DB 12;
71.4%; Pred. No. 1.4e+02;
iive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                             309 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transcriptional regulator, LysR family.
                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=MC58 / SEROGROUP B;
MEDLINE=20175755; PubMed=10710307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       substrate; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000847; HTH LysR.
InterPro; IPR005119; LysR_subst.
Pfam; PF00126; HTH 1; 1.
Pfam; PF03466; LysR_substrate; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 287:1809-1815(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 71.1.,
Factorive 5; Conservative
Query Match
Best Local Similarity 71.49
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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140 ОННЯСНРН 147
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01-JUN-2001
01-JUN-2002
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Q9C865
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X MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayrakearoglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
A Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7227;
                                                                                         Neisseria meningitidis (serogroup A).
Bacteria: Proteobacteria: beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                      MEDLINE=20222556; PubMed=10'661919;
Parkhill J. Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davies P., Devlin K., Feltwell T., Hamlin N., Holroyd S., Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Rutherford K.M., Simmonda M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G., "Complete DNA sequence of a serogroup A strain of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: TO THE LYSR FAMILY OF TRANSCRIPTIONAL REGULATORS.
EMBL; AL162753; CAB83682.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                          DNA-binding; Transcription regulation; Complete proteome.
SEQUENCE 309 AA; 34835 MW; 74D2137E7BA00601 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2002 (TrEMBLrel. 20, Last annotation update)
TIN protein (GG7895 protein)
TIN OR NK-4 OR CG7895.
                                      01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Putative transcriptional activator protein METR.
                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00044; HTH_LYSR_FAMILY; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 416 AA.
309 AA
                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=Z2491 / SEROGROUP A / SEROTYPE 4A;
                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly)
PRT;
                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00126; HTH 1; 1.
Pfam; PF03466; LysR substrate; 1.
                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000847; HTH LysR.
InterPro; IPR005119; LysR_subst.
                         (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 71.9
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                 404:502-506(2000)
                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00039; HTHLYSR
PRELIMINARY;
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                                                                                                                                                                                                                                                                                    meningitidis 22491
                                                                                                                     NCBI_TaxID=65699;
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                                                                               METR OR NMA0381.
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                         01-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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Q9JWG7
Q9JWG7
                                                                                                                                                                                                                                                                                                    Nature
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de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

By Dutbin K.J., Evangelista C.C., Ferraz C., Ferraca S., Felsischmann W.,

R. Fosler C., Gabriellian A.E., Garral N.B., Galbart W.M., Glasser K.,

R. Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

R. Harris N.L., Harvey D., Hennan T.J., Hernandez J.R., Houck J.,

R. Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ibegwam C.,

Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

R. Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

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R. Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

R. Mount S.M., Moy W., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

R. Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

R. Shier B.C., Siden-Kiamos I., Singson M., Skupski M.P., Smith T.,

Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

Syliskas R., Tector C., Turner R., Venter E., Wang A.H.,

R. Jensen K.H., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

R. Jensen S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

R. Jensen S.M., Moyers E.W., Rubinstock G.M., Weissenbach J.,

R. The genome sequence of Drosophila melanogaster.",

R. The genome sequence of Drosophila melanogaster.",
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 49.3 kDa protein (SH3 domain-containing protein 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00389; HUA; L. PROSTER; BOROSTER; PS00027; HOMEOBOX_1; 1. PROSTER; PSS0071; HOWEOBOX_2; 1. DNA-binding; Homeobox; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       regulatory elements.";
J. Biol. Chem. 0:0-0(1997).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 86:7716-7720(1989)
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Pred. No. 2e+02;
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(TrEMBLrel. 17, Last seq
(TrEMBLrel. 21, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=90046666; PubMed=2573058;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interPro; IPR001356; Homeobox.
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SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.1%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 287:2185-2195(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Query Match
Best Local Similarity 62.30,
Best Local Similarity 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-15 FROM N.A.
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Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria, Proteobacteria, beta subdivision, Ralstonia group,
                           01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative amidotransferase amidase protein (EC 3.5.1.-).
  01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
                                                                             RSC0589 OR RS04871
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                    NCBI_TaxID=305;
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MEDLINE=21016719; PubMed=11130712;

A PEDLINE=21016719; PubMed=11130712;

A White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

A Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hudhes B., Huizar L.,

A Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.P.,

Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

Militscher J., Miranda M., Nguyen M., Ngoren W., Roomey T., Rowley D.,

Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

A Bai G., Peterson J., Pham P.K., Shinn P., Southwick A.M.,

Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

Wu D., Yu G., Fraser C.M., Verter J.C., Davis R.W.;

H. Haliana H., Tallon L., L., Tambunga G., Toriumi M.J., Town C.D.,

Wu D., Yu G., Fraser C.M., Verter J.C., Davis R.W.;

T. "Sequence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
A Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
A Gorninci P., Chen H., Chenk R., Hayashizaki Y., Ishida J., Jones T.,
A Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
A Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
A Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
Theologis A.,
"Arabidopsis Full Length cDNa Clones.";
L. Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
L. Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
R. EMBL; AG51264.1;
R. EMBL; AG51264.1;
R. EMBL; AG50773; AAL32438.1;
R. EMBL; AV808035; AAL32438.1;
R. InterPro; IPR001452; SH3:
R. Pffm; FP0018; 
                   Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-21558796; PubMed=11701884;
Lam B.C.-H., Sage T.L., Bianchi F., Blumwald E.;
"Role of SH3 domain-containing proteins in clathrin-mediated vesicle
"trafficking in Arabidopsis.";
Plant Cell 13:2499-2512(2001).
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SEQUENCE 439 AA; 49258 MW; 41A42B784BE8AC25 CRC64;
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PRT;

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QBY1V0 QBY1V0 RESULT 40 Q8Y1V0 ID Q8Y1V AC Q8Y1V DT 01-MA

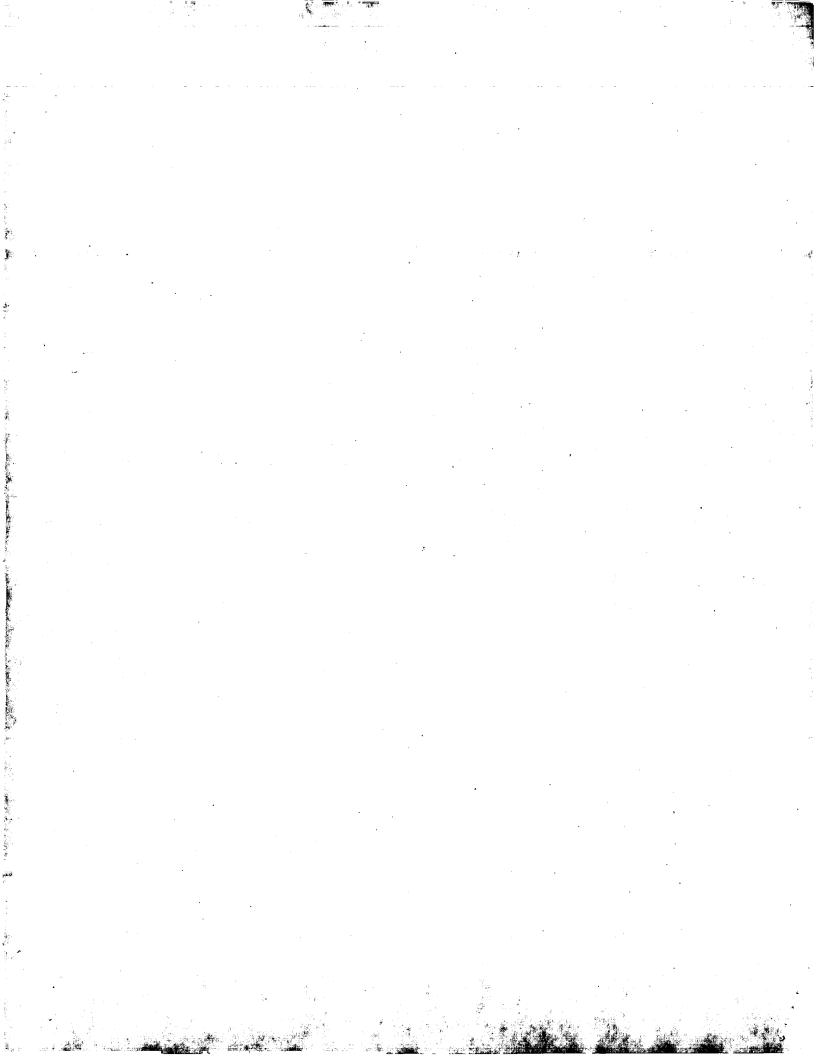
01-MAR-2002 (TrEMBLrel. 20, Created)

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                                         Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Remard C., Cunnacc S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.;

"Genome sequence of the plant pathogen Ralstonia solanacearum.";

Nature 415:497-502(2002).

EMBL; AL646060; CAD1411911;
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Pred. No. 2.1e+02;
0; Mismatches 1
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STRAIN=GM11000;
MEDLINE=21681879; PubMed=11823852;
                                                                                                                                                                                                                                                                       InterPro; 1rrovara...
Pfam; PF01425; Amidase; 1.
Hydrolase; Complete proteome.
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85.7%;
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July 18, 2003, 15:01:44; Search time 23.66 Seconds (without alignments) 39.423 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                      OM protein - protein search, using sw model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

0.7			Description	Murine PIP3 recogn	Murine anti-PAb-42	. Hepatitis B virus	Hypercalcaemia age	Murine anti-CD3 MA	HBV specific singl	Anti-DNA antibody	Heavy chain variab	Murine antibody S2	Murine VH group 1
COLUMNICO			ID	AAY87657	AAY70805	AAU70794	AAR27008	AAR30771	AAY05361	AAW04593	AAR79244	AAB50793	AAR21267
			DB	21	21	23	13	14	20	18	16	22	13
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Claim 7; Page 12; 15pp; Japanese

ope ermoentenromit	hypercarcaemia age	3	ر درانا درانا	WOL a	heavy	J7.6 VH	scFv U7.6 VH (K19N	ń	Murine PIP3 recogn	Murine anti-PAb-42	Hepatitis B virus		H regi	28	Murine 128.1 VH/hu	7	Murine 128.1 VH/hu	Murine 128.1 VH/hu	Anti-mesothelin sc	Antimesothelin ant	➣	Fv(GP-4) immunosup	Anti-5T4 secreted	5T4 scFv antibody	Murine anti-5T4 an			-ri		Human B7-1.5T4.1 p	acid sequen	o acid	Anti-5T4 single ch	0	Diphtheria toxin/U	•
200	13 AAKZ/UIU	0707044	AABOYOO	AAB6969	AAR5998	17 AAR88752	AAR88754	·	·	21 AAY70791	AAU7076	AAW0644		14 AAR38259	4	4	14 AAR41707	14 AAR41715	0	N	m	ທ	20 AAY42294	20 AAY27407		ď	m.	0 AAY0536	S	20 AAW86004	α.	S.	0	-	۳	
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## ALIGNMENTS

PIP3; phosphatidylinositol-3,4,5-triphosphate; variable region; CDR1; immunogen; antibody; heavy chain; complementarity determining region. Murine PIP3 recognizing Mab variable region heavy chain CDR1 region. (FUKU/) FUKUI Y. (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK. A monoclonal antibody recognizing phosphatidylinositol-3,4,5-triphosphate AAY87657 standard; Protein; 7 AA. 98JP-0252921. 98JP-0252921 11-AUG-2000 (first entry) WPI; 2000-353334/31. JP2000083664-A. 07-SEP-1998; 07-SEP-1998; 28-MAR-2000. AAY87657; Mus sp. RESULT 1 AAY87657  ó

Sequence

X S

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This invention describes a novel antibody specifically recognizing phosphaticaldylinosation-3,4.5-triphosphate (PIP3). The antibody of the invention is used in immunogenic compositions in which a dead Salmonella genus microbe is used as an adjuvant and mixed with PIP3. The antibody can be used in an immunosasay contraining a step in which the above antibody or its variable region is reacted with PIP3 present in a sample and the bond based on their immunological reaction. The method can determine PIP3 easily in a high sensitivity. This sequence respresents the murine PIP3 recognizing monoclonal antibody variable region heavy chain complementarity determining region, CDR1 described in the method of
                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                           the invention.
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heavy chain variable region; VH; complementarity determining region; CDR; dernatological; immunosuppressive; antiinflammatory; autoimmune response; SLE; systemic lupus erythematosus; diagnosis; treatment; autoantigen; DNA-binding domain; anti-idiotypic antibody. monoclonal antibody; mAb; PAb-421; IDI-2; IDI-2 H1; Murine anti-PAb-421 IDI-2 mAb heavy chain CDR based peptide IDI-2 H1. Murine, p53 protein,

AAY70805 standard; peptide; 20 AA.

(first entry)

31-JUL-2000

AAY70805;

99WO-US24443. WO200023082-A1. 19-0CT-1999; 27-APR-2000 Mus sp. 

(YEDA ) YEDA RES & DEV CO LTD

98US-0104816

19-OCT-1998;

Cohen IR, Rotter V, Erez-Alon N, Herkel J; WPI; 2000-339512/29 Treatment of systemic lupus erythematosus by down-regulating the autoimmune response to the C-terminal DNA-binding domain of the p53 protein by an active compound comprising of antibodies to p53 or fragments of p53

Claim 78; Fig 10; 87pp; English.

The patent discloses a method for the treatment of systemic lupus erythematosus (SLB) by down-regulating the autoimmune response to the C-terminal DNA-binding domain of p53 protein by an active compound. The present sequence is a IDI-2 H1 peptide which comprises the complementarity determining region (CDR) of the heavy chain of IDI-2 monoclonal antibody (Mab). The IDI-2 mab is an anti-idotypic antibody/Ab2 mAb specific for PAb-421 which is an Ab1 mAb specific to the C-terminal DNA-binding domain of murine p53 protein. The peptide corresponds to residues 19-38 of IDI-2 heavy chain the diagnosis, prevention and treatment of SLE in humans.

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Novel peptide that binds to hepatitis B virus core or E antigen, useful for treating and preventing hepatitis B virus infection
                                                                                                                                                                    Hepatitis B virus, virucide, immunomodulator; hepatotropic; HBV, antiinflammatory; HBV core antigen; HBcAg; HBV E antigen; HBeAg; B cell mediated processing; T cell proliferation; cytokine production;
                         Gaps
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        Score 41; DB 21; Length 20; Pred. No. 0.68;
                         Indels
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                                                                                                                                                     Hepatitis B virus antigen binding partner #26.
                         Mismatches
                                                                                                   AAU70794 standard; Peptide; 20 AA.
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       100.0%;
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Query Match
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                                                                                                                                                                                                               Synthetic.
                                                                                                                    AAU70794;
                                                                                    RESULT 3
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The invention relates to an isolated or purified peptide (I) which binds Hepatitis B virus (HBV) core antigen (HBCAg) or HBV E antigen (HBCAg).

(I) is useful for treating or preventing Hepatitis B virus (HBV) infection, by identifying a subject in need of a molecule that inhibits HBV infection, and providing the subject with (I). (I) is also useful for determining the presence of HBV in a biological sample, and for hBCAg and/or HBCAg and processing and uptake of HBCAg and/or HBCAg and or youther (I) inhibits B cell mediated processing and uptake of HBCAg and/or HBCAg and/or HBCAg and or youther (I) inhibits B cell mediated processing and proliferation or yotokine production. (I) is also useful for modulating poptides, derivatives or modified peptides, synthetic molecules including peptides, derivatives or modified peptides, synthetic molecules including peptides, derivatives or modified peptides, confidential as biocechnological conjugations and chemicals. (I) is also useful as detection reagents in conventional immunohistochemical techniques, as diagnostic reagents to detect HBV in protocol by monitoring the levels of HBCAg and/or HBCAg and/or HBCAg and doring and after treatment. AAU70766-AAU70876 represent Hepatitis B virus (HBV) core in the investion of the investion (HBCAg) or HBV E antigen (H 20 AA; Sequence

Query Match

100.0%; Score 41; DB 23; Length 20;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Humanisation of antibodies - by molecular modelling of the variable domains and alteration by gene conversion mutagenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single-stranded antibody against hepatitis B virus core protein, applicable as (gene) therapeutic agents for treatment of hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single stranded antibody; hepatitis B virus; HBV core protein; HBV infection; viral proliferation inhibitor; viral DNA synthesis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence is that of the heavy chain variable domain of murine anti-CD3 monoclonal antibody UCHTI (muxCD3, Shalaby 1992).
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Pred. No. 3.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 41; DE Best Local Similarity 100.0%; Pred. No. 3.3 Matches 7; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                            Carter PJ, Presta LG;
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                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1993-018139/02.
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N-PSDB; AAX33929.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99 AA;
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                                    Mus musculus.
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                                                                                                                                                                                             15-JUN-1992;
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                                                                                       WO9222653-A.
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                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treatment and preventive agent for hypercalcaemia - contg. one of anti-human para-thyroid-hormone-related protein monoclonal antibody, a rodent or chimera monoclonal antibody, fused gene and cell line, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequences given in AAR27008-11 are fragments which were used in the construction of an agent for the treating and prevention of hypercalcaemia. The agent contained a portion of the antihuman parathyroid hormone-related protein monoclonal antibody funtihuman PTHYP MAD). The MAD was used as the active component in the agent. The agent further comprises a rodent/human chimeric MAD which has a rodent variable region and a human constant region and recognises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antihuman parathyroid hormone-related protein; monoclonal antibody; variable region; rodent/human chimeric MAb; constant region; PTHFP.
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     Pred. No. 0.68;
0; Mismatches
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                                                                                                                                                                                                                                                                          AAR27008 standard; peptide; 98 AA.
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100.0%;
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Best Local Similarity 100.
Matches 7; Conservative
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GYSFTGY 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
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AAR27008
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Lopez O,
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                                                                                                                                             Sequence
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      This sequence is the single-stranded antibody of the invention, that has the capability of binding to a hepatitis B virus (HBV) core protein. Therapeutic agents can be formulated with the antibody for treatment of HBV infections by stopping proliferation of the virus through inhibition of viral DNA synthesis, and the gene encoding the antibody can be applied
                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-DNA antibody which specifically binds DNA hairpin - useful to develop prods. for diagnosis and treatment of disorders, e.g. glomerulonephritis or systemic lupus erythematosus
                                                                                                                                                                                                                                                                                Heavy chain; variable region; anti-DNA; monoclonal; antibody;
MAb 7b3; hairpin; diagnosis; inflammatory glomerulonephritis;
systemic lupus erythematosus; screening; treatment; prevention;
                                                                                                                 ö
                                                                                             100.0%; Score 41; DB 20; Length 108; 100.0%; Pred. No. 3.6;
                                                                                                                 Indels
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label= CDR_II
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/label= CDR_I
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                                                        as an agent to gene therapy
                                                                                                       Local Similarity 100.
nes 7; Conservative
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/label= .
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                                                                                                                                   GYSFTGY
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                                                                                                                                                                                                                       AAW04593;
                                                                           Seguence
                                                                                             Query Match
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Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hybridoma antibodies have been produced with the spleen cells of BALB/C mouse that had received multiple injections of mercuric ions reacted with glutathione to produce a mercuric ion coordinate covalent compound which was covalently bound to keyhole limpet hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 5B6, 5B6 and 3B8) were producing MADS that were strongly positive against glutatione-mercuric ions but negative against glutathione without mercuric ions. RNA was isolated from hybridoma cells with guanidine isothiocyanate. First strand cDNA synthesis was catelyysed were complementary to the 5' end of the CH1 domain of the heavy
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
The present sequence is the heavy chain variable region of the anti-DNA monoclonal antibody (MAb) 7h3, which has a high affinity for single stranded DNA, low or no affinity for double stranded DNA and specifically binds a DNA hairpin. The MAb can be used diagnose disorders associated with the pathological complexation of DNA, e.g. inflammatory glomerulonephitis and systemic lupus erythematosus. It can also be used to generate reagents to screen
                                                                                                                                                               disorder.
Calf thymus DNA was used to immunise a MRL-1pr mouse, spleen cells
                                                                                                                                                                                                  from which were then fused with Sp2/0 myeloma cells to give hybridomas producing the anti-DNA MAb. 7b3 was found to react strongly with poly(dT), poly(dG) and poly(dI), moderately with single stranded DNA and weakly with poly(G).
                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                        for pharmaceutical agents, and treat and/or prevent an above
                                                                                                                                                                                                                                                                                                                                           Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monoclonal antibody; heavy metal; mercury; variable region;
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Pred. No. 3.7;
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                                                                                                                                                                                                                                                                                                                                           100.0%;
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wagner FW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1995-275415/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 GYSFTGY 24
                                                                                                                                                                                                                                                                                                      111 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              heavy chain.
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an appropriate V region primer. In addition, the VH primer AAQ97518 was used to amplify the mAb 2D5 and 5B6 heavy chains. The sequences of the PCR amplified nucleotides were determined. These are given in AAQ97498-097510 and the deduced AA sequences in AAR79241-R79250 & AAR78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45 and in the claims are different from the descriptions in the sequence listings are
chain expressed by the hybridoma of interest, or to the 5' and of the C kappa domain. Some of the primers used for cDNA synthesis are shown in AAQ97511-Q97518. The primer used for cDNA synthesis of the variable region of a particular antibody polypeptide was also used for PCR amplification of that variable region, in conjunction with
                                                                                                                                                                                                                                                                                                                                                                                114 AA;
                                                                                                                                                                                                                                                                                                                         used here.
                                                                                                                                                                                                                                                                                                                                                                             Sequence
     050000000000000x8
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ö 100.0%; Score 41; DB 16; Length 114; 100.0%; Pred. No. 3.8; ive 0; Mismatches 0; Indels ( Best Local Similarity 100. Matches 7; Conservative 20 GYSFTGY 26 1 GYSFTGY 7 Query Match 8

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Gaps

RESULT 9

AAB50793 standard; Protein; 114 AA. (first entry) 21-MAR-2001 AAB50793; 

Murine antibody S2C6 heavy chain variable region.

Mouse; antibody; S2C6; heavy chain variable region; CD40; cancer; inflammatory disease; immune system disorder.

Mus musculus.

WO200075348-A1

14-DEC-2000

08-JUN-2000; 2000WO-US15749.

99US-0328296. 08-JUN-1999;

(SEAT-) SEATTLE GENETICS INC

Fell HP; Francisco JA, Siegall CB, Wahl AF,

WPI; 2001-071080/08 N-PSDB; AAC91890 Anti-CD40 antibodies which immunospecifically bind CD40, useful for prevention and treatment of cancer, inflammatory diseases and disorders or deficiencies of immune system

Claim 3; Fig 2; 91pp; English.

The present invention provides the protein and coding sequences of anti-CD40 antibodies. These can be used in the treatment of cancer and inflammatory and immune system diseases, including systemic lupus erythematosus, scleroderma, inflammatory myositis, Sjogren's syndrome, mixed connective tissue disease, rheumatoid arthritis, multiple sclerosis, inflammatory bowel disease, acute respiratory distress syndrome, pulmonary inflammation, osteoporosis, delayed type hypersensitivity, asthma, primary biliary cirrhosis and idiopathic thrombocytopaenic purpura.

114 AA; Sequence

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hoogenboom HRJ, Griffiths AD;
Clackson TP, Chiswell DJ;
                                                                                                                                                                                                                                                                                         Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus; g3p; binding; adsorption; gene VIII; diverse repertoire; specific binding pairs; replicable genetic display package.
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100.0%; Score 41; DB 22; Length 114; 100.0%; Pred. No. 3.8;
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                                                                                                                                                                                                                                                            Murine VH group 1 chain D specific for phOx.
                              0; Mismatches
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/label= CDR3
/note=" D/N-X-G-X-X motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McCafferty J, Pope AR, Johnson KS,
Jackson RH, Holliger KP, Marks JD,
Winter GP, Bonnert TP;
                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 21; Fig 24; 209pp; English.
                                                                                                                                                                    AAR21267 standard; Protein; 115 AA.
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/label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                   50..66
/label= CDR2
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90GB-0022845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91GB-0010549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAMB-) CAMBRIDGE ANTIBODY.
                                                                                                                                                                                                                               (first entry)
               Best Local Similarity 100.
Matches 7; Conservative
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                                                                                         26 GYSFTGY 32
                                                            1 GYSFTGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-OCT-1990;
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                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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                                                                                                                                                                                                   AAR21267;
 Query Match
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Murine, immunoglobulin; CDR; non immunogenic; cytomegalovirus; gH; heavy chain; variable region; framework; human; Wol.

Location/Qualifiers

Mus musculus

/note= "CDR"

Region Region

Humanised VH region of the mouse CMV5 antibody.

13-JAN-1993

AAR25730;

AAR25730 standard; Protein; 119 AA

RESULT 12 AAR25730

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one, "E", being of gp 2 (VHox1). Of the twenty three clones sequenced, three were of type "D". Most of the clones were Vk-d combinations. The Kd of VH-B/Vk-d for phox-GABA was 10 nM Only two other combinations (of eleven tested) were found to have higher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequences given in AAR27008-11 are fragments which were used in the construction of an agent for the treating and prevention of hypercalcaemia. The agent contained a portion of the antihuman parathyroid hormone-related protein monoclonal antibody (antihuman PTHYP MAb). The MAb was used as the active component in the agent. The agent further comprises a rodent/human chimeric MAb which has a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antihuman parathyroid hormone-related protein; monoclonal antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             variable region; rodent/human chimeric MAb; constant region; PTHrP
                                                              values. This suggests that phage bearing scFv fragments having weak affinities can be selected with antigen, probably due to the avidity of the multiple antibody heads on the phage. See also AAR21260-307, 309-311; AAR22450, 565-581.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rodent variable region and a human constant region and recognises
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                                                                                                                                                                          DB 13; Length 115;
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                                                                                                                                                                         100.0%; Score 41; DB 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypercalcaemia agent portion 3.
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Best Local Similarity luv.
7; Conservative
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Best Local Similarity
7; Conserv?
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N-PSDB; AAQ28522.
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                                                                                                                                                                                                                                       1 GYSFTGY 7
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The sequence shows the humanised mature heavy chain variable region of the mouse CMV5 antibody. Murine CDRs were used in a human WO I framework to produce a pure humanised immunoglobulin (Ig) which is capable of binding to the gH gHycoprotein of cytomegalovirus. The Ig is non immunogenic, due to the human framework, and has a strong affinity for its predetermined antiqen. They can be produced in large quantities via recombinant DNA and monoclonal antibody technology. The humanised Igs may be used alone or in combination with chemotherapeutic agents such as see also AAR25721-32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New immunoglobulin(s) having murine CDRs in human framework regions - have lower antigenicity; useful for treating e.g. HSV, CMV, T-cell disorders, myeloid disorders and auto-immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schneider WP;
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                                                                                                                                                                                                            'note= "mutated residue"
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Gaps

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Mismatches

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Homo sapiens
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                        RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a method of producing humanised immunoglobulins involving expressing in a cell a nucleic acid encoding a humanised version of an immunoglobulin. This is obtained by comparing a donor and human immunoglobulin and producing a combined antibody which contains part of each. These are useful in the treatment of
                                                                                                                                                                                                                                              Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes; light chain; graft versus host disease; transplant; autoimmune disease; multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus; myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Producing humanized immunoglobulin, involves producing a cell containing DNA segments encoding humanized heavy and light chain variable regions, and expressing the DNA segments in the cell -
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                                100.0%; Score 41; DB 13; Length 119; 100.0%; Pred. No. 3.9; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                         Humanised CMV5 antibody heavy chain SEQ ID NO: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Producing humanized immunoglobulin,
                                                                                                                                                       AAB69680 standard; Protein; 119 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Fig 6, 145pp, English.
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89US-0310252.
90US-0590274.
90US-0634278.
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1es 7; Conservative
                                            Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                 GYSFTGY 32
                                                                           1 GYSFTGY 7
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           119 AA;
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13-FEB-1989;
28-SEP-1990;
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                                                                                                                                                                                                                                                                                                                  Homo sapiens,
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           Sequence
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26 GYSFTGY 32

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immunoglobulins involving expressing in a cell a nucleic acid encoding a humanised version of an immunoglobulin. This is obtained by comparing a donor and human immunoglobulin and producing a combined antibody which contains part of each. These are useful in the treatment of graft-versus-host disease, transplant rejection, autoimmune diseases such as diabetes, rheumatoid arthritis, myasthenia gravis, multiple sclerosis and systemic lupus erythematosus, herpes infections, CMV virus infections demonstrate the method of the invention.
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                                                                                                                                                                                                       Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes; light chain; graft versus host disease; transplant; autoimmune disease; multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus; myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Producing humanized immunoglobulin, involves producing a cell containing DNA segments encoding humanized heavy and light chain variable regions, and expressing the DNA segments in the cell-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a method of producing humanised
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. 3.9;
0;
                                                                                                                                                        Human Wol antibody heavy chain SEQ ID NO: 89.
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Pred. No.
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AAB69692 standard; Protein; 119
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Best Local Similarity 100.
Matches 7; Conservative
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when the VH (AARR8752) and VL (AAR88753) regions of anti-DNP scFv U7.6 were expressed in COS-7 cells transfected with a vector carrying the encoding DNA sequences (AAT12612 and AAT12613), only low levels of secretion were achieved; exit from the endoplasmic reticulum was identified as the rate-limiting step. Increasing the degree of glycosylation of the scFv, by replacing VH Lysl9 with Asn (see also AAR88754), increased the secretion rate. Additional glycosylation can also decrease antigenicity, modify ligand binding affinity and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Single-chain Fv molecules with additional glycosylation sites increased rates of secretion, decreased antigenicity, modified ligand binding affinity and are protected from proteolytic degradation
                                              Single-chain Fv molecules with additional glycosylation sites increased rates of secretion, decreased antigenicity, modified ligand binding affinity and are protected from proteolytic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A modified VH chain (AAR88754) of anti-DAP scFv U7.6 (see also
                                                                                                                                                                                                                                                                                                                                                                         Score 41; DB 17; Length 120;
Pred. No. 3.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Single-chain Fv; scFv; glycosylation; protein secretion; endoplasmic reticulum; antibody engineering.
                                                                                                                                                                                                                                                                                                                                                                                                          .
                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Glycosylation site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR88754 standard; Protein; 120 AA.
                                                                                                                                    Claim 6; Page 40-41; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CREA-) CREATIVE BIOMOLECULES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 7; Page 42; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Segal DM;
                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95WO-US10348.
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                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                         protect from proteclysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jost CR,
WPI; 1996-139645/14.
N-PSDB; AAT12612.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    scFv U7.6 VH (K19N)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 GYSFTGY 32
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GYSFTGY 7
                                                                                                                                                                                                                                                                                                                                            120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9605228-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Huston JS,
                                                                                                   degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR88754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR88754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence is that of the U7.6 heavy chain variable region produced by PCR from murine mRNA using the CH1-Xba primers. The protein was used to produce a fusion protein of light chain variable region-linker-heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                          Delivering agents to target cells - where monospecific binding proteins are administered to a host and bind to target cells, followed by admin. of multivalent antibodies to direct the agents to the target cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single-chain Fv, scFv, glycosylation, protein secretion, endoplasmic reticulum, antibody engineering.
                   Marker; antibody; single chain Fv fusion protein; sFv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 41; DB 1
100.0%; Pred. No. 3.9;
ive 0; Mismatches
                                                                                                                                                                                                                       (CREA-) CREATIVE BIOMOLECULES INC.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CREA-) CREATIVE BIOMOLECULES INC.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR88752 standard; Protein; 120 AA.
                                                                                                                                                                                                                                                                           Segal DM
                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 3; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Segal DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95WO-US10348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94US-0292124.
                                                                                                                                                                                         93US-0002324.
                                                                                                                                                        94WO-US00261.
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Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                             George AJT, Huston JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jost CR,
                                                                                                                                                                                                                                                                                                           WPI; 1994-248905/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  See also AAR59984-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GYSFTGY 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GYSFTGY
                                                                                                                                                                                                                                                                                                                            N-PSDB; AAQ69933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-AUG-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCFV U7.6 VH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9605228-A1
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                                                     Mus musculus
                                                                                                                                                        17-JAN-1994;
                                                                                                                                                                                         38-JAN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-FEB-1996.
                                                                                                                        21-JUL-1994.
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                                                                                      WO9415642-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR88752;
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AAR88752

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This invention describes a novel antibody specifically recognizing phosphatically institution. A.f.-triphosphate (PIP3). The antibody of the invention is used in immunogenic compositions in which a dead Salmonella genue microbe is used as an adjuvant and mixed with PIP3. The antibody can be used in an immunoassay containing a step in which the above antibody or its variable region is reacted with PIP3 present in sample and the bond based on their immunological reaction. The method the mutrine PIP3 easily in a high sensitivity. This sequence represents the mutrine pIP3 recognizing monoclonal antibody variable region heavy chain described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murine; p53 protein; PAb-421; monoclonal antibody; mAb; IDI-2; anti-idiotypic antibody; DNA-binding domain; dermatological; immunosuppressive; antiinflammatory; autoimmune response; SLE; systemic lupus erythematosus; diagnosis; treatment; autoantigen; heavy chain variable region; VH; complementarity determining region; CDR.
                                                                            Murine PIP3 recognizing Mab variable region heavy chain protein.
                                                                                                             PIP3; phosphatidylinositol-3,4,5-triphosphate; variable region; immunogen; antibody; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 41; DB 21; Length 124; 100.0%; Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murine anti-PAb-421 IDI-2 mAb heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                              (FUKU/) FUKUI Y. (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phosphatidylinositol-3,4,5-triphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY70791 standard; Protein; 130 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A monoclonal antibody recognizing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 11; 15pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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/label= CDR
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nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-353334/31.
N-PSDB; AAA12202.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GYSFTGY
                                                                                                                                                                                                             JP2000083664-A.
                                                                                                                                                                                                                                                                                                                           07-SEP-1998;
                                                                                                                                                                                                                                                                                        07-SEP-1998;
                                           11-AUG-2000
                                                                                                                                                                                                                                                  28-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-JUL-2000
     AAY87655;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Region
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Matches
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ID AAY7
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                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Humanisation of antibodies - by molecular modelling of the variable domains and alteration by gene conversion mutagenesis
                 position 19. The asparagine site increases the degree of glycosylation of recombinant scrv U7.6 produced by COS-7 cell transfectants, leading to an increased rate of glycosylation from the endoplasmic reticulum. The method allows scrv molecules sepable of binding to specific ligands to be produced in, and secreted by, eukaryoric cells. Decreased antigenicity and increased resistance to proteolysis may also result from
                                                                                                                                                                                                                                                                    ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
AAR88752) has asparagine substituting for lysine at amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 41; DB 14; Length 122; 100.0%; Pred. No. 4; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                               DB 17; Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence is that of the heavy chain variable domain of a humanised variant of murine anti-CD3 monoclonal antibody (muxCD3, Shalaby 1992).
                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    huxCD3v9, humanised muxCD3 heavy chain variable domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Humanisation; rapid; monoclonal antibody; anti-CD3
                                                                                                                                                                                                                           100.0%; Score 41; DB 17
100.0%; Pred. No. 3.9;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR30772 standard; protein; 122 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY87655 standard; Protein; 124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 5; 126pp; English.
                                                                                                                                                      additional glycosylation sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92WO-US05126.
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                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Presta LG;
                                                                                                                                                                                                                                                                                                                                 GYSFTGY 32
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                                                                                                                                                                                                                                                                                                       1 GYSFTGY 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GYSFTGY 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9222653-A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carter PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR30772;
                                                                                                                                                                                            Sequence
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RESULT 19 AAY87655 ID AAY8 XX

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The invention relates to an isolated or purified peptide (I) which binds Hepatitis B virus (HBV) core antigen (HBCAG) or HBV E antigen (HBCAG).

(I) is useful for treating or preventing Hepatitis B virus (HBV) infection, by identifying a subject in need of a molecule that inhibits HBV infection, and providing the subject with (I). (I) is also useful for determining the presence of HBV in a biological sample, and for inhibiting B cell mediated processing and uptake of HBCAG and/or HBCAG, by determining whether (I) inhibits B cell mediated processing and uptake of HBCAG and/or HBCAG and/or HBCAG and/or HBCAG and/or HBCAG and/or HBCAG and/or HBCAG and (I) is also useful for modulating an immune system response. (I) is useful as a template for a design of synthetic molecules including peptides, derivatives or modified peptides, coptionized on expression of each of modulating and immune system response. (I) is also useful as biotechnological tool, diagnostic reagent and as active inqueredient in pharmaceuticals. (I) is also useful as detection reagents in conventional immunchiscochemical techniques, as diagnostic reagents to detect HBV in protocol by monitoring the levels of HBCAG and/or HBCAG and/or HBCAG and to the efficiency of an HBV treatment protocol by monitoring the levels of HBCAG and/or HBCAG and during and after treatment. AMUTO766, AMUTO766, represent HBCAG and with a protocol by monitoring the levels of HBCAG and/or HBCAG and and a protocol by monitoring the levels of HBCAG and/or HBCAG and/or HBCAG and/or HBCAG and/or HBCAG and/or
                                                                                                                                                                                                                                        Novel peptide that binds to hepatitis B virus core or E antigen, useful for treating and preventing hepatitis B virus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Humanised antibody, variable heavy region; buried residue modification; VH; HuMc3 VH; BA46 antigen; human; milk fat globule; HMFG; lactation; fat globule membrane; murine; mammal; epithelial cell; breast cancer; breast membrane glycoprotein; therapy; immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antigen (HBcAg) or HBV E antigen (HBeAg) binding partners as described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 41; DB 2 100.0%; Pred. No. 4.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW06446 standard; Protein; 136 AA.
                                                                                                                                                                                                                                                                                                                         Claim 2; Page 11; 82pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HuMc3 VH region BR-R version.
                           21-APR-2000; 2000US-0556605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95WO-US11683
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Best Local Similarity luv.
7; Conservative
                                                                                                                                                                                      VPI; 2002-055347/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 GYSFTGY 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GYSFTGY
                                                                                (TRIP-) TRIPEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW06446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 22
  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The patent discloses a method for the treatment of systemic lupus erythematosus (SLE) by down-regulating the autoimmune response to the C-terminal DNA-binding domain of p53 protesin by an active compound. The present sequence is a heavy chain variable region of IDI-2 an anti-idiotypic antibody/Ab2 monoclonal antibody (mAb) specific for PAb-421 which is an Ab1 mAb specific to the C-terminal DNA-binding domain of murine p53 protein. The Ab1 and Ab2 mAbs and peptides based on complementarity determining regions of light and heavy chain variable regions of these antibodies, are examples of active compounds useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis B virus, virucide; immunomodulator; hepatotropic; HBV; antiinflammatory; HBV core antigen; HBcAg; HBV E antigen; HBeAg; B cell mediated processing; T cell proliferation; cytokine production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treatment of systemic lupus erythematosus by down-regulating the autoimmune response to the C-terminal DNA-binding domain of the p53 protein by an active compound comprising of antibodies to p53 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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'note= "Complementarity determining region"
                                                                                "Complementarity determining region"
                                                                                                                                                             /note= "Complementarity determining region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the diagnosis, prevention and treatment of SLE in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis B virus antigen binding partner 9C8 VH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Herkel J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 41; DB 2
100.0%; Pred. No. 4.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Erez-Alon N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 78; Fig 9; 87pp; English.
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                           50..66
/label≂ CDR
                                                                                                      99..113
/label= CDR
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Best Local Similarity 100..
7, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rotter V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-339512/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||||||||
GYSFTGY 32
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07-JUN-1995; 16-SEP-1994;

20-APR-2001; 2001WO-IB00844.

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                                                                                                                                                                                                                                                                                                                                                                                                   AAR38259
    Dp
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                                                                                                                                           murine antibody Huxca VI. The Most Will, was humanised using the buried residue retention (BR-R) technique. The Most sequences can also be modified using the buried residuemedification, where important non-human framework residues are unaffected (see AAW06442 and AAW06443). The Most antibody binds to the BA46 antigen of the human milk fat globule (HMG5). The milk fat globule membrane is derived from the apical surface of the mammalian epithelial cell during lactation, and therefore is a source for breast membrane glycoproteins. The antibody can be used in an intro method to detect a HMG5 antigen (or antigen fragment), and to diagnose the presence of the antigen in a subject. The antibody can also be used to deliver an agent to a target (within a subjects body). Containing a HMG5 antigen. The antibodies can also be used for the humanised antibodies retain their high affinity binding to the antigen, they are useful for immunodiagnostic and immunotherapeutic
                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Humanised antibody; variable heavy region; buried residue modification; VH; HuMc3 VH; BA46 antigen; human; milk fat globule; HMFG; lactation; fat globule membrane; murine; mammal; epithelial cell; breast cancer; breast membrane glycoprotein; therapy; immunotherapy.
                                                                                                                                    This sequence represents the variable heavy (VH) chain of the humanised
                                                                 Recombinant Mc3 antibody which binds BA46 antigen of HMFG -comprises a modified heavy or light chain variable region, useful in the diagnosis and therapy of breast cancer
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 41; DB 1.
100.0%; Pred. No. 4.5;
ive 0; Mismatches
                        Ceriani RI, Do Couto FJR, Peterson JA;
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(CANC-) CANCER RES FUND CONTRA COSTA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW06442 standard; Protein; 136 AA.
                                                                                                               Example 7; Fig 14; 91pp; English.
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                                                                                                                                                                                                                                                                                                                                                  Query Match
Query Match
Best Local Similarity 100.00
Best Local Similarity 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                  applications in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-179941/18.
N-PSDB; AAT42717.
                                           WPI; 1996-179941/18
                                                                                                                                                                                                                                                                                                                                                                                                                        GYSFIGY 51
                                                                                                                                                                                                                                                                                                                                                                                                           1 GYSFTGY 7
                                                                                                                                                                                                                                                                                                                                          136 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HuMc3 VH region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-FEB-1997
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16-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 23
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This sequence represents the variable heavy (VH) chain of the humanised murine antibody HuMc3 VH. The Mc3 VH sequence was humanised using the buried residue modification technique, where important non-human framework residues are unaffected. The Mc3 antibody binds to the BA46 antigen of the human milk fat globule (HMFG). The milk fat globule common the far globule (HMFG). The milk fat globule coll during lactation, and therefore is a source for breast membrane glycoproceins. The antibody can be used in an in vitro method to detect antigen (or antigen for antibody can be used in an in vitro method to detect antigen in a subject. The antibody can also be used to deliver an agent to a target (within a subjects body), containing a HMFG antigen. The antibody can also be used to deliver an agent to a target (within a subjects body), containing a HMFG antigen. The antibodies can also be used for diagnosis, prognosis, and therapeutic applications of breast cancer. As the humanised antibodies retain their high affinity binding to the antigen, they are useful for immunodiagnostic and immunotherapeutic applications in humans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Recombinant Mc3 antibody which binds BA46 antigen of HMFG -comprises a modified heavy or light chain variable region, useful in the diagnosis and therapy of breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polymerase chain reaction; primer; PCR; amplify; murine; heavy; light; chain; variable; constant; region; anti-human; transferrin; receptor; antibody; brain; capillary; endothelial cell; conjugate; neuropharmaceutical; diagnostic; agent; tumour; AIDS; stroke; epilepsy; Parkinsons disease; Alzheimers disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 41; DB 17; Length 136; 100.0%; Pred. No. 4.5; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric 128.1 VH, mouse kappa subgroup IIB.
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                                                                                                                                       Claim 13; Fig 18; 91pp; English
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/label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18..126
/label= CDR3
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/label= FR4
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/label= FR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0..50
|abel= FR1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
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/label=
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|abel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GYSFTGY
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pAH4807. This vector represents the cloning of the human gamma isotype, gamma 3, with the variable region of the murine monoclonal antibody 128.1. This plasmid encodes a chimeric monoclonal antibody in which the heavy chain (VH) is derived from a murine source and the sequences encoding CH1. CH2 and CH3 are derived from a human source. This vector, in combination with the chimeric light chain vector, pAG4611 (see also AAQ43845), was transfected into SP2/0 cells and clones were isolated. 128.1 is an anti-human transferrin receptor antibody which binds to the transferrin receptor on brain capillary endothelial cells. This antibody may be used in a conjugate in which it is linked used to prevent neurological disorders eg. brain tumours, also be used for diagnostic methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequences given in AAR41710-14 are encoded by the expression vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polymerase chain reaction, primer; PCR; amplify; murine; heavy; light; chain; variable; constant; region; anti-human; transferrin; receptor; antibody; brain; capillary; endothelial cell; conjugate; neuropharmaceutical; diagnostic; agent; tumour; AIDS; stroke; epilepsy; Parkinsons disease; Alzheimers disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cimeric antibody comprising VH from 128.1 and CH from human gammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 41; DB 14; Length 233; 100.0%; Pred. No. 7.5;
                                                                                                                                                                                                                                                                                                                                                                       Antibody conjugates specific for transferrin receptor - used for diagnosis and treatment of cancer, AIDS and neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Fig 18G-H; 151pp; English.
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                    138..233
/label= CH1
                                                                                                                                                         92WO-US10206
                                                                                                                                                                                               91US-0800458
/label= FR4
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Matches 7; Conservative
                                                                                                                                                                                                                                    (ALKE-) ALKERMES INC.
                                                                                                                                                                                                                                                                                                                    WPI; 1993-196742/24.
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                                                                                                                                                           4-NOV-1992;
                                                                                                                                                                                               26-NOV-1991;
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                                                                             WO9310819-A.
                                                                                                                    10-JUN-1993.
                                                                                                                                                                                                                                                                           Friden PM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                  disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Peptide
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AAR41682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                    The sequences given in AAR38258-59 represent the light and heavy chains respectively, of the chimeric antibody 128.1. 128.1 is an anti-human transferrin receptor antibody which binds to the transferrin receptor on brain capillary endothelial calls. This antibody may be used in a conjugate in which it is linked to a neuropharmaceutical or diagnostic agent. The conjugate may be used to treat or prevent neurological disorders eg. brain tumnours, AIDS, stroke, epilepsy, Parkinsons and Alzheimers disease. It may also be used for diagnostic methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625; heavy; light; chain; variable; constant; region; anti-human; pAH4807; transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2; endothelial cell; conjugate; neuropharmaceutical; gamma-3; gamma-4; diagnostic; agent; tumour; AIDS; stroke; epilepsy; monoclonal; Parkinsons disease; Alzheimers disease; SP2/0 cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                  Antibody conjugates specific for transferrin receptor - used for diagnosis and treatment of cancer, AIDS and neurological disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine 128.1 VH/human gamma-3 CH1 encoded by plasmid pAH4807.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 14; Length 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 41; DB 1
100.0%; Pred. No. 4.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "Leader peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR41710 standard; Protein; 233 AA.
                                                                                                                                                                                                                                                                                                                  Table 6; Page 57; 151pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69..85
/label= CDR2
86..117
/label= FR3
118..126
/label= CDR3
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/label= CDR1
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/label= FR2
                    92WO-US10206
                                                           91US-0800458
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Query Motch
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Best Acan 7; Conservative
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/label=
                                                                                                  (ALKE-) ALKERMES INC
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GYSFTGY 51
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                                                                                                                                                                                                 N-PSDB; AAQ43843
                                                           26-NOV-1991;
                    24-NOV-1992;
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                                                                                                                                          Friden PM;
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RESULT 25

Peptide Region Region Region Region Region Region Region

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(first entry)

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Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625; heavy; light; chain; variable; constant; region; anti-human; pAH4807; transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2; endothelial cell; conjugate, neuropharmaceutical; gamma-3; gamma-4; diagnostic; agent; tumour; AIDS; stroke; epilepsy; monoclonal; Parkinsons disease; Alzheimers disease; SP2/0 cell.
                                    Murine 128.1 VH/human gamma-2 CH1 encoded by plasmid pAH4625.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibody conjugates specific for transferrin receptor - used for diagnosis and treatment of cancer, AIDS and neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ALKE-) ALKERMES INC
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                                                                                                                                              Synthetic
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   The sequences given in AAR41682-85 are encoded by the expression vector, pAH4602. This vector contains open reading frames encoding the heavy chain variable region (VH) of the antibody 128.1, an ampicillin resistance gene and a histidine (histidinol) selection marker. Transcription of the VH gene is from the VH promoter of the murine 27.44 gene. The vector also includes a heavy chain immunoglobulin enhancer and the human gammal constant region (CH). The VH region of 128.1 was isolated by polymerase chain reaction and cloned into plasmid pAH4274. This was achieved by digesting the plasmid and the product with EcoRV and NheI. The VH gene was inserted in-frame with the human gammal CH region CH at the 3' end of the VH-J region by means of a NheI site. 128.1 is an anti-human transferrin receptor antibody which binds to the transferrin receptor on brain capillary endothelial cells. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibody may be used in a conjugate in which it is linked to a neuro-pharmaceutical or diagnostic agent. The conjugate may be used to treat or prevent neurological discorders eg. brain tumours, AIDS, stroke, epilepsy, Parkinsons and Alzheimers disease. It may also be used for
                                                                                                                                                                                                                                                                                                                                                                                          Antibody conjugates specific for transferrin receptor - used for diagnosis and treatment of cancer, AIDS and neurological disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 41; DB 14; Length 235; 100.0%; Pred. No. 7.6; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                  /note= "Human gamma1 CH"
                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 11H-I; 151pp; English
            note= "128.1 HV"
                                                                      57..85
/label= CDR2
86..117
/label= FR3
                                                                                                                     118..126
/label= CDR3
127..137
/label= FR4
                                                 30..56
/label= CDR1
                          20..49
/label= FR1
                                                                                                                                                                                                                                                         92WO-US10206
                                                                                                                                                                                                                                                                                                       (ALKE-) ALKERMES INC
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N-PSDB; AAQ43844.
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                                                                                                                                                                                                                                                         24-NOV-1992;
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"Leader peptide"

note=

20..50 /label= FR1

L= CDR1

51..55 /label=

69..85 /label= CDR2 86..117 /label= FR3 18..126 |abel= CDR3 127..137 /label= FR4

56..68 /label= FR2

138..235 /label= CH1

92WO-US10206. 91US-0800458

Location/Qualifiers

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The sequences given in AAR41707-09 are encoded by the expression vector pAH4625. This vector represents the cloning of the human gamma isotype, gamma-2, with the variable region of the murine monoclonal antibody 128.1. This plasmid encodes a chimeric monoclonal antibody in which the heavy chain (VH) is derived from a murine source and the sequences encoding CHI, CH2 and CH3 are derived from a human source. This vector, in combination with the chimeric light chain vector, pAG4611 (see also AAQ43845), was transfected into SP2/0 cells and clones were isolated. 128.1 is an anti-human transferrin receptor antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                were isolated. 128.1 is an anti-human transferrin receptor. which binds to the transferrin receptor on brain capillary endothelial cells. This antibody may be used in a conjugate in which it is linked to a neuropharmaceutical or diagnostic agent. The conjugate may be used to treat or prevent neurological disorders eg. brain tumours, AIDS, stroke, epilepsy, Parkinsons and Alzheimers disease. It may
Disclosure, Fig 17G-H; 151pp; English.
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Gaps

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Best Local Similarity 100. Matches 7; Conservative

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1 GYSFTGY 7

AAR41707 standard; Protein; 235 AA.

AAR41707

AAR41707 ID AAR4 XX AC AAR4 RESULT

clones

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Gaps

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in which the heavy chain (VH) is derived from a murine source and the sequences encoding CH1, CH2 and CH3 are derived from a human source. This vector, in combination with the chimeric light chain vector, pAG4511 (see also AAG43845), was transfected into SP2/0 cells and clone were isolated. 128.1 is an anti-human transferrin receptor antibody which binds to the transferrin receptor on brain capillary endothelial cells. This antibody may be used in a conjugate in which it is linked to a neuropharmaceutical or diagnostic agent. The conjugate may be used to treat or prevent neurological disorders eg. brain tumours, AIDS, stroke, epilepsy, Parkinsons and Alzheimers disease. It may
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region 2"
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223..231
/note= "light chain complementarity determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "heavy chain complementarity determining
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "heavy chain complementarity determining
                                                                                                                                                                                                                   Score 41; DB 14; Length 235;
Pred. No. 7.6;.
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       stomach cancer; squamous cell cancer; antitumour; therapy;
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                                                                                                                                         AIDS, stroke, epilepsy, Parkinsons a also be used for diagnostic methods.
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                                                                                                                                                                                                                                                                                                                                                                                               ABB76197 standard; Protein; 241 AA.
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100.0%;
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Best Local Similarity 1000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis; immunotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=
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                                                                                                                                                                                                                                                                                                                  5
                                                                                                                                                                                          235 AA;
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                                                                                                                                                                                                                                                                                                       45 GYSFTGY
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                                                                                                                                                                                                                                                                                                Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625; heavy; light; chain; variable; constant; region; anti-human; pAH4807; transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2; endothelial cell; conjugate, neuropharmaceutical; gamma-3; gamma-4; diagnostic; agent; tumour; AIDS; stroke; epilepsy; monoclonal; Parkinsons disease; Alzheimers disease; SP2/0 cell.
                                   Gaps
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   100.0%; Score 41; DB 14; Length 235; 100.0%; Pred. No. 7.6; ive 0; Mismatches 0; Indels
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                                                                                                                                                                            AAR41715 standard; Protein; 235 AA
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/label= CDR3
127..137
/label= FR4
138..235
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/label= CDR2
86..117
/label= FR3
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/label= CDR1
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/label= CH1
                                                                                                                                                                                                                                      (first entry)
   Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
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/label= 1
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                                                                7
                                                                  GYSFTGY
                                                                                              GYSFTGY
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                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
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                                                                                                                                             RESULT 28
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mesothelioma; ovarian cancer;

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17-0CT-2000; 2000US-240816P.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
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                                        27-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-JUN-2000;
17-OCT-2000;
 07-DEC-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-JAN-2002,
                                                                                  Pastan I,
                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP45937;
                                                                                                                                                            cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP45937
 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                       The present sequence is the protein sequence of anti-mesothelin scFV antibody SS. This single-chain antibody was produced by immunising a mouse with cDNA encoding mesothelin, creating a phage library from mRNA isolated from the spleen of the immunised animal, and enrichment of anti-mesothelin phage over 3 rounds of panning. scFV SS is composed of a heavy chain variable region (WH) joined to a light chain variable region (WL) via a peptide linker. According to Kabat's classification, the VH belongs to sub-group IIA and family V and the VL belongs to sub-group IIA and family V and the VL belongs to sub-group IIA and adissociation constant of less than 3 x 10 power -8 M and specifically pinds to cells expressing mesothelin on their cell surface. The antibody comprises SS scFV, the VH and VL region of SS scFV or the complementarity determining regions of SS scFV. It is preferably conjugated to a therapeutic agent, particularly becudomonas exotoxin or its cytotoxic fragment. The resulting the growth of a mailgnant cell that expresses mesothalin on its call cancer. The antibody can also be used to detect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 41; DB 20; Length 241; 100.0%; Pred. No. 7.8; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mesothelin; SS antibody; single-chain Fv; scFv; cytostatic; cancer therapy; ovarian cancer; mesothelioma.
                  "light chain framework region 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antimesothelin antibody SS single-chain Fv protein.
                                                                                                                          (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB50019 standard; protein; 241 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          mesothelin in a biological sample.
region 3"
                                                                                                                                                                                                   New anti-mesothelin antibodies
                                                                                                                                                                                                                       Claim 2; Fig 1; 63pp; English.
                                                                                  98WO-US25270.
                                                                                                      97US-0067175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
         232..241
/note= "1
                                                                                                                                              Chowdhury PS;
                                                                                                                                                                    WPI; 1999-371123/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GYSFTGY 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GYSFTGY 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 AA;
                                                                                                                                                                               N-PSDB; ABL57231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200073346-A1
                                                                                 25-NOV-1998;
                                                                                                      01-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
                                        WO9928471-A2
                                                            10-JUN-1999
                                                                                                                                               Pastan IH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB50019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
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BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive, immunostimulati, immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immundeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is antimesothelin antibody SS single chain Fv protein. This sequence was used to generate mutant antibody heavy or light chain variable regions, which have 5 times higher binding affinity for mesothelin antigen than the parental antibody (the present sequence). The mutant proteins of the present invention have substition(s) in the complementarity determining region (CDR). Malignant cells express mesothelin on their surfaces, and so the mutant proteins of the present invention can be used to target immunoctoxin to cells expressing the present invention can their surface i.e. malignant cells. The mutant proteins of the present invention can therefore be used to treat ovarian cancers, mesotheliomas, and several other types of human cancers in which the cells bear the mesothelin antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                       Novel polypeptides comprising mutated antimesothelin antibody heavy o
light chain variable region, having greater binding affinity for the
antigen, useful as diagnostic and therapeutic agents for ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 41; DB 22; Length 241; 100.0%; Pred. No. 7.8; ive 0; Mismatches 0; Indels
                                                                                                                                                                   USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human BLyS binding scFv SEQ ID 1948.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP45937 standard; Protein; 241 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 1; 70pp; English.
26-MAY-2000; 2000WO-US14829
                                                                                    99US-0160071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                       Chowdhury PS;
                                                                                                                                                                                                                                                                                                                                       WPI; 2001-061517/07.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GYSFTGY 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 AA;
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Gaps

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Length 243; Indels

Ruben ŚM,

(HUMA-) (CAMB-)

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This sequence represents an example of a secreted single chain antibody Fv fragment (in this case, directed against the 5T4 antigen), which is involved in transcellular localisation. A secreted single chain antibody Fv fragment can be fused to cytochrome P450 reductase (P450R) derivatives such as anchorless P450R (AAY42287) or FN fragment (AAY42288). This enables the fusion protein to be delivered to other ectls where it is then transported to the nucleus. Many drugs' sites of action are in the nucleus, rather than the cytoplasm, where P450R normally functions. P450R or its derivatives can be used to activate prodrugs to their active form via reduction. Administration of a prodrug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytochrome, targetting; localisation; cancer; tumour; prodrug; reduction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New prodrug activating agent targeted to selected cells or tissues, particularly hypoxic cells, for treating e.g. tumors -
                                                                                                                                       MAb capable of binding to the gamma chain of the IL-2 receptor, and thus of blocking the IL-2 response, is produced by mouse hybridoma line GP-4 (FREM BP-4640). DNA encoding the variable region of this MAb was expressed in E. coli, yielding Fv(GP-4) with
                                    Immunosuppressant polypeptide - has ability to block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-5T4 secreted single chain antibody Fv fragment.
                                                                                                                                                                                                                                                                               Score 41; DB 15; Let
Pred. No. 7.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patterson AV, Kingsman SM,
                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                 Claim 9; Page 27-28; 37pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY42294 standard; Protein; 243 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 9; Fig 3; 187pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (OXFO-) OXFORD BIOMEDICA UK LTD
                                                                                                                                                                                                                                                                                                       100.0%;
100.0%;
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98GB-0018103:
99GB-0002081.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-GB00674.
                                                                                                                                                                                                                          immumosuppressive activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-DEC-1999 (first entry)
                                                                                                                                                                                                                                                                                    interleukin-2 response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-551046/46.
                                                                                                                                                                                                                                                                                                                                                                                                                              148 GYSFTGY 154
                                                                                                                                                                                                                                                                                                                                                                                        1 GYSFTGY 7
                                                                                                                                                                                                                                                                 243 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAZ19786.
N-PSDB; AAQ73679.
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Mitrophanous K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-MAR-1998;
19-AUG-1998;
29-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9945127-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY42294;
                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY42294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó;
                                                                                                                                                                                                                                                          This invention describes novel antibodies that immunospecifically bind to Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNP) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antitheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common wariable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method
                                                                                                                                                             Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 41; DB 23; Length 241; 100.0%; Pred. No. 7.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAb; monoclonal antibody; hybridoma; interleukin-2; IL-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                Hilbert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nakazawa H, Shimamura T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibody variable region; GP-4; Fv(GP-4);
                                                                              Choi GH, Vaughan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                          Claim 1; Page 2725-2726; 3148pp; English
                   HUMAN GENOME SCI INC.
CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR60781 standard; Protein; 243 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93JP-0094491.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94EP-0106257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fv(GP-4) immunosuppressive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Капауаша У,
                                                                                Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AJIN ) AJINOMOTO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1994-325948/41.
                                                                                                                    WPI; 2002-114799/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GYSFTGY 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GYSFTGY 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunosuppressive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-APR-1993;
07-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Takeshita T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-OCT-1994
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Seguence

Query Match

Matches

ð 셤 AAR60781;

Mus sp.

56

Griffiths L;

Kan 0,

Hamura J,

Gaps

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arthritis, or conditions associated with hypoxia, hypoglycemia or ischemia, or conditions associated with hypoxia, hypoglycemia or ischemia, or to deliver antibiotics, antiviral agents, analgesics, anesthetics, anti-inflammatories, antineoplastic agents and diagnostic agents. LD optimize activity of PAD, e.g. by delivering it to selected locations or by delivering it to neighboring cells (bystander effect) and allow a reduction in dose of prodrug, and thus of systemic side-effects. Nucleic acids encoding the agent may be expressed selectively in hypoxic cells. The present sequence represents the single chain variable antibody fragment against the tumor antigen 5T4 (5T4 scPv). 5T4 scPv and a human P450 reductase derivative alP450R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New vector encoding a tumour interacting protein for treating cancer - contains a desired nucleotide sequence and/or protein which recognises tumours, and is used as a gene delivery system to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This amino acid sequence comprises an scFv, termed 5T4scFv.1, comprising the heavy chain variable region (VH) from the murine 5T4 monoclonal antibody followed by a 15-amino acid flexible linker and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumour interacting protein; cancer; gene therapy; vector;
5T4 antigen; monoclonal antibody; single chain antibody; scFv;
mouse; 5T4scFv.1.
                                                                                                                                                                                                                                                          20; Length 243;
                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kingsman SM;
                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murine anti-5T4 antigen monoclonal antibody scFv.
                                                                                                                                                                                                                                                         Score 41; DB 2
Pred. No. 7.9;
                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bebbington CR, Carroll MW, Ellard FM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "encoded by GDT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW86002 standard; Protein; 243 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Fig 1A; 82pp; English.
                                                                                                                                                                                                                                                                                           .;
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                                                                                                                                                                                                                                                         100.0%;
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97GB-0011579.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric - Mus sp.
Chimeric - synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-059910/05.
                                                                                                                                                                                                                                                                                                                                                          26 GYSFTGY 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAV80290.
                                                                                                                                                                                                                           243 AA;
                                                                                                                                                                                                                                                                                                                           1 GYSFTGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OXFO-) OXFORD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9855607-A2
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                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW86002:
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                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                AAW86002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prodrug, localization domain; tumor-selective antibody; cytochrome P450; prodrug activating domain; modified hematopoietic stem cell; MHSC; tumor; inflammation; atherosclerosis; muscular dystrophy; cerebral malaria; rheumatoid arthritis; hypoxia; ischemia; hypoglycemia; tumor antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention provides a new prodrug activating agent that comprises: (i) a localization domain (LD; other than a tumor-selective antibody) and a prodrug activating domain (PAD); (ii) at least one nucleic acid encoding a cytochrome P450 and under control of at least one constitutive or inducible expression control sequence or (iii) a modified hematopoietic stem cell (MHSC) containing at least one nucleic acid encoding a PAD and under control of elements as in (ii). The prodrug activating agent or vectors that express them, are specifically used to treat tumors, inflammation, atherosclerosis and muscular dystrophy, but may also be
is useful where the active drug may be metabolised before it reaches its site of action or where the active drug is cytotoxic, e.g., anticancer drugs. Targetred delivery of such prodrug activators allows a reduction in dose of the prodrug, and thus of systemic side-effects. P450R derivative fusion proteins, or vectors that express them, are specifically used to treat tumours, inflammation, atherosclerosis and muscular dystrophy, but may also be used to treat many other conditions, e.g., cerebral malaria, rheumatoid arthritis, or conditions associated with hypoxia, ischaemia or hypoglycemia, or to deliver antibiotics, antiviral agents, analgesics, anaesthetics, anti-inflammatories, antineoplastic agents and disgnostic agents.
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New prodrug activating agent targeted to selected cells or tissues, particularly hypoxic cells, for treating e.g. tumors or inflammation
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99GB-0002081.
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Best Local Similarity
7; Conserv?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified
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the light chain variable region (VL) of the mouse 5T4 antibody. The trophoblast cell surface antigen defined by monoclonal antibody 5T4 is expressed at high levels on the cells of a wide variety of human tumours. 5T4scFv.1 DNA (see AAV80290) can be used to construct single-chain antibodies (see AAV80039) and scFv fusion constructs (see AAV860040-05). The invention relates to a vector comprising a nucleotide sequence coding for a tumour interacting protein (TIP) and optionally a nucleotide sequence of interest (NOI) which conditions a protein of interest (POI), the vector being capable of delivering the NOI and/or POI to the tumour recognised by the TIP. Delivery can be in vivo or ex vivo. The vector is used to treat cancer, and may also used as a gene delivery system for introducing at least 1 gene encoding a TIP (preferably a tumour binding protein) conto a haematopoietic cell lineage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Single chain antibody; ScFv; inflammatory disease; arthritis; cancer; hypersensitivity; autoimmune disease; central nervous system disorder; Parkinson's disease; periodontal disease; cardiopulmonary disease; cardiovascular disease; gastrointestinal disorder; infection; diabetes; Helicobacter-related disease; immune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of single chain antibody capable of recognizing a disease associated molecule for manufacturing a medicament for preventing and/or treating a disease condition associated with disease associated
                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                        Mismatches
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Misc-difference 169
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15-FEB-2000; 2000GB-0003527.
02-MAR-2000; 2000GB-0005071.
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Matches
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Claim 3; Fig 1; 118pp; English.

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which is capable of recognizing a disease associated molecule in the manufacture of a medicament for the prevention and treatment of a disease condition. The ScFv antibody is useful in the manufacture of a medicament for affecting a disease in vivo, for preparing a pharmaccutical composition, for in vivo imaging and/or for adjuvant treatment of a disease. The ScFv antibody is also useful for treatment of a disease. The ScFv antibody is also useful for adjuvant treating inflammatory diseases, including arthritis, hypersensitivity, autoimmune diseases, cancers, central nervous system disorders including Parkinson's disease, periodontal diseases, cardiovalumenary diseases, and other immune diseases. The present sequence related diseases, and other immune disorders. The present sequence represents a ST4 ScFv of the invention. The antibody comprises the VH and VL regions from murine ST4 monoclonal antibody, joined by a linker sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BLys; B lymphocyte stimulator; TNF superfamily; human, cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomobulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimme disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
             specification describes the use of a single chain antibody (ScFv)
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibodies against B Lymphocyte Stimulating polypeptides, useful the diagnosis and treatment of cancers and immune disorders -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 2668-2669; 3148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human BLyS binding scFv SEQ ID 1900.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP45889 standard; Protein; 245 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUN-2001; 2001WO-US19110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-MAR-2001; 2001US-276248P
21-MAR-2001; 2001US-277379P
25-MAY-2001; 2001US-293499P
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2001US-276248P
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Best Local Similarity 100.
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Score 41; Pred. No.

100.0%; 100.0%;

Query Match 100. Best Local Similarity 100. Matches 7; Conservative

65 GYSFTGY 71

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1 GYSFTGY

Length 297; Indels

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tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiALDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency syndrome (ALDS)). ABP473290 represent the antibodies and fragments of the antibodies described in the method
                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Single stranded antibody; hepatitis B virus; HBV core protein;
HBV infection; viral proliferation inhibitor; viral DNA synthesis;
gene therapy.
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                                                                                                                                                                                                                                  100.0%; Score 41; DB 23; Length 245; 100.0%; Pred. No. 7.9; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        HBV specific single stranded antibody.
                                                                                                                                                                                                                                                                                                                                                                             AAY05363 standard; Protein; 297 AA.
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Best Local Similarity 100.v.
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                                                                                                                                                                                                                                                                                                                26 GYSFTGY 32
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                                                                                                                                                                                  of the invention.
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fusion protein; recombinant bispecific single chain antibody; helical peptide linker; anti-L6 antibody; tumour cell antigen; anti-CD3 antibody; variable region.

Synthetic

Peptide Region 275..302 /label= Fv\_helical\_linker

94EP-0300692

31-JAN-1994;

10-AUG-1994 EP610046-A.

hinge

272..274 /label= hi

Region Region

Region

/label= (Gly4Ser)3\_linker 1abel= CD3\_VL~VH\_fusion

134..148

label L6\_VL\_leader location/Qualifiers

Bispecific CD3-L6FvIg antibody derivative.

14-MAR-1995

AAR60206;

AAR60206 standard; Protein; 302 AA.

RESULT 39

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amplified by PCR methods. A gene fusion was constructed from the two amplified domains and a (Gly4Ser)3 linker. The amino terminus of the VL-VH fusion cassette was fused at the SalI site to the L6 light chain variable region leader peptide and the carboxy-terminus was fused directly to the hinge region of the FC domain at the BclI site and/or to a short "helical" peptide linker to construct the bispecific CD3-L6FvIg antibody derivative. The variable regions for L6 were fused in frame to the opposite end of
                                                                                                                                                                                                                                                                                                                                                                                                                                         Fell PH, Gilliland LK, Hayden MS, Ledbetter JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Expression vector encoding bispecific fusion protein - having binding domains for separate targets joined by helical peptide, useful e.g. for diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The VL and VH sequences of the anti-CD3 hybridoma G19-4 were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Fig 11 and Page 29-31; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the helical linker (not included in AAR60206)
                                                                                                                                                                                                                                                                                                                                                                                                                 BRIM ) BRISTOL-MYERS SQUIBB CO
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93US-0121054.
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N-PSDB; AAQ81076.
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13-SEP-1993;
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Linsley PS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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This sequence is the single-stranded antibody of the invention, that has the capability of binding to a hepatitis B virus (HBV) core protein. Therapeutic agents can be formulated with the antibody for treatment of HBV infections by stopping proliferation of the virus through inhibition of viral DNA synthesis, and the gene encoding the antibody can be applied as an agent to gene therapy.

297 AA;

Sequence

Single-stranded antibody against hepatitis B virus core protein, applicable as (gene) therapeutic agents for treatment of hepatitis viral infections

Claim 5; Page 55-57; 72pp; English.

Yamamoto M;

Hayashi N, Tohdoh N, Yamamoto H,

WPI; 1999-243623/20.

N-PSDB; AAX33931

(SUMU ) SUMITOMO PHARM CO LTD

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Gaps
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 Length 302;
                            0; Indels
100.0%; Score 41; DB
100.0%; Pred. No. 9.7
:ive 0; Mismatches
  Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
                                                     1 GYSFIGY 7
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||||||| 176 GYSFTGY 182

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AAW86004 standard; Protein; 488 AA AAW86004 ID AAW

AAW86004; 

(first entry) 15-MAR-1999 Human B7-1.5T4.1 protein fusion, specific for human 5T4.

Tumour interacting protein, cancer, gene therapy, vector, 5T4 antigen, monoclonal antibody, single chain antibody; mouse, human, B7-1; co-stimulatory molecule.

Chimeric - Mus sp. Chimeric - Homo sapiens. Chimeric - synthetic.

WO9855607-A2

10-DEC-1998

98WO-GB01627 04-JUN-1998;

04-JUL-1997; 04-JUN-1997; 20-JUN-1997;

97GB-0014230. 97GB-0011579. 97GB-0013150.

(OXFO-) OXFORD BIOMEDICA UK LTD.

Kingsman SM; Ellard FM, Carroll MW, Bebbington CR, Myers KA;

WPI; 1999-059910/05. N-PSDB; AAV80292.

New vector encoding a tumour interacting protein for treating cancer - contains a desired nucleotide sequence and/or protein which recognises tumours, and is used as a gene delivery system to treat cancer

Example 5; Fig 2; 82pp; English

This is the amino acid sequence of B7-1.5T4.1, a fusion protein comprising the extracellular domain (amino acids 1-215) of human co-stimulatory molecule B7-1 joined via a flexible peptide linker to an scFV (see AAW8602) derived from murine 5T4 monoclonal antibody. B7-1.5T4.1 cDNA (see AAV80292) can be inserted into vector por to allow expression of the fusion protein in mammalian cells. The trophoblast cell surface antigen defined by 5T4 is expressed at high levels on the cells of a wide variety of human timours. The invention relates to a vector comprising a nucleotide sequence invention relates to a vector comprising a nucleotide sequence coing for a tumour interact (NOI) which encodes a protein of interest (POI), the vector being capable of delivery can be in vivo or ex vivo. The vector being capable of delivery can be in vivo or ex vivo. The vector is used to treat cancer, and may also used as agene delivery system for introducing at least 1 gene cencoding a TIP (preferably a tumour binding protein) into a mammalian collaboration at TIP (preferably a tumour binding protein) into a mematopoietic cell lineage. B7-1 is expected to bind specifically to CD28 and CTLA-4 present on human T-cells.

488 AA Sequence

ö Gaps .. 0 Query Match
100.0%; Score 41; DB 20; Length 488;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels

1 GYSFTGY

1|||||| 272 GYSFTGY 278

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Search completed: July 18, 2003, 15:06:39 Job time: 28.66 secs

333, 133, 128, 128,

Sequence Sequence Sequence Sequence

Title: Perfect score:

Sequence:

protein

Run on:

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Minimum DB Maximum DB

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Sequence

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GENERAL NO. 591.1524
; GENERAL INFORMATION:
; APPLICANT: Sallberg, Matti
; APPLICANT: Lazdina, Una
TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE
; TITLE OF INVENTION: HEPATITIS B VIRUS CORE AND E ANTIGENS
; TITLE REFERENCE: TRIPEP.020A
; CURRENT APPLICATION NUBER: US/09/556,605
; CURRENT FILING DATE: 2000-04-21
NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 41; DB 4; Length 7; Pred. No. 2e+05;
                            US-09-556-605-3
US-08-525-539A-47
US-08-525-539A-63
US-08-444-644-17
US-08-242-246A-17
US-08-232-246A-13
US-08-232-246A-33
US-08-444-644-28
US-08-444-644-28
US-08-444-644-28
          US-09-257-069-2
PCT-US93-07832-19
                                                                                                                                      US-08-232-246A-19
US-08-232-246A-28
                                                                                                                                                           US-08-232-246A-42
US-08-230-843-4
US-08-636-936-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANIZAM: Artificial Sequence
PRGANIZE:
OTHER INFORMATION: Artificial Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
18-09-556-605-29
Sequence 29, Application US/09556605
Patent No. 6417324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Mus musculus
US-09-257-069-5
1 GYSFTGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GYSFTGY
                                                                                                                                                                                                                                                            US-09-257-069-5
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                                                                                    (without alignments)
25.365 Million cell updates/sec
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Sequence
Sequence
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Sequence
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                                                                         July 18, 2003, 15:03:46 ; Search time 8.12 Seconds
                                                                                                                                                                                                                                                                                                               Issued_Patents_AA:*
: /cgn2_6/ptodata1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata1/iaa/6B_COMB.pep:*
: /cgn2_6/ptodata1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata1/iaa/PCTUS_COMB.pep:*
         GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
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US-08-146-206C-26
                                                                                                                                                                                            262574 segs, 29422922 residues
                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                   - protein search, using sw model
                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                     seq length: 0
seq length: 200000000
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                                                                                                                  US-10-007-790-5
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Match Length
                   Copyright
                                                                                                                                       1 GYSFTGY 7
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Score

Result Š ö

Gaps

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ITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 41; DB 2; Length 114; 100.0%; Pred. No. 0.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: DO COUTO, FERNANDO J.R.
APPLICANT: CERIANI, ROBERTO L.
TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE
TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY PEPTIDE
WINDLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDE
    STREE: 90 South 7th Street, 3100 No. 5972656west Ctr. CITY: Minneapolis STATE: NN
                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/187,407
FILING DATE: 27-7AN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,542
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 'US 07/493,299 FILING DATE: 14-MAR-1990 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/324,392 FILING DATE: 14-MAR-1989 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/888,366 FILING DATE: 03-JUL-1997
                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 76, Application US/08525539A Patent No. 6309636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 755 Page Mill Road CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35,093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Carter, Charles G. REGISTRATION NUMBER: 35, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 100
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON
                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 GYSFTGY 26
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                                                                                                                                                                      55402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: CA
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Pred. No. 0.87;
                                       100.0%; Score 41; DB 4; Length 20; 100.0%; Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037
FILING DATE: 23-UN-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                     APPLICANT: Glick, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Poerster
                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/ACENT INFORMATION:
NAME: Konski, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442110710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
US-08-888-366-8
Sequence 8, Application US/0888366; Patent No. 5972666; GENRRAL INFORMATION:
APPLICANT: Lopez, Osvaldo; APPLICANT: Wylie, Dwane E.
APPLICANT: Wagner, Fred W.
                                                                                                                                                                                                                                                                         Sequence 20, Application US/08881037
Patent No. 6080588
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
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SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-08-881-037-20
                                                                                                                                                      GYSFIGY 11
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                                       Query Match
Best Local Similarity
Matches 7; Conserv
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US-09-556-605-29
                                                                                                                                                                                                                                                        JS-08-881-037-20
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Gaps

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100.0%; Score 41; DB 1; Length 119; 100.0%; Pred. No. 0.94; tive 0; Mismatches 0; Indels
                                                                                                                                                 Score 41; DB 4; Length 117;
Pred. No. 0.92;
                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Townsend and Townsend Khourie and Crew
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COMPUTER READMELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION UNMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLGSSIFICATION: 424
PRIORS APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
FILING DATE: 18-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION:
                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 65, Application US/07634278 Patent No. 5530101
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100.0%;
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 119 amino acids
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Best Local Similarity 100.0
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Palo Alto STATE: California
      amino acid
                                                             linear
                                                                                                                                                                                                                                                                                                                              26 GYSFTGY 32
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STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                  STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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                                                                          JS-08-525-539A-78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Patent No. 309636
GENERAL INFORMATION:
APPLICANT: DO COUTO, FERNANDO J.R.
APPLICANT: PETERSON, JERRY A.
TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
TITLE OF INVENTION: Mc3 ANTI-BA46 ANTIBODY, METHODS OF USE I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 41; DB 4; Length 117; 100.0%; Pred. No. 0.92;
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ZIP: 94304-1018

COMUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,539A
FILING DATE: 14-SEP-1995
CLASSIFICATION: 424
ATORNEY/AGENT INFORMATION:
NAME: DYLAN, TYLER
REGISTRAION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 27633-20001.21
TELECOMMUNICATION INPERMATION:
                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,539A
FILING DATE: 14-SEP-1995
CLASSIFICATION: 424
ATTONREY/AGERT INFORMATION:
NAME: DYLAN, TYLER
REGISTRATION NUMBER: 37,612
REFRENCE/FOOCKET NUMBER: 27,633-20001.21
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: (415) 813-5600
TELEFRAX: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEE: MORRISON & FOERSTER
: 755 Page Mill Road
Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 494-0792
TELEX: 706141
INPORRATION FOR SEQ ID NO: 76
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 81
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||||||||
26 GYSFTGY 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
STREET: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
US-08-525-539A-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
US-08-525-539A-78
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Gaps

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CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 GYSFTGY 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GYSFTGY 7
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                                                                                                                                                                        94111
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                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
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                                                                                     Sequence 89, Application US/07634278
Patent No. 5530101
GENERAL INFORMATION:
APPLICANT: CO. Man Sung
APPLICANT: ALANDOLFI, Nilliam P.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SECTION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION NUMBER: US 07/590,274
FILING DATE: 13-FEB-1990
PRIOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
ATTORNEY/AGENT INPORMATION:
NAME: SMITCH, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 33,0223
REFERENCE/DOCKET NUMBER: 31823-002600
                                                                                                                                                                                                                                                                                                                           379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (415) 326-2422 INFORMATION FOR SEQ ID NO: 8 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 119 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                        CITY: Palo Alto
STATE: California
26 GYSFTGY 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GYSFTGY 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
STREET: 37
                                                        RESULT 8
US-07-634-278-89
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                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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APPLICANT: SCHNEIDER, william P.
APPLICANT: SCHNEIDER, william P.
ITILE OF INVERTION: IMPROVED HUMANIZED IMMUNOCLOBLINS
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS: 1 OF A PAPEL OF A
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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNDER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-58P-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTATION NUMBER: 30,233
REFERENCE/DOCKET NUMBER: 130-280
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 89, Application US/08474040
Patent No. 5693761
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 65.
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-474-040-65
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 65, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
    APPLICANT: QUEEN, Cary L.
    APPLICANT: SCHNEIDER, William P.
    APPLICANT: COELINGH, Kathleen L.
    APPLICANT: COELINGH, Kathleen L.
    APPLICANT: ANDOFFI, Nicholas F.
    APPLICANT: AND F.
    APPLICANT: AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                          MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 13-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1989
PRIOR APPLICATION NUMBER: US 07/290,975
FILING DATE: 13-FEB-1989
ATTORNEY AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE JOCKET MIMPER: 11823-002600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Townsend and Townsend Khourie and Crew 379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
ITELEPHONE: (415) 326-2422
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: peptide US-08-477-728-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Abbac.
STREET: 372 _,
CITY: Palo Alto
~~*TE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-474-040-65
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100.0%; Score 41; DB 1; Length 119; 100.0%; Pred. No. 0.94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, Milliam P.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
APPLICANT: SELICK, Harold E.
APPLICANT: SELICK, TARROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IPP
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Parentin Release #1.0, Version #1.25
CURRATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/634,278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: 379 Lytton Avenue
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Gaps

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Score 41; DB 1; Length 119;
Pred. No. 0.94;
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APPLICANT:
CO, Man Sung
APPLICANT: CC, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: COELINGH; Nicholas F.
APPLICANT: COELINGH; Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION WHERE: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTOMEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REPRERENCE PLOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2400
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 89:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 89, Application US/08487200 Patent No. 5693762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11
                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
100.0%;
                                                                                                                                                                                                     | LENGTH: 119 amino acids
| TYPE: amino acid
| STRANDEDNESS: single
| TOPOLOGY: linear
| MOLECULE TYPE: peptide
| US-08-487-200-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 379 Lytton Avenue CITY: Palo Alto STATE: California COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |||||||
26 GYSFTGY 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GYSFTGY 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-487-200-89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 65, Application US/08487200

Patent No. 5693762

GENERAL INFORMATION:

APPLICANT: CO, Man Sung

APPLICANT: SCHNEIDER, William P.

APPLICANT: LANDLEFF, Nicholas F.

APPLICANT: CALINGH, Kathleen L.

APPLICANT: SELICK, Harold E.

TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-190
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-198
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
FILING DATE: 13-FEB-1989
FILING DATE: 28-DEC-1988
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Townsend and Townsend and Crew
       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M REGISTRATION NUMBER: 30,223
REPERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPAX: (415) 326-2400
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-474-040-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 379 Lytton
CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||||||||
26 GYSFTGY 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GYSFTGY 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-08-487-200-65
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Gaps

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Query Match 100.0%; Score 41; DB 4; Length 119; Best Local Similarity 100.0%; Pred. No. 0.94; Matches 7; Conservative 0; Mismatches 0; Indels
100.0%; Score 41; DB 4; Length 119; 100.0%; Pred. No. 0.94;
                                                                                                                                                                                                                                                                                                                        APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sungl
APPLICANT: CO, Man Sungl
APPLICANT: SCHNEIDER, William P.
APPLICANT: COELINGH, Nicholas F.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PROOR APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
FILING DATE: 28-DEC-1988
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Pelocial
                                                                                                                                                                                                                                US-08-484-537-89
; Sequence 89, Application US/08484537
; Patent No. 6180370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFRENCE/DOCKET NUMBER: 1182:
TELECOMMUNICATION INFORMATION:
TELEPRONE: (415) 326-2400
TELEPRAT: (415) 326-2400
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      379 Lytton Avenue
Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-484-537-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                     26 GYSFTGY 32
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                                                                                                                                                                                100.0%; Score 41; DB 1; Length 119; 100.0%; Pred. No. 0.94;
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Patent No. 6180370

GENERAL INPORMATION:

APPLICANT: QUEBN, Cary L.

APPLICANT: SCHNEIDER, William P.

APPLICANT: LANDOLET, Nicholas F.

APPLICANT: SELICK, Harold E.

TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: 379 Lytton Avenue CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PUCKASIFICATION DATA:
PUCKASIFICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEFONE: (415) 326-2400
TELEFONE: (415) 326-2400
TELEFAX: (415) 326-2400
                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                   LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                             Query Match
Best Local Similarity 100.
SEQUENCE CHARACTERISTICS
                                                                                 TOPOLOGY: linear;

MOLECULE TYPE: peptide
US-08-487-200-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) MOLECULE TYPE: peptide US-08-484-537-65
                                                                                                                                                                                                                                                                                                                      GYSFTGY 32
                                                                                                                                                                                                                                                                           1 GYSFTGY 7
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
GAPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVORTION: Immunoglobulin Variants
WIMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
APPLICATION NUMBER: PCT/US94/00261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-07-934-373C-19; Sequence 19, Application US/07934373C; Patent No. 5821337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                           ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40,378
                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                    TELECOMMUNICATION INFORMATION TELEPHONE: (617) 981-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: P.
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                        TELEFAX: (617) 981-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genentech, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                             LENGTH: 120 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 122 amino acids
Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.

Best Local Similarity 100.

Matches 7; Conservative
                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear; MOLECULE TYPE: protein PCT-US94-00261-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Lee, Wendy M. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 GYSFTGY 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GYSFTGY 7
                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-07-934-373C-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                               Sequence 2. Application US/08002324

Patent No. 5861156

GENERAL INFORMATION:
APPLICANT: George, Andrew J.T.
APPLICANT: Hoston, James S.
TILLE OF INVENTION: METHODS OF DELIVERING AGENTS TO TARGET
TITLE OF INVENTION: GELLS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 41; DB 2; Length 120; Best Local Similarity 100.0%; Pred. No. 0.95; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: 1
TITLE OF INVENTION: METHODS OF DELIVERING AGENTS TO NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER FEADABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/002,324
FILING DATE: 19930108
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: BROOK, David E.
REGISTRATION NUMBER: 22,552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: CBM92-02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 981-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT-US94-00261-2; Sequence 2, Application PC/TUS9400261; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (617) 981-9540
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 120 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-002-324-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GYSFTGY 7
                                                                                                                                                                                                                                                                                                                               Lexington
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                                           US-08-002-324-2
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Pred. No. 0.96;
; Mismatches 0; Indels
                                                                                                           ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
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COMPUTER READABLE FORM:

MEDIUM TYPE: 35. inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wilbeatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530
PRIOR APPLICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING APPLICATION DATA:
APPLICATION NUMBER: 08/146206
                                                                                                                                                                                                                                                                                                                   FILING DATE: 21-ANG-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Lee, wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P070
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
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100.0%;
                                               South San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: 1.4-170
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Best Local Similarity 100.
Matches 7; Conservative
               1 DNA Way
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                                                                                              USA
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                                                                                           COUNTRY:
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                                               Indels
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18-07-34-373C-20
18-07-34-373C-20
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18-07-37-37-37-37
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                  Pred. No. 0.96;
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Patent No. 582137
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION:
ITLE OF INVENTION: 1 mmunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
100.00t; ex
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INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 122 amino acids
Amino Acid
                  Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                      26 GYSFTGY 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: Linear
US-07-934-373C-20
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26 GYSFTGY 32
                                                                                         1 GYSFTGY 7
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US-07-934-373C-45
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Gaps

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Query Match 100.0%; Score 41; DB 3; Length 122; Best Local Similarity 100.0%; Pred. No. 0.96; Matches 7; Conservative 0; Mismatches 0; Indel's
                                                                                                                                                                                    100.0%; Score 41; DB 3; Length 122; 100.0%; Pred. No. 0.96;
                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 45. Application US/08437642B
Sequent No. 6654297
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Winderin (Genencech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/34373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 15-JUN-1991
PRIOR APPLICATION NUMBER: 07/71572
FILING DATE: 15-JUN-1991
ATTORNEY/AGBNT INFORMATION:
NUMBER: LEG, WENDRY NUMBER: 07/71572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P0709P2C1
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REFERENCE/DOCKET NUMBER: PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
                     ... NO: 2
...: 122 amino acids
...: TYPE: Amino Acid
...: TOPOLOGY: Linear
US-08-437-642B-20
Querv W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 122 amino acids
Amino Acid
                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
TELEPAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         650/952-9881
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26 GYSFTGY 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZUDWAIT: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winheatin (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIFICATION NUMBER: US/08/437,642B
FILING DATE: 109-May-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/334373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/15272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20, Application US/08437642B
Patent No. 6054297
GENERAL INFORMATION:
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
  FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REGISTRATION NUMBER: 40,378
REGISTRATION NUMBER: P0709P2C1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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REFERENCE/DOCKET NUMBER: POTELECOMMUILCATION:
TELECOMMUILCATION:
TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                    TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                           : 122 amino acids
Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
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; Sequence 26, Application US/08146206C
; Patent No. 1070213
; Patent No. 670213
; Patent No. Faul J.
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41; DB 4; Length 122; Pred. No. 0.96;
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COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,206C
FILING DATE: 17-No. 6407213-1993
CLASSIFCATION NUMBER: 07/715272
APPLICATION NUMBER: 07/715272
RILING DATE: 14-JUM-1991
ATTORNEY/AGENT INPORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                               SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,206C
FILING DATE: 17-No. 6407213-1993
CLASSIFICATION: 530.
                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 07/70991
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: 65/225-1994
         IBM PC compatible
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
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INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
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CITY: South San Francisco
STATE: California
COUNTRY: USA
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TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GYSFIGY 7
                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20, Application US/08146206C
Patent No. 6407213
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 41; DB 4; Length 122; 100.0%; Pred. No. 0.96;
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
SOFTWARE: Winheatin (Genentech)
SOFTWARE: Winheatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,206C
FILING DATE: 17-NO. 6407213-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INPORMATION:
NAME: Lee, Wendy W.
REGISTRATION NUMBER: 40,378
REGISTRATION NUMBER: 9070991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: P0709P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
                                                                                                                              Sequence 19, Application US/08146206C Patent No. 6407213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 650/952-9001
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
26 GYSFTGY 32
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-08-146-206C-19
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Gaps

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100.0%; Score 41; DB 5; Length 129; 100.0%; Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                         100.0%; Score 41; DB 4; Length 124; 100.0%; Pred. No. 0.98;
                       Phosphatidylinositol-3,4,5-Triphosphate
                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
TITLE OF INVENTION: Monoclonal Antibody Specific for TITLE OF INVENTION: Phosphatidylinositol-3,4,5-Tripho FILE REFERENCE: M3-008-US CURRENT APPLICATE M99-02-24 PRIOR APPLICATION NUMBER: US 1998-252921 PRIOR PILING DATE: 1998-09-07 NUMBER OF SEQ ID NOS: 10 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 30
PCT-US93-07832-19
; Sequence 19, Application PC/TUS9307832
; GENERAL INFORMATION:
; APPLICANT: Genencech, Inc.
; TITLE OF INVENTION: Immunoglobulin Variants
; VUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
; STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRICE APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATH:
APPLICATION NUMBER: PCT/US93/07832
FILING DATE: 19930820
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TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFERMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acids
TOPOLOGY: 1.
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                      ) ORGANISM: Mus musculus
US-09-257-069-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 GYSFTGY 32
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Best Local Similarity
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                                                                                                                                                                                                                             LENGTH: 124
                                                                                                                                                                                                                                                      TYPE: PRT
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0
                                                  100.0%; Score 41; DB 4; Length 122; 100.0%; Pred. No. 0.96;
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Patent No. 6348580
GENERAL INFORMATION:
APPLICANT: Medical & Biological Laboratories Co.,Ltd.
                                                                                                                                                                                                                                               RESULT 28
PCT-US93-07832-20
; Sequence 20, Application PC/TUS9307832
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Immunoglobulin Variants; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: Datin (Genentech)
CURRENT APPLICATION DATA:
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                                                                                                0; Mismatches
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APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA: PCT/US92/05126
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA: 07/934373
FILING DATE: 07/934373
ATTORNEY/AGENT INFORMATION:
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FILING DATE: 19930820
CLASSIFICATION:
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REFERENCE/DOCKET NUMBER: 70:
FELECOMMUNICATION INFORMATION:
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
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amino acid
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Matches 7; Conservative
                                                                                                Conservative
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26 GYSFTGY 32
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                                                  Query Match
Best Local Similarity
Matches 7; Conserv
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         US-08-146-206C-26
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US-09-257-069-2
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Gaps

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GENERAL INFORMATION:

APPLICANT: DO COUTO, FERNANDO J.R.

APPLICANT: CERIANI, ROBERTO L.

APPLICANT: PETERSON, JERRY A.

TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
NUMBER OF SEQUENCES: 81

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
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ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,539A
FILING DATE: 14-SEP-1995
CLASSIPICATION: 424
ATTORNEY AGENT INPORMATION:
NAME: DYLAN, TYLER
REGISTRATION: WIMBER: 37,612
REGISTRATION NUMBER: 37,612
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; Sequence 63, Application US/08525539A
; Patent No. 6309636
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TELECOMMUNICATION INFORMATION:
TELEPAM: (415) 813-560
TELEPAX: (415) 494-0792
                                                                  : 136 amino acids
amino acid
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Best Local Similarity 100.
Matches 7; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                              ; MOLECULE TYPE: protein US-08-525-539A-47
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US-08-444-644-17
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                                                                LENGTH:
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APPLICANT: CERLANI, ROBERTO L.
APPLICANT: CERLANI, ROBERTO L.
APPLICANT: PETERSON, JERRY A.
TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
OVERESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 755 Page Mill Road
CITY: Palo Alto
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      0; Indels
                                                                                                                                                                                                                                                  APPLICANT: SALIBERG, Matti
APPLICANT: Saliberg, Matti
APPLICANT: Lazdina, Una
TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE
TITLE OF INVENTION: HEPATITIS B VIRUS CORE AND E ANTIGENS
FILE REFERENCE: TRIPEP.020A
CURRENT APPLICATION NUMBER: US/09/556,605
CURRENT FILING DATE: 2000-04-21
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FRAEESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: EL PR PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/525,539A
FILING DATE: 14-SEP-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Artificial Oligonucleotide
US-09-556-605-3
    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INPORMATION:
NAME: DYLAN, TYLER
REGISTRATION NUMBER: 37,612
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 32
US-08-525-539A-47
; Sequence-47, Application US/08525539A
; Patent No. 6309636
; GENERAL INFORMATION:
                                                                                                                                              RESULT 31
US-09-556-605-3
F Sequence 3, Application US/09556605
F Patent No. 6417324
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 7; Conservative
7; Conservative
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26 GYSFTGY 32
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                                          1 GYSFTGY 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 3
LENGTH: 130
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  Matches
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TRANSFERRIN RECEPTOR SPECIFIC
ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
CONJUGATES
46
      ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
CONJUGATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 1.137
OTHER INFORMATION: /note= "Chimeric 128.1 Heavy Chain
OTHER INFORMATION: V-Region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                        ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington
                                                                                                                                                                                                                                                                                               CALP: 0.41.9 U. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Hamilton, Brook, Smith & Reynolds, P.C. Two Militia Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Wagner, Richard W. REGISTRATION NUMBER: 34,480 REPERENCE/DOCKET NUMBER: ALK88-15AAA TELECOMMUNICATION INFORMATION: TELEBONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 33, Application US/08444644 Patent No. 6015555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 137 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide FRAGMENT TYPE: N-terminal
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APPLICANT: Friden, Phill:
TITLE OF INVENTION: TRANI
TITLE OF INVENTION: ANTII
TITLE OF INVENTION: CONJII
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
STREET: Hamilton, BI
STREET: Two Militia Dri
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Best Local Similarity 100.
Matches 7; Conservative
            TITLE OF INVENTION: ANY TITLE OF INVENTION: CON NUMBER OF SEQUENCES: 46 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Peptide
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45 GYSFTGY 51
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02173
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Sequence 17, Application US/08444644
Patent No. 6015555
GENERAL INFORMATION:
APPLICANT: Friden, Phillip M.
TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
TITLE OF INVENTION: CONJUGATES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS: ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
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V-Region"
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TRANSFERRIN RECEPTOR SPECIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REPERENCE/DOCKET NUMBER: ALK88-15AAAZ
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/232,246
FILING DATE: 07-JUL-1994
FILING DATE: 07-JUL-1994
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
FILING DATE: 07-SEP-1990
APPLICATION DATA:
APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1989
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Peptide
LOCATION: 1..137
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45 GYSFTGY 51
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US-08-232-246A-17
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STATE:
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Gaps .. 0

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Phillip M.
TRANSFERRIN RECEPTOR SPECIFIC
ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
CONJUGATES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive
CITY: Lexington
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,644
                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: WAGNET INFORMATION:
NAME: WAGNET INFORMATION:
TELECOMMUNICATION SEQ ID NO: 33:
SUCCESSION SEQ ID NO: 33:
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/232,246
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
APPLICATION NUMBER: US 07/800,05077
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATE: US 07/404,089
FILING DATE: 07-SEP-1989
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Patent No. 6015555
GENERAL INFORMATION:
APPLICANT: Friden, Phillip M.
TITLE OF INVENTION: TRANSFERRIN REC
TITLE OF INVENTION: CONJUGATES
ITILE OF INVENTION: CONJUGATES
ITILE OF INVENTION: CONJUGATES
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acids
TOPOLOGY: 14
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FRAGMENT TYPE: N-terminal
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Best Local Similarity 100...
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Patent No. 6129508
GENERAL INFORMATION:
APPLICANT: Friden, Phillip M.
TITLE OF INVENTION: TRANSFERIN RECEPTOR SPECIFIC
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
TITLE OF INVENTION: CONJUGATES
NUMBER OF SEQUENCES: 46
CORRESPONDENCES. 46
CORRESPONDENCE ADMILTON, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,246A
FILING DATE: 04-MAY-1994
                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/232,246
FILING DATE: 07-ULL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1989
ATTORNEY AGENT INPORMATION:
                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 233 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 7; Conservative
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ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STREET: Two
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                                                                                                                                                                                                     FILING DATE:
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COUNTRY:
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TYPE: amino acids TYPE: amino acids TOPOLOGY: linear OLEGETH
    SEQUENCE CHARACTERISTICS
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Best Local Similarity
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                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: PHILLIP M.

TITLE OF INVENTION: TRANSFERIN RECEPTOR SPECIFIC

TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT

TITLE OF INVENTION: CONJUGATES

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Bronk
CITY
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CITY: Lexington
STATE: MA
STATE: MA
STATE: MA
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,644
                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 34,480
REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
FELECOMMUNICATION INFORMATION:
TELECHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/232,246
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1980
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1980
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-444-644-28
; Sequence 28, Application US/08444644
; Patent No. 6015555
; GENERAL INFORMATION:
APPLICANT: Friden, Phillip M.
                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                    TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO: 2
                                                                                                                                                                                  235 amino acids
                                                                                                                                                                                                                                                                                                  FRAGMENT TYPE: N-terminal US-08-444-644-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Wagner, Richard W
REGISTRATION NUMBER: 34
                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                       amino acid
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APPLICANT: Friden, Phillip M.

TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC

TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT

TITLE OF INVENTION: CONJUGATES

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

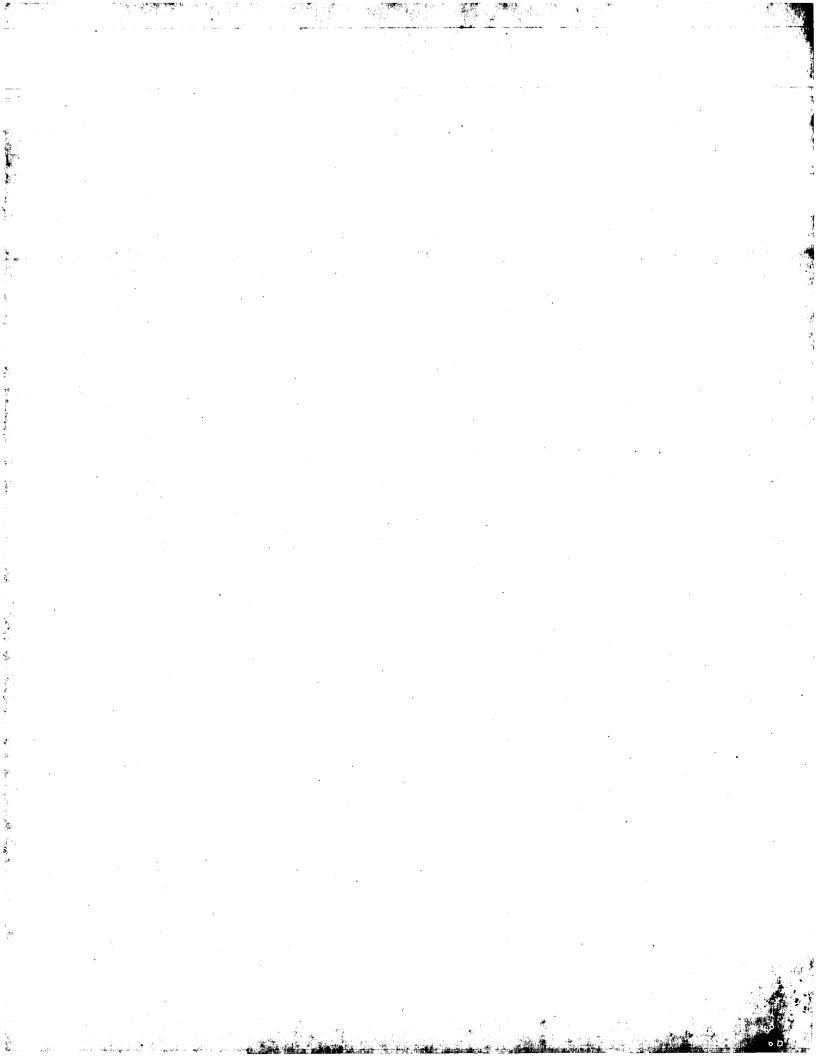
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 235;
                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                    E: Hamilton, Brook, Smith & Reynolds, P.C.
Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41; DB 3;
Pred. No. 1.9;
                                                                                             0; Mismatches
                                                             100.0%; Score 41; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                  Sequence 42, Application US/08444644 Patent No. 6015555
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100.0%;
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MOLECULE TYPE: protein
; FRAGMENT TYPE: N-terminal
US-08-444-644-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 235 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
FRAGMENT TYPE: N-terminal
                                                             Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                               STREET: Two
                                                                                                                                             45 GYSFTGY 51
                                                                                                                          1 GYSFTGY 7
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0; Mismatches 7; Conservative Matches ò

0; Gaps 0;

0; Indels

Search completed: July 18, 2003, 15:11:47 Job time : 9.12 secs



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Length 20
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AND E ANTIGENS
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Publication No. US20030082186A1
GENERAL INFORMATION:
APPLICANT: Sallberg, Matti
TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE
US-09-900-766-1

US-10-025-687-17

US-10-125-687-17

US-10-125-687-17

US-09-880-748-2008

US-09-880-748-2001

US-09-880-748-2021

US-09-880-748-2021

US-09-880-748-2021

US-09-880-748-2009

US-09-880-748-2009

US-09-880-748-2019

US-09-880-748-2019

US-09-880-748-2019

US-09-880-748-2010

US-09-880-748-2011

US-09-880-748-2011

US-09-880-748-2017

US-09-880-748-2017

US-09-880-748-2017

US-09-880-748-2016

US-09-880-748-2016

US-09-880-748-2016

US-09-880-748-2016

US-09-880-748-2016

US-09-880-748-2016

US-09-880-748-116

US-09-880-748-116

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US-09-880-748-118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB 10;
Pred. No. 0.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 29, Application US/09839447A
| Sequence 29, Application US/09839447A
| Patent No. US20020058247A1
| GENERAL INFORMATION:
| TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIN |
| TITLE OF INVENTION: HEBATITIS B VIRUS CORE AND |
| FILE REPERRICE: TRIPEP 020CP1 |
| CURRENT APPLICATION NUMBER: US/09/839,447A |
| PRIOR APPLICATION NUMBER: 09/556605 |
| PRIOR APPLICATION NUMBER: 09/556605 |
| RINGER FILING DATE: 2000-04.21 |
| NUMBER OF SEQ ID NOS: 111 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| SEQ ID NO 29 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Artificial Peptide US-09-839-447A-29
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 7; Conservative
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Sequence 3, Appli
Sequence 47, Appl
Sequence 63, Appl
Sequence 1948, Ap
Sequence 1960, Ap
                                                                                                                                               July 18, 2003, 15:09:56; Search time 18.06 Seconds (without alignments) 46.031 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 78,
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Sequence
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1: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/NSO6_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/RCTUB_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/NSO8_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/NSO8_PUBCOMB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

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16: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-153-271-29
US-09-956-206A-76
US-09-839-447A-3
US-09-956-206A-47
US-09-956-206A-47
US-09-956-206A-63
US-09-880-748-1948
US-09-880-748-1948
US-09-880-748-1900
US-10-207-655-318
US-09-813-659-18
US-09-813-659-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                          OM protein - protein search, using sw model
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seq length: 200000000
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Match Length
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Sequence 1388, Ap Sequence 48, Appl Sequence 1635, Ap Sequence 1722, Ap

Sequence 2042, Sequence 2116, Sequence 1386,

Sequence 2107, Requence 2109, Sequence 2109, Sequence 2011, Requence 2026, Requence 2037, Sequence 2004, Requence 2004, Requen

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DB 11; Length 117;
1.8;
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100.0%; Pred. No. 1.6
:ive 0; Mismatches
                         TOPOLOGY: linear SEQ ID NO: 76: US-09-956-206A-76
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US-09-956-206A-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                               Sequence 78, Application US/09956206A Patent No. US20020164339A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 19-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 117 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
TYPE: amino acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                  Query Match
Best Local Similarity 100
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CERIANI, ROBERTO L.
PETERSON, JERRY A.
TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 41; DB 15; Length 20; 100.0%; Pred. No. 0.28;
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  HEPATITIS B VIRUS CORE AND E ANTIGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 44,408
REFERENCE/DOCKET NUMBER: 276332000101
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/956,206A
FILING DATE: 19-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 14-SEP-1995
APPLICATION NUMBER: PCT/US95/11683
FILING DATE: 14-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/525,539
                                                                                 PRIOR APPLICATION NUMBER: 09/556,605
PRIOR FILING DATE: 2000-04-21
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
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FILING DATE: 7-JUNE-1195
APPLICATION NUMBER: 08/307,868
FILING DATE: 16-SEPT-1994
TITLE OF INVENTION: HEPATITIS B VIRUS COI
THE REPERBRACE: TRIPEP. O20DVU
CURRENT APPLICATION NUMBER: US/10/153,271
CURRENT FILLING DATE: 2002-05-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: DO COUTO, FERNANDO J.R
                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Artificial Peptide US-10-153-271-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 76, Application US/09956206A Patent No. US20020164339A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TELEFAX: (650) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -09-956-206A-76
                                                                                                                                                                                                                          TYPE: PRT
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Gaps
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CERIANI, ROBERTO L.
PETERSON
TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/956,206A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 44,408
REFERENCE/DOCKET NUMBER: 276332000101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/525,539
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: PCT/US95/11683
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: 08/487,598
FILING DATE: 7-JUNE-1995
APPLICATION NUMBER: 08/307,868
FILING DATE: 16-SEPT-1994
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AAL INFORMATION:
APPLICANT: DO COUTO, FERNANCO C...
CERIANI, ROBERTO L.
PETERSON, JERRY A.
TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
METHODS OF HUMANIZING ANTIBODY PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: DO COUTO, FERNANDO J.R.
CERIANI, ROBERTO L.
PETERSON, JERRY A.
TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
MC3 ANTI BA46 ANTIBODY, METHODS OF USE THEREOF, AND
METHODS OF HUMANIZING ANTIBODY PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 41; DB 11; Length 136; 100.0%; Pred. No. 2.1;
                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/956,206A
FILING DATE: 19-Apr-2002
CLASSIFICATION: <u >- Unknown></u>
PRIOR APPLICATION DATA:</u>
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/525,539
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: PCT/US95/11683
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: 08/487,598
FILING DATE: 7-JUNE-1995
APPLICATION NUMBER: 08/307,868
ATTORNEY AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: WITT, ERIC
REGISTRATION NUMBER: 44,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 63, Application US/09956206A Patent No. US20020164339A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 136 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 706141
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              GENERAL INFORMATION:
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US-09-956-206A-63
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                                                                                                                                                                                                                          APPLICATION MACHINE SALIDARY
TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE
TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE
TITLE OF INVENTION: HEPATITIS B VIRUS CORE AND E ANTIGENS
FILE REFERENCE: TRIPED-020CP1
CURRENT APPLICATION NUMBER: US/09/839,447A
CURRENT APPLICATION NUMBER: 09/556605
PRIOR APPLICATION NUMBER: 09/556605
PRIOR FILING DATE: 2000-04-21
NUMBER OF SEQ ID NOS: 111
SOFTWARE: FASTERQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/10153271
Publication No. US20030082186A1
GENERAL INFORMATION:
APPLICANT: Sallberg, Matti
APPLICANT: Sallberg, Matti
TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE
TITLE OF INVENTION: HEPATITIS B VIRUS CORE AND E ANTIGENS
FILE REFERENCE: TRIPEP.020DV1
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100.0%; Pred. No. 2; .
:ive 0; Mismatches 0;
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CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: 09/556,605
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FASEUSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Artificial Peptide US-09-839-447A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Artificial Peptide US-10-153-271-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/09956206A
                                                                                                                                                            Sequence 3, Application US/09839447A; Patent No. USZ0020058247A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 130
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100...
7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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                                               26 GYSFTGY 32
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LENGTH: 130
TYPE: PRT
                                                                                                                 RESULT 5
US-09-839-447A-3
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US-09-880-748-1900

JS-09-880-748-1900

JS-09-880-748-1900

JS-09-880-748-1900

JS-09-880-748-1900

JS-09-880-748-1900

JS-09-880-748-1900

JILE APPLICATION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF23-

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR PILING DATE: 2000-10-17

PRIOR FILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ledbetter, Jeffrey A. APPLICANT: Ledbetter, Martha S. TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS FILE REFERENCE: 300.694.401C.
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
SEQ ID NO 13
LENGTH: 259
TYPE: PRT
ORGANISM: Mus musculus
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CTHER INFORMATION: MOUSE ANTI-HUMAN CD37 SCFV US-10-207-655-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                      Mismatches
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Pred. No.
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                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%;
Matches 7; Conservative 0
                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
US-09-880-748-1900
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FILE REFRENCE: P5523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-10-17
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-05-25
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REFERENCE/DOCKET NUMBER: 276332000101
                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/525,539
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: PCT/US95/11683
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: 08/487,598
FILING DATE: 7-UNG-1995
APPLICATION NUMBER: 08/307,868
FILING DATE: 16-SEPT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/956,206A FILING DATE: 19-Apr-2002 CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: bingle sequence sequence sequence DESCRIPTION: SEQ ID NO: 63: US-09-956-206A-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :09-880-748-1948
Sequence 1948, Application US/09880748
Publication No. US20030059937A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (650) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                     ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 136 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (650) 494-0792
TELEX: 706141
                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 63: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1948
LENGTH: 241
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Best Local Similarity 100.
Matches 7; Conservative
                             CITY: Palo Alto
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PRIOR FILING DATE: 1993-09-13
PRIOR APPLICATION WUMBER: 08/013,420
PRIOR FILING DATE: 1993-02-01
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Petentin Ver. 2.0
SEQ ID NO 18
LENGTH: 302
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100.0%;
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SEQ ID NO 32
LENGTH: 302
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
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Best Local Similarity 100.
Matches 7; Conservative
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CAGANISM: Homo sapiens
US-09-813-659-18
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US-09-813-659-32
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Sequence 18, Application US/09813659

Patent No. US20020012999A1

GENERAL INFORMATION:

APPLICANT: Ledbetrer, Jeffrey A.

APPLICANT: Bajorath, Jurgen

APPLICANT: Gilliand, Lisa K.

TITLE OF INVENTION: EXPRESSION VECTORS ENCODING BISPECIFIC FUSION PROTEINS

TITLE OF INVENTION: AND METHODS OF PRODUCING BIOLOGICALLY ACTIVE BISPECIFIC

TITLE OF INVENTION: PUSION PROTEINS IN A MAMMALIAN CELL

FILE REFERENCE: 30436.18USD2

CURRENT APPLICATION NUMBER: US/09/813,659

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 09/549,067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PERDEAL INFORMATION:

APPLICANT: Ledbetter, Jeffrey A.

APPLICANT: Ledbetter, Jeffrey A.

APPLICANT: Lansley, Peter S.

APPLICANT: Linsley, Peter S.

APPLICANT: Linsley, Peter S.

APPLICANT: Linsley, Peter S.

APPLICANT: Fell, H. Peter Y.

APPLICANT: Bajorath, Jurgen

APPLICANT: Bajorath, Jurgen

APPLICANT: Bajorath, Lisa K.

TITLE OF INVENTION: AND WETHODS OF PRODUCING BISPECIFIC FUSION PROTEINS

TITLE OF INVENTION: AND WETHODS OF PRODUCING BISPECIFIC

TITLE OF INVENTION: PUSION PROTEINS IN A MAMMALIAN CELL

TITLE OF INVENTION: PUSION PROTEINS IN A MAMMALIAN CELL

TITLE OF INVENTION: PUSION PROTEINS IN A MAMMALIAN CELL

TITLE OF INVENTION: PUSION PROTEINS IN A MAMMALIAN CELL

TITLE OF INVENTION: PUSION PROTEINS IN A MAMMALIAN CELL

FILE REFERENCE: 30436-1849,067

PRIOR FILING DATE: 2000-04-13

PRIOR FILING DATE: 1993-09-13

PRIOR FILING DATE: 1993-09-13

PRIOR FILING DATE: 1993-09-13

PRIOR FILING DATE: 1993-09-13

PRIOR FILING DATE: 1993-02-01

NUMBER OF SEQ ID NOS: 32

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 30

LEVENT APPLICATION NUMBER: PATENT NUMBER:
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                         100.0%; Score 41; DB 15; Length 259; ilarity 100.0%; Pred. No. 4.1; Conservative 0; Mismatches 0: Indels (
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APPLICATION NUMBER: 08/539,436
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PRIOR FILING DATE: 1995-10-05
PRIOR APPLICATION NUMBER: 08/121,054
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US-05-813-659-30
; Sequence 30, Application US/09813659
; Patent No. US20020012989A1
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Matches 7; Conservative
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Query Match
Best Local Similarity
7; Conserv
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; OTHER INFORMATION: Conjugate protein US-09-900-766-1
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Best Local Similarity 85.7.
6; Conservative
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Matches 6; Conservative
                                                                 Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
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US-10-194-975-1
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ORGANISM: Homo sapiens
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APPLICANT: Lake, Philip
APPLICANT: Lake, Philip
APPLICANT: Wight, Richard M.
TITLE OF INVENTION: Anti-CD3 Immunotoxins and Therapeutic Uses Therefor FILE REFERENCE: CGC 4-31157A/USN
CURRENT APPLICATION NUMBER: US/09/480,236
CURRENT FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: FORSBERO, GORAN
APPLICANT: FORSBERO, GORAN
APPLICANT: BALANDSSON, EBR
APPLICANT: WALONSON, EBR
APPLICANT: WALONSON, ERR
APPLICANT: WALSE, BJORN
TITLE OF INVENTION: A NOVEL ENGINEERD SUPERANTIGEN FOR HUMAN THERAPY
FILE REFERENCE: PO2188USO;10104199
CURRENT APPLICATION UNMBER: US/09/900,766
CURRENT FILING DATE: 2001-07-06
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                                                                                                                                                        ; OTHER INFORMATION: fusion polypeptide US-10-207-655-348
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09480236
Patent No. US20020142000A1
GENERAL INFORMATION:
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Publication No. US20030039655A1
GENERAL INFORMATION:
  NUMBER OF SEQ ID NOS: 426
SOFTWARE: PatentIn version 3.0
SEQ ID NO 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.0
                                                                                         TYPE: PRT ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                     174 GYSFTGY 180
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|153 GYSFTGY 159
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LOCATION: (1)..(672)
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LENGTH: 672
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LENGTH: 601
                                                                                                                                      FEATURE:
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TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
FILE REFERENCE: 26050-705
CURRENT APPLICATION WUMBER: US/10/025,687
CURRENT FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.1
SEQ ID NO 17
LENGTH: 98
                                          Gaps
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  Length 672;
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                                        Indels
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100.0%; Score 41; DB 12; 100.0%; Pred. No. 11;
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US-10-194-975-1
i Sequence 1, Application US/10194975
publication No. US20030039649A1
GENERAL INFORMATION:
APPLICANT: Foote, Jefferson
TITLE OF INVENTION: Super Humanized Antibodies
FILE REPERENCE: 501231.01
CURRENT FILING DATE: 2002-10-10
CURRENT FILING DATE: 2002-10-10
PRIOR PRILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 98
                                        Mismatches
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Pred. No. 5.
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                                                                                                                                                                                   RESULT 18
US-10-025-687-17
'Sequence 17, Application US/10025687
'Publication No. US20020142255A1
'GENERAL INFORMATION:
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DB 12; Length 241;

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    Mismatches

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Pred. No.
                      92.7%;
85.7%;
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85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
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ORGANISM: Homo sapiens
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26 GYTFTGY 32
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Best Local Similarity
Matches 6; Conserv
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ORGANISM:
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APPLICANT: Luo, Peter
TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
FILLE REFERENCE: 26050-705
CURRENT APPLICATION NUMBER: US/10/125,687
CURRENT FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 28
SSEY TARE: PatentIn version 3.1
LENGTH: 98
                                                                                                                                                                                                                                                                                                           Gaps
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GENERAL INCOMPATION:

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR PILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-25

NUMBER OF SEQ ID NOS: 3239
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Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS; FILE REPERBRECE PFS23
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
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Pred. No. 13;
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Pred. No. 5.2;
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US-09-880-748-2008
US-09-880-748-2008
Sequence 2008, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
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Best Local Similarity 85.7
                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
US-10-125-687-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2008
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US-09-880-748-2031
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Sequence 2032, Application US/09880748

Publication No. US20030059937A1

GRENEAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PFS23

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2001-017

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-06-25

NUMBER OF SEQ ID NOS: 3239

SEQ ID NO 2032

LENGTH: 241
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; Sequence 2021, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF5.3
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR APPLICATION NUMBER: 60/240,816
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13;
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Pred. No.
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92.7%;
85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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US-09-880-748-2106
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26 GYTFTGY 32
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Publication No. US2030059937A1
GENERAL INFORMATION:
I TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PLING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2001-03-16
PRIOR PLICATION NUMBER: 60/276,248
PRIOR PLICATION NUMBER: 60/277,379
PRIOR PLING DATE: 2001-03-16
PRIOR PLING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PLING DATE: 2001-03-21
PRIOR PLING DATE: 2001-05-25
NUMBER OF SEC ID NOS: 3239
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Sequence 2106, Application US/09880748

Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT PILNG DATE: 2001-06-15

PRIOR FILING DATE: 2000-06-15
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Pred. No. 13;
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Pred, No. 13;
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PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR PILING DATE: 2001-03-16
PRIOR PLING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR APPLICATION NUMBER: 60/293,499
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PACENTIN Ver. 2.0
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Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6, Conservative
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; ORGANISM: Homo sapiens
US-09-880-748-2046
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ORGANISM: Homo sapiens
US-09-880-748-2021
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GYTFTGY 32
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26 GYTFTGY 32
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| PRIOR PRELICATION NUMBER: 60/246,216
| PRIOR PRICING NUMBER: 60/246,248
| PRIOR LINING DATE: 2000-10-17
| PRIOR PRICING NUMBER: 60/276,248
| PRIOR PLINING DATE: 2001-01-6/249
| PRIOR PLINING PRIOR PRIOR
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Sequence 2109, Application.US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2107, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
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Pred. No. 13;
1; Mismatches
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-10-17
PRIOR PILING DATE: 2000-10-17
PRIOR PILING DATE: 2001-07
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-17
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-05-25
NUMBER OF SEC ID NOS: 3239
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 2107
LENGTH: 243
                                     PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 2063
LENGTH: 243
                    APPLICATION NUMBER: 60/212,210
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85.7%;
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Best Local Similarity 85.7
Matches 6, Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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CORGANISM: Homo sapiens
US-09-880-748-2063
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CORGANISM: Homo sapiens
US-09-880-748-2107
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26 GYTFTGY 32
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US-09-880-748-2107
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Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PPS23

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-21
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US-09-880-748-2063
; Sequence 2063, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS; FILE REFERENCE: PFS-23; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
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Pred. No. 13;
1; Mismatches 0; Indels
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PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR PILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR PLING: DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PATENTIN Ver: 2.0
SEQ ID NO 2012
LENGTH: 243
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Best Local Similarity 85.7%;
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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US-09-880-748-2012
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; ORGANISM: Homo sapiens
US-09-880-748-2014
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GYTFTGY 32
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LENGTH: 243
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GENERAL INCURATION:
GENERAL INCURATION:
GENERAL INCURATION:
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REPRENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-66-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
SEQ ID NOS: 3239
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 2026
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13;
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Pred. No. 13;
1; Mismatches
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Pred. No.
                                 PRIOR APPLICATION NUMBER: 60/212, 210
PRIOR FILING DATE: 2000-06-15
PRIOR PLING DATE: 2000-06-15
PRIOR PLING DATE: 2000-10-17
PRIOR PLING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276, 248
PRIOR APPLICATION NUMBER: 60/277, 379
PRIOR PRIOR DATE: 2001-03-16
PRIOR PRIOR DATE: 2001-03-21
PRIOR PRIOR DATE: 2001-03-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PARENTIN Ver: 2.0
SEQ ID NO 2011
LENGTH: 244
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Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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; ORGANISM: Homo sapiens
US-09-880-748-2026
                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-2011
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US-09-880-748-2037
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; Sequence 1908, Application US/09880748
; Fublication No. US-030308937A1
; Fublication No. US-030308937A1
; Fublication No. US-030308937A1
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; TILE REFERENCE: PF523
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212, 210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2001-01-17
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR PRIOR DATE: 2001-03-21
; PRIOR PRIOR DATE: 2001-03-21
; ROMBER OF SEQ ID NOS: 3239
; SOFTWARE: PARCETIN VET. 2.0
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
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13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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Pred. No. 13;
1; Mismatches 0
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Pred. No. 13;
1; Mismatches
                PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PLIING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-05-25
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2001-06-15
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Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 323
SOFTWARE: Patentin Ver. 2
                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , ORGANISM: Homo sapiens
US-09-880-748-1908
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26 GYTFTGY 32
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US-09-880-748-2011
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                                                                                                                                                                                                                                                                                                     SEQ ID NO 2109
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GENERAL INVENTALION:
GENERAL INVENTALION:
GENERAL INVENTALION:
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PILING DATE: 2000-61-15
PRIOR PILING DATE: 2000-61-5
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PATCHTION NUMBER: 60/293,499
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PATCHTION PRIOR TILION DATE: 2010-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PATCHTION VAILED
MANDER OF SEQ ID NOS: 3245
                 TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
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Pred. No. 13;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 245;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 12;
13;
                               TILLE REPERBNCE: PF5.3
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-10-17
PRIOR PLING DATE: 2000-10-17
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-25
PRIOR PILING DATE: 2001-03-35

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Pred. No.
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US-09-880-748-2116
'S Sequence 2116, Application US/09880748
'Publication No. US20030059937A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-880-748-2042
Sequence 2042, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
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85.7%;
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Best Local Similarity 85...
Schen 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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; ORGANISM: Homo sapiens
US-09-880-748-2042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT; ORGANISM: Homo sapiens
US-09-880-748-2004
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; Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFRENCE: PF523
CURRENT PELING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR PRILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PATENTIN VEY: 2.0
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1; Mismatches
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-10-17
PRIOR PILING DATE: 2001-01-17
PRIOR PILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-05-25
SOFTWARE: PATENT NUMBER: 60/293,499
PRIOR PILING DATE: 2001-05-25
SOFTWARE: PATENT NOS: 3239
SOFTWARE: PATENT NOS: 3239
SOFTWARE: PATENT NOS: 3239
SOFTWARE: PATENT NOS: 3239
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 2004, Application US/09880748; Publication No. US20030059937A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2037
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; ORGANISM: Homo sapiens
US-09-880-748-1946
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26 GYTFTGY 32
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26 GYTFTGY 32
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US-09-880-748-1946
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g

Gaps

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GENERAL INFORMATION:

APPLICANT: Ruben et al

RESULT 38

g

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Gaps

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### APPLICANT: Ruben et al.

### TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

### FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

### FILOR PRIOR PERIOR OF CONCESS

### PRIOR PELING DATE: 2000-06-15

### PRIOR PELING DATE: 2000-010-17

### PRIOR APPLICATION NUMBER: 60/270,319

### PRIOR APPLICATION NUMBER: 60/270,379

### PRIOR PILING DATE: 2001-03-21

### PRIOR PILING DATE: 2001-03-21

### PRIOR PILING DATE: 2001-03-21

### PRIOR PILING DATE: 2001-03-25

### OFTHARE: PARENT NUMBER: 60/293,499

### PRIOR PILING DATE: 2001-03-25

### NUMBER OF SEQ ID NOS: 3239

### SOFTHARE: PARENT NOS: 3239
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Search completed: July 18, 2003, 15:35:51 Job time: 19.06 secs

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July 18, 2003, 15:03:05; Search time 9.1 Seconds (without alignments) 73.950 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                               OM protein - protein search, using sw model
                                                                                                                                                Run on:
```

283224 segs, 96134422 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 US-10-007-790-5 1 GYSFTGY 7 Perfect score: Scoring table: Searched: Sequence: Title:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Iq heavy chain V r	heavy cha		heavy chain V	heavy chain va	heavy chain V	heavy chain V	Ig heavy chain V r	heavy chain V	heavy chain V	heavy chain V	anti-DNA autoantib	heavy chain V	chain N	Ig heavy chain V r	anti-qlycoprotein	Ig heavy chain V r		heavy chain		tinase (EC 3	heavy chain	g heavy chain V	g heavy chain V	g heavy chain V	g heavy	g heavy chain pr	g heavy chain V	chain V
SUMMARIES	ID	836383	S17604	B37263	PH0978	S67941	PH0971	826320	PH0972	PH0977	\$26319	PL0084	PL0200	F30502	B53285	A49982	F45722	PH0887	PH0100	PS0057	H32513	JC6551	S26938	S26912	869899	PH1668	PH1669	HVHU35	S18551	S36265
ok*	DB	7	~	N	N	~	~	7	N	0	7	7	~	~	~	~	7	7	7	~	~	~	7	~	~	~	~	Н	~	7
	Length	63	98	102	105	105	107	. 107	108	108	114	118	118	119	119	120	120	122	125	135	137	457	98	98	104	109	110	117	117	118
	Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	92.7	92.7	92.7	92.7	92.7	92.7	92.7	92.7
	Score	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	38	38	38	38	38	38	38	38
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Iq heavy chain V r	Iq heavy chain V r	~	genome polyprotein	hypothetical prote	Ig heavy chain V r	Ig heavy chain V r	Iq heavy chain V r	hypothetical prote			_	Ig heavy chain V r	_	Ţ.	
144151	5,46393	S49530	JQ1734	S69468	S33404	PH1239	PH0099	F75116	PH1429	PH1274	826907	S12424	S12428	S12431	PH1240
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126	129	135	1718	173	40	102	119	862	98	86	86	101	101	101	102
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92	92	92	92.7	90	87	87	87	87	85	82	85	82	85.4	85	82
38	38	38	38	37	36	36	36	36	35	35	35	35	35	35	35
30	31	32	. 33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1

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Systems Vergion - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Musrig97 #sequence_revision 29-Aug-1997 #text_change 23-Jul-1999
C;Accession: S36383; S33398
R;Ansell, K.H.
submitted to the EMBL Data Library, April 1993
A;Reference number: S36376
A;Reference number: S36383
A;Molecule type: mENA
A;Residues: 1-63 -ANS-
A;Molecule type: mENA
A;Residues: 1-63 -ANS-
A;Cross-references: EMBL:X73016; NID:g295883; PIDN:CAA51502.1; PID:g939945
R;Kettleborough, C.A.; Saldanha, J.; Ansell, K.H.; Bendig, M.M.
Bur. J. Immunol. 23, 206-211, 1993
A;Title: Optimization of primers for cloning libraries of mouse immunoglobulin genes usir A;Reference number: S33391; MUID:93122092; PMID:8419173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Igheavy chain V region - mouse
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C; Accession: S17604
R; Clackson, T; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 64-652, 1991
A; Title: Making antibody fragments using phage display libraries.
A; Reference number: S17230; MUID:91326098; PMID:1907718
A; Accession: S17604
A; Status: preliminary
A; Molecule type: nucleic acid
A; Residues: 1-98 < CLA>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 8-91/Domain: immunoglobulin homology < IMM>
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A;Residues: 1-40,'X' <KET>
A;Residues: 1-40,'X' <KET>
A;Cross-references: EMBL:X73016
A;Experimental source: strain BALB/c
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-63/Domain: immunoglobulin homology (fragment) <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 41; DB 2, Length 63;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 7; Conservative 0; Mismatches 0; Indels
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836383
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Autoimmunity 12, 135-141, 1992
A;Title: Cloning of a human autoimmune response: preparation and sequencing of a human ar
A;Reference number: S67940; MUID:92314301; PMID:1617110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C'Species: Mus musculus (house mouse)
C'Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C'Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C'Accession: PH0971
R'Itilman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 779, 1992
A'Fille: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B ct A;Reference number: PH0971; MUID:92381444; PMID:1512540
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C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S26320
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                                                                                                                                                                                                                                                                          100.0%; Score 41; DB 2; Length 105; 100.0%; Pred. No. 0.82; ive 0; Mismatches . 0; Indels
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A;Rostdues: 1-107 <57RA
A;Cross-references: BMBL:X59206
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heteroterzamer; immunoglobulin
F;3-86/Domain: immunoglobulin homology <IMM>
                                                                                     A;Accession: S67941
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-105 cHEXA
A;Cross-references: EMBL:X73851
C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Molecule type: mRNA
A,Residues: 1-107 <TIL>
A,Residues: 1-107 <TIL>
A,Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;11-94/Domain: immunoglobulin homology <IMM>
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(c) Species: Mus musculus (house mouse)
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Best Local Similarity 100.0%; Pred. No. 0.6
Matches 7; Conservative 0; Mismatches
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A;Status: nucleic acid sequence not shown
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J. Exp. Med. 174, 613-624, 1991
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Best Local Similarity 100.
Matches 7; Conservative
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Matches 7; Conservative
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A,Status: preliminary
A,Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                   B37263
Ig heavy chain V region (1G3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: B37263
R;Goshorn, S.C.; Retzel, E.; Jemmerson, R.
A;Title: Chem. 266, 2134-2142, 1991
A;Title: Common structural features among monoclonal antibodies binding the same antigen A;Reference number: A38601; MUID:91115823; PMID:1703527
A;Accession: B37263
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C;Species: Mus musculus (house mouse)
C;Species: 30-899-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH0978
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective 1A;Reference number: PH0971; MUID:92381444; PMID:1512540
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C.Date: 19-7 #sequence_revision 09-May-1997 #text_change 30-May-1997
C.Accession: S67941
C.Accession: S67941
C.Accession: J.M.; Furmaniak, J.; Pegg, C.; Burton, D.R.; Smith, B.R.
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                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Cross-references: GB:M57997; NID:g195426; PIDN:AAA63335.1; PID:g195427
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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                                         DB 2; Length 98;
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                                                               0.76;
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                                         100.0%; Score 41; 100.0%; Pred. No.
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                Query Match
Best Local Similarity 100.
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Best Local Similarity الان،
م، 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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GYSFTGY 25
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GYSFTGY 24
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A;Residues: 1-105 <TIL>
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A; Residues: 1-102 <GOS>
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A;Status: nucleic acid sequence not shown

Query Match Best Local Similarity 100.

25 GYSFTGY 31

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GYSFTGY

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C; Accession: PL0084
R; Meek, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.; Car
J. Exp. Med. 169, 519-533, 1989
A; Title: Structural characterization of antidiotypic antibodies; evidence that Ab2s are
A; Reference number: PL0080; MUID:89094248; PMID:2492056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: PL0084
A;Accession: PL0084
A;Molecule type: mRNA
A;Residues: 1-118 <MEE>
A;Cross-references: GB:X58595; GB:Y00794; NID:G51573; PIDN:CAA41470.1; PID:G938254
A;Cross-references: GB:X58595; GB:Y00794; NID:G51573; PIDN:CAA41470.1; PID:G938254
A;Experimental source: strain BALB/c
A;Note: 66-Gly is translated as "X" from the codon GGN
A;Note: the sequence shown here is from the VH region of an antidiotypic monoclonal anti
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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R;Smith, R.G.; Voss Jr., E.W.
Mol. Immunol. 27, 463-470, 1990
A.Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from N;
A;Reference number: PL0198: WUID:90309768; PMID:2114528
                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Mus musculus (house mouse)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 21-Jan-2000
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
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C;Species: Mus musculus (house mouse)
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                                                                                       Length 114;
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Pred. No. 0.92;
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F;50-66/Region: complementarity-determining 2
F;99-110/Region: complementarity-determining 3
F;99-106/Region: D region
C; Keywords: heterotetramer; immunoglobulin F;11-94/Domain: immunoglobulin homology <IMM>
                                                                                       Score 41;
Pred. No.
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                 Query Match
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Matches 7, Conservative
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Matches 7; Conservative
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C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH0977
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J; Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B A;Reference number: PH0971; MUID:92381444; PMID:1512540
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$26319
Ig heavy chain V region - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000
C;Accession: S26319
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein A;Reference number: $26309; MUID:91341421; PMID:1908510
                                                                                                                                                                                                  C,Accession: PH0972
R,Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A,Title: Both Igm and IgG anti-DNA antibodies are the products of clonally selective B A;Reference number: PH0971; MUID:92381444; PMID:1512540
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                                                                                                                                         C.Species: Mus musculus (house mouse)
C.Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
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                                                                                                                                                                                                                                                                                                                                                                                                             A.Molecule type: mRNA
A.Residues: 1-108 <TLL>
A.Experimental source: B cell, strain [NZB x NZW]Fl
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Keywords: heterotetramer; immunoglobulin
F;14-97/Domain: immunoglobulin homology <IMM>
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A; Experimental source: B cell, strain (NZB x NZW]F1
C; Superfamily: immunoglobulin v region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
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                                                                                                                chain V region (clone 17s.128) - mouse (fragment) s: Mus musculus (house mouse)
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A;Status: nucleic acid sequence not shown

Molecule type: mRNA

Best Local Similarity 100. Matches 7; Conservative

Query Match

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A,Accession: S26319 A,Molecule type: mRNA A;Residues: 1-114 <STA>

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anti-glycoprotein H monoclonal antibody heavy-chain variable domain (Mab 33) - mouse (free Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Musculus (house mouse)
C;Accession: F45722
R;Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasque J. Virol. 67, 489-496, 1993
A;Fitle: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hum A;Reference number: A45722; MUID:93100833; PMID:7677958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Shalaby, M.R.; Shepard, H.M.; Presta, L.; Rodrigues, M.L.; Beverley, P.C.L.; Feldmann, J. Exp. Med. 175, 217-225, 1992
A;Title: Development of humanized bispecific antibodies reactive with cytotoxic lymphocyt
A;Reference number: PH0885; MUID:92113462; PMID:1346155
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Ig heavy chain V region (anti-cyclosporin E) - mouse (fragment)
Ig heavy with musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 21-Jan-2000
C;Accession: PH0100
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C;Species: Mus musculus (house mouse)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
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A.Residues: 1-122 «SHA»
A.Residues: 1-122 «SHA»
A.Note: the authors translated the codon TTC for residue 70 as Leu
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                       Length 120;
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A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-120 <SIM>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
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C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
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F;15-99/Domain: immunoglobulin homology <IMM>
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Best Local Similarity
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A49982
Lip heavy chain V region (BA7.1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: A49982
R;Lin (Richer-Emmons, T.; Villalobos, A.P.; Foster, M.H.; Wahlgren, C.; Kleyman, T.R J. Biol. Cham. 269, 2805-2813, 1994
A;Title: Topology of an amiloride-binding protein.
A;Reference number: A49982; MUID:94132051; PMID:8300613
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: B53285
R; Sawada, J; Mizusawa, S.; Terao, T.; Naito, M.; Kurosawa, Y.
Mol. Immunol. 28, 1063-1072, 1991
Mol. Immunol. 28, 1063-1072, 1991
A; Title: Molecular characterization of monoclonal anti-steroid antibodies: primary struct
                                                                                                                                                                                                                                             mic
                                                                           C;Species: Mus musculus (house mouse)
C;Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000
C;Datesesion: 193602
R;Eilat, D.; Webster, D.M.; Rees, A.R.
J. Immunol. 141, 1745-1753, 1988
A;Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 1878-Eference number: A30502; MUID:88315787; PMID:2457627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig heavy chain V and J regions, monoclonal antibody OHP101.Bl1.1 - mouse (fragment) C;Species: Mus musculus (house mouse) C;Species: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
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A Modecule type: mRNA; protein
A; Modecule type: mRNA; protein
A; Note: sequence inconsistent with nucleotide translation
A; Note: sequence extracted from NCB1 backbone (NCBIN:63295, NCBIP:63300)
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
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*Residues: 1-120 <LIN.*
A;Cross-references: GB:L24802; NID:g452096; PIDN:AAA98740.1; PID:g452097
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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A;Reference number: A53285; MUID:92017897; PMID:1922102
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                                                           Ig heavy chain V region (A52) - mouse C; Species: Mus musculus (house mouse)
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Matches 7; Conservative C
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Best Local Similarity 100.00
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A,Molecule type: mRNA
A,Residues: 1-119 <ELL>
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Gene 208, 315-322, 1998
A,Title: The Ld Cht1 gene encodes the secretory chitinase of the human pathogen Leishmanj
A,Reference number: JC6551, MUID:98201628, PMID:9524285
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A;Residues: 1-457 ×SHA>
A;Crost-references: DBBJ:AF009354
C;Comment: This enzyme cleaves the beta-1-4 linkage between N-acetyl-glucosamine residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Keywords: glycoprotein; glycosidase; glycosyltransferase; hexosyltransferase; hydrolase F;1-15)Comain: signal sequence #status predicted <SIG> F;20-457/Product: chitinase #status predicted <AIG> F;20-457/Product: chitinase #status predicted <AIT> F;384/Binding site: carbohydrate (Asn) (covalent) #status predicted
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R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mollo 1. 227, 776-798, 1992
J. Mille: The repertoire of human germline V(H) sequences reveals about fifty groups of V.
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26938
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Leishmania donovani
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 07-May-1999
C;Accession: JG655;
R;Shakarian, A.M.; Dwyer, D.M.
Gene 208, 315-322, 1998
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Ig heavy chain V region (DP-75) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov_1993 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
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                              Pred. No. 1.1;
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Pred. No. 2.8;
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85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
                         Best Local Similarity 100.
Matches 7; Conservative
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Best Local Si
Matches 7,
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A;Residues: 1-135 <YAO.
A;Residues: 1-135 </AC.
A;Residue
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H2513
H2513
H2513
H2513
H2513
G. Action precursor V region (BXW16) - mouse
C; Species: Mus musculus (house mouse)
C; Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C; Accession: H3513
F; Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.; J. Ciln. Invest. 82, 852-860, 1988
A.Title: Immunoglobulin kappa light chain variable region gene complex organization and A; Reference number: A94689; MUID:88331394; PMID:3138286
R;Schmitter, D.; Poch, O.; Zeder, G.; Heinrich, G.F.; Kocher, H.P.; Quesniaux, V.F.J.;
Mol. Immunol. 27, 1029-1038, 1990
Mol. Immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin homology < IMM>
Mol. Immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin homology < IMM>
Mol. Immunoglobulin | Immunoglobulin homology < IMM>
Mol. Immunoglobulin | Immun
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F;50-66/Region: complementarity-determining 2
F;99-112/Region: complementarity-determining 3
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-137 <KOF>
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C.Species: Homo sapiens (man)
C.Date: 24-Feb-1994 #Sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C.Accession: PH1669
R.Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A.Fitle: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyloc
A.Reference number: PH1642; MUID:93301610; PMID:8315388
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Cibate: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 21-Jul-2000
Cibate: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 21-Jul-2000
Cibacession: S00476; $34013
R;Matsuda, F:; Lee, K.H.; Nakai, S.; Sato, T.; Kodaira, M.; Zong, S.O.; Ohno, H.; Fukuhai EMBO J. 7, Jud7-1051, 1988
EMBO J. 7, Jud7-1051, 1988
A;Ttele: Dispersed localization of D segments in the human immunoglobulin heavy-chain loc A;Reference number: S00476; MUID:88296408; PMID:2841108
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*Residues: 1-117 < MATS.

*Note: the authors translated the codon AGT for residue 89 as Met.

*Mariette, X.; Tsapis, A.; Brouet, J.C.

*Mariette, X.; Tsapis, A.; Brouet, J.C.

*Trine munol. 23, 846-851, 1991

*Title: Nucleotidic sequence analysis of the variable domains of four human monoclonal 3

*Reference number: S34001; MUID:93209281; PMID:7681398
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C;Keywords: heterotetramer; immunoglobulin
F;1.19,Domain: signal sequence #status predicted <SIG>
F;20-117/Product: Ig heavy Chain V region (V35) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>
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A;Molecule type: mRNA
A;Residues: 1-110 cHHI>
A;Experimental source: B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: hereroterzamer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>
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85.7%; Pred. No. 3.3;
ive 1; Mismatches 0; Indels
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                                                                                                                                                                                               Ig heavy chain V region (clone 3B2) - human (fragment)
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Pred. No. 3.1;
1; Mismatches
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A;Map position: 14q32.33-14q32.33
A;Introns: 16/1
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85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
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Molecule type: mRNA
Residues: 20-116 <MAR>
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18 GYTFTGY 24
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Best Local Similarity
Matches 6; Conserv
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PH1668

Igheavy chain V region (clone 3G5) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996

C;Accession: PH1668

R;Hille: TH1668

R;Hille: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylc

A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig heavy chain V region (clone RFTS7H), rheumatoid factor - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C;Accession: 569899
R;Randen, I.; Pascual, V.; Victor, K.; Thompson, K.M.; Forre, O.; Capra, D.J.; Natvig, J R;Randen, I.; Pascual, V.; Victor, K.; Thompson, K.M.; Forre, O.; Capra, D.J.; Natvig, J A;Title: Synovial IgG rheumatoid factors show evidence of an antigen-driven immune respons A;Reference number: S69896; MUID:93272805; PMID:8500520
      C;Accession: S26912
R;Tomlinson, 1. M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Stetus: preliminary
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A;Cross-references: EMBL: 234893; NID: 9509803; PIDN: CAA84376.1; PID: 9509804
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology rinA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:Z12310; NID:g32979; PIDN:CAA78180.1; PID:g32980
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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A;Residues: 1-109 <HIL>
A;Residues: 1009 <HIL>
A;Experimental source: B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 98;
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Pred. No. 2.8;
1; Mismatches
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Pred. No. 3.1;
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85.7%;
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Best Local Similarity 85.77
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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Matches 6; Conservative
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A; Residues: 1-98 <TOM>
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C;Accession: I44151

R;Zebedee, S.L; Barbas III, C.F.; Hom, Y.L.; Caothien, R.H.; Graff, R.; DeGraw, J.; Pyat Price, S.L.; Barbas III, C.F.; Hom, Y.L.; Caothien, R.H.; Graff, R.; DeGraw, J.; Pyat Pritle: Human combinatorial antibody libraries to hepatitis B surface antigen. A;Feference number: A44151, MUID:92228746; PMID:1373487
A;Accession: I44151
A;Accession: I44151
A;Accession: Legen RNA
A;Redule: preliminary; not compared with conceptual translation
A;Redules: Preliminary;
A;Residues: 1-126 - 2EB>
A;Nose-references: GB MR8309; NID:g183952; PIDN:AAA35967.1; PID:g183953
A;Note: nucleotide translation not given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D. J. Mol. Biol. 239, 68-78, 1994
A; Title: In vitro assembly of repertoires of antibody chains on the surface of phage by A; Reference number: S46390; MUID: 94254092; PMID: 8196048
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submitted to the EMBL Data Library, October 1994
A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
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A,Cross-references: EMBL:231680; NID:9509786; PIDN:CAA83485.1; PID:91335146
C;Superfamily: immunoglobulin V region; immunoglobulin homology.
C;Reywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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C;Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
C;Accession: S49530
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C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
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A;Residues: 1-135 <MAH>
A;Cross-references: EMBL:246348; NID:9560839; PIDN:CAA86467.1;
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMA
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Pred. No. 3.9;
1; Mismatches 0; Indels
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0
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Pred. No. 3.6;
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Pred. No. 3.7;
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85.7%;
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Best Local Similarity 85.7%;
Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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A;Status: preliminary
A;Molecule type: DNA
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C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C;Accession: S36.56
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries. A;Reference number: S36.256; MuID:93178448; PMID:7679990
A;Accession: S36.265
A;Status: preliminary; nucleic acid sequence not shown
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A;Cross-references: EMBL:X62106; NID:g37831; PIDN:CAA44016.1; PID:g37832
A;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.;
J. Exp. Med. 175, 831-842, 1992.
A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from the A;Reference number: S23623; MUID:92156804; PMID:1740665
                                                                                                             C;Species: Homo sapiens (man)
C;Date: 13.-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C;Datession: 818551, 823625
C;Accession: 818551, 823625
R;Shin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; EMBO J. 10, 3641-3645, 1991
A;Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: c A;Reference number: 818551; MUID:92037524; PMID:1935893
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144151
Ig heavy chain V region (BO) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 28-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-117/Product: Ig heavy chain V region (VI-2) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Residues: 1-117 <OLE>
A,Cross.references: EMBb:X59704; NID:g32552; PIDN:CAA42225.1; PID:g32553
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836265
Ig heavy chain V region (clone alpha-MUC1-1) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38; DB 2; Length 117;
Pred. No. 3.3;
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                              RESULT 28
S18551
Ig heavy chain V region precursor (VI-2) - human (fragment)
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Pred. No. 3.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92.7%;
85.7%;
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85.7%;
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Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                     A;Accession: S18551
A;Molecule type: DNA
A;Residues: 1-117 <SHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GYSFTGY 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GYSFTGY 7
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A; Residues: 1-118 <GRI>
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GYTFTGY 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: S23625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Introns: 16/1
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R;Schmitter, D.; Poch, O.; Zeder, G.; Heinrich, G.F.; Kocher, H.P.; Quesniaux, V.F.J.; Ve Mol. Immunol. 27, 1029-1038, 1990
A;Title: Analysis of the structural diversity of monoclonal antibodies to cyclosporine. A;Reference number: PH0087; MUID:91042649; PMID:2122240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VHS gene in human B cell chroni
mouse immunoglobulin genes usir
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C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Mus musculus (house mouse)
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                     A; Experimental source: strain BALB/c
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: B cell chronic lymphocytic leukemia C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterocteramer; immunoglobulin P;19-102/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-119 <SCH>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer: immunoclobulin
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A,Title: Extensive and selective mutation of a rearranged
A,Reference number: PH1232, MUID:93018822, PMID:1402653
A,Title: Optimization of primers for cloning libraries of A,Reference number: $33391; MUID:93122092; PMID:8419173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig heavy chain V region (clone CLL8) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36; DB 2;
Pred. No. 6.9;
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Pred. No. 8;
                                                                                                                                                                                                                                        F;15-40/Domain: immunoglobulin homology (fragment)
                                                                                                                                                                                                                                                                                          Score 36; DB :
Pred. No. 2.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Keywords: heterotetramer; immunoglobulin;15-98/Domain: immunoglobulin homology <IMM>;15-98/Domain: complementarity-determining 1
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                                                                                                                                                                                                                                                                                          87.8%;
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                                                                                                                                    A; Cross-references: EMBL: X73024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 85...
Best Local 6; Conservative
                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       26 GYSFTGH 32
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Accession: PH1239
A,Molecule type: mRNA
A,Residues: 1-102 <CAI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GYSFTGY 7
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                                                       A;Accession: S33404
A;Molecule type: mRNA
A;Residues: 1-40 <KET>
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A;Residues: 1-173 <FUL>
A;Cross-references: EMBL:U40829; NID:g1066476; PID:g2347174; GSPDB:GN00016; MIPS:YPR150w
                                                                                                                                                                                                                                                                                                                                                 R;Kanyuka, K.V.; Vishnichenko, V.K.; Levay, K.E.; Kondrikov, D.Y.; Ryabov, E.V.; Zavriev
G. Gen. Virol. 73, 2553-2560, 1992
A;Title: Nucleotide sequence of shallot virus X RNA reveals a 5'-proximal cistron closel
A;Reference number: JQ1734; MUID:93019008; PMID:1339468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;MOJecule type: genomic RNA
A;Residues: 1-1718 «KAN»
A;Cross-references: GB:M97264; NID:g295078; PIDN:AAA47787.1; PID:g295079
C;Superfamily: eggplant mosaic virus RNA-directed RNA polymerase
C;Keywords: ATP; nucleotide binding; nucleotidyltransferase; P-loop; RNA biosynthesis;
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IG heavy chain V region - mouse (fragment)
IS pecies: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 17-Jul-1998
C;Accession: S33404
R;Kettleborough, C.A.; Saldanha, J.; Ansell, K.H.; Bendig, M.M.
                                                                                                                                                                                 genome polyprotein - shallot virus X
N'Alternate names: RNA nucleotidyltransferase (RNA-directed); RNA replicase
N'Contains: RNA-directed RNA polymerase (EC 2.7.7.48)
C'Species: shallot virus X
C'Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
C'Accession: JQ1734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Saccharomyces cerevisiae
C;Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 19-Apr-2002
C;Accession: S69468
R;Fulton, L.
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    yeast (Saccharomyces cerevisiae)

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A.Cross-references: SGD:S0006354
A.Map position: 16R
C.Superfamily: Saccharomyces hypothetical protein YPR150w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rifulton, L. submitted to the EMBL Data Library, November 1995
Alpescription: The sequence of S. cerevisiae cosmid 9659.
Alference number: $69022
Alfecesion: $69468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;915-922/Region: nucleotide-binding motif A (P-loop)
F;978-983/Region: nucleotide-binding motif B
F;921/Binding site: ATP (Lys) #status predicted
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Matches 6; Conservative
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GFSFTGY 141
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GYSYTGY 629
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                                                          GYTFTGY
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- human (fragment)

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Gaps .; 0

Length 98; 1; Indels

DB 2; 10;

Score 35; DB 2 Pred. No. 10; 0; Mismatches

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Clackes Journal of the Management of the Managem
                                                                                                                            C.Species: Homo sapiens (man)
C.Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: July 18, 2003, 15:10:42 Job time : 10.1 secs
                                                              region (clone PBL5)
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85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
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A;Experimental source: strain Orsay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;anonymous, Genoscope submitted to the EMBL Data Library, July 1999 submitted to the EMBL Data Library, July 1999 submitted to the EMBL Data Library, July 1999 strong the EMBL Data Library abjecting into archaeal chromosome stru A;Reference number: A75001 A;Reference number: P75116 A;Accession: F75116 A;Accession: F75116 A;Accession: P75116 A;
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A; Residues: 1-98 < VAN>
A; Residues: 1-98 < VAN>
A; Residues: 1-98 < VAN>
J: Exp. Med. 168, 229-245, 1988
A; Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin
A; Reference number: PL0116; MUID:88286083; PMID:2840480
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C;Date: 03-Feb-1994 #text_change 21-Jan-2000
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Accession: PH1429; PL0119
B;Van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
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Pred. No. 61;
0; Mismatches 1; Indels
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iive 0; Mismatches
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A, Residues: 1-862 < KAW>
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RESULT 40

Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

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Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
Johno H., Fukuhara S., Honjo T.;
"Dispersed localization of D segments in the human immunoglobulin
heavy-chain locus.";
                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Pred. No. 2.1;
1; Mismatches
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01-NOV-1991 (Rel. 20, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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                                                                                                                                                         ALIGNMENTS
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                                HV43_MOUSE
CRB3_BOVIN
CRB3_HUMAN
CRB3_HOUSE
CRB3_RAT
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YKU5_CAEEL
GIGA_CLOAB
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INTERPRO; IPR003006; IG MHC.
INTERPRO; IPR003596; IG_V.
Ffan; PP00047; ig; 1.
SMART; SM00406; IGV; 1.
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85.7%;
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                                                                         July 18, 2003, 15:02:20 ; Search time 4.34 Seconds (without alignments) 66.897 Million cell updates/sec
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          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Score

Result è S ö

1718 AA.

PRT;

RESULT 2
RRPO SHVX
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AC Q04575;
DT 01-JUN-1994 (Rel. 29, Created)

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UL95\_HSV6U CGA1\_CARAU HFE1\_HAEIN GARD\_BACSU

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SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are the EMBL outstations the Buropean Bioinformatics Institutes. There are content is in no its by non-profit institutions at long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-88144476; PubMed=3125551;
Wilson M.R., Middleton D., Warr G.W.;
"Immunoglobulin heavy chain variable region gene evolution: structure
and family relationships of two genes and a pseudogene in a teleost
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig heavy chain V region 3 precursor.
Carassius auratus (Goldfish).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
Cyprinidae, Carassius.
NCBI_TaxID=7957;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP-binding; Helicase; RNA replication; RNA-directed RNA polymerase;
                                                                                                                                                                                                                                                                                                                                                FUNCTION: RNA-replication. The central part of this protein possibly functions as an ATP-binding helicase. CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                Kanyuka K.V., Vishnichenko V.K., Levay K.E., Kondrikov D.Y., Ryabov E.V., Zavriev S.K., Vishuichenko V.K., Levay K.E., Kondrikov D.Y., Involeotide sequence of shallot virus X RNA reveals a 5'-proximal cistron closely related to those of potexviruses and a unique arrangement of the 3'-proximal cistrons.";
J. Gen. Virol. 73:2553-2560(1992).
                                                                                                           Viruses; ssRNA positive-strand viruses, no DNA stage; Allexivirus
  01-JUN-1994 (Rel. 29, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
RNA replication protein (194 kDa protein) (ORF 1) [Contains: RNA-directed RNA polymerase (EC 2.7.7.48); Probable helicase].
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Pred. No. 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    915 922 ATP (POTENTIAL).
1718 AA; 194529 MW; 820FEAEIEB62415C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR005123; 20G-FeII Oxy.
InterPro; IPR001788; RNA_dep_RNapol2.
InterPro; IPR000606; Viral_helicasel.
Pfam; PF00978; RNA_dep_RNapol2; 1.
Pfam; PF01443; Viral_helicasel; 1.
Pfam; PF03171; 20G-PeII Oxy; 1.
                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=93019008; PubMed=1339468;
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Best Local Similarity 85.7°,
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                         Shallot virus X (ShVX)
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GYSYTGY 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; JQ1734; JQ1734.
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                                                                                                                                    NCBI_TaxID=31770;
                                                                                                                                                                                                                                                                                                                                                                                                                      RNA (N)
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ID HV03 C
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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--- ALTERNATIVE PRODUCTS: 4 ISOFORMS; 1/P45 (SHOWN HERE), 2/P42, 3/P40
AND 4/P37; ARE PRODUCED BY ALTERNATIVE SPLICING.
--- SIMILARITY: CONTAINS 2 RNA RECOGNITION MOTIFS (RRM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UDN-2002 (Rel. 41, Last annotation update)
Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Differential expression of AUF1 isoforms in rat tissues.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: BINDS WITH HIGH AFFINITY TO RNA MOLECULES THAT CONTAIN
AU-RICH ELEMENTS (ARES) FOUND WITHIN THE 3-PRIME UNTRANSLATED
REGIONS OF MANY PROTOONCOGENES AND CYTOKINE MRNAS (BY SIMILARITY)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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FRAMEWORK-2.
COMPLEMENTARITY - DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 34; DB 1; Length 117; Pred. No. 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAMEWORK
                                                                                                                                                                                                                                                                                                                                        HSSP; P01772; 2FB4.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGY; 1.
Immunoglobulin V region; Signal.
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Q9JJ54; Q9JJ53; Q9JJ52; Q9JJ51;
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                                                                                                                                                                                                                                                                        EMBL; J03616; AAA50807.1; -
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HSSP; P09651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIM; 601324;
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K6P1_STRCO
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Q14101; Q14101; Q14102;
Q1-5001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 41, Last annotation update)
Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element HNR-D OR AUFI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPSQNWNQGYSNYWNQGYGSYGYNS
YYGYGDYSN -> D (IN ISOFORM 3 AND ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE=58403404; PubMed=7673125;
Kajita Y., Nakayama J., Aizawa M., Ishikawa F.;
"The UNG-specific RNA binding protein, heterogeneous nuclear ribonucleoprotein D0. Common modular structure and binding properties of the 2xRB-Gly family.";
J. Biol. Chem. 270:22167-22175(1995).
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Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: BINDS WITH HIGH AFFINITY TO RNA MOLECULES THAT CONTAIN
-!- FUNCTION: BINDS WITH HIGH AFFINITY TO RNA MOLECULES THAT CONTAIN
BEGIONS OF MANY PROTOCONCOGENES AND CYTOKINE MRNAS.
-!- SUBCELLULAR LOCATION: NUCLEAR; component of ribonucleosomes.
-!- ALTERNATIVE PRODUCTS: 4 ISOFORMS; 1 (SHOWN HERE), 2, 3 AND 4; ARE
-!- PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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MEDLINE-28277449; PubMed-5915222;
Dempsey L.A., Li M.-J., DePace A., Bray-Ward P., Maizels N.;
"The human HNRPD locus maps to 4q21 and encodes a highly conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISSING (IN ISOFORM 2 AND ISOFORM 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
EMBL, AB046615; BAB03465.1; -.
EMBL, AB046616; BAB03466.1; -.
EMBL, AB046618; BAB03466.1; -.
EMBL, AB046618; BAB03468.1; -.
EMBL, AB046618; BAB03468.1; -.
EMBL, AB046618; BAB03468.1; -.
EMBL, AB046618; BAB03468.1; -.
EMBL, AB046618; EMB03468.1; -.
EMBL, EMB0360; EMM, 2.
EMBCSTE; PS50102; EMM; 2.
EMCSTE; PS50030; RRM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 34; DB 1; Length 353;
Pred. No. 32;
1; Mismatches 1; Indels
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RNA-BINDING (
RNA-BINDING (
GLY-RICH.
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71.4%;
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les 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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VARSPLIC
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YYGYGDYSN -> D (IN ISOFORM 3 AND ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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STRAIN=A3(2) / 1109,
MEDLINE=97208211; PubMed=9055413;
Alves A.M.C.R., Euverink G.J.W., Bibb M.J., Dijkhuizen L.;
MIdentification of ATP-dependent phosphofructokinase as a regulatory
steep in the glycolytic pathway of the actinomycete Streptomyces
coelicolor A3(2).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNA-BINDING (RRM) 1.
RNA-BINDING (RRM) 2.
GLY-RICH.
MISSING (IN ISOFORM 2 AND ISOFORM 4).
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
6-phosphofructokinase 1 (EC 2.7.1.11) (Phosphofructokinase 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34; DB 1; Length 355;
Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000504; RNA_rec_mot.
Pfam; PF00076; rrm; 2.
SMART; SM00360; RRM; 2.
PROSITE; PS50102; RRM; 2.
PROSITE; PS00030; RRM RNP 1; 2.
Nuclear protein; RNA-binding; Ribonucleoprotein; Repeat;
Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D0B6EA177BEF789E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Phosphohexokinase 1) (ATP-PFK).
PFKA1 OR PFKA OR PFK1 OR SC02119 OR SC6E10.13c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       342 AA
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SEQUENCE FROM N.A.
STRAIN=A3(2) / M145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALA-RICH
                                                                                                                                                                                                                                                                                                                                                      AF026126; AAC23474.1;
AF026126; AAC23475.1;
AF026126; AAC23476.1;
AF039575; AAB96683.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 355 AA; 38434 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.9%;
71.4%;
                                                                                                                                                                                                                                                                       D55671; BAA09522.1; -. D55672; BAA09523.1; -. D55673; BAA09524.1; -.
                                                                                                                                                                                                                                           EMBL; D55674; BAA09525.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genew; HGNC:5036; HNRPD.
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Best Local Similarity 85.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  153 GVŠFTGY 159
                                                                                                                                                                                                                                                                                                                                      JR; A41238; A41238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     304
392 AA;
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Q60362;
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MOD_RES
SEQUENCE
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TRANSMEM
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  ID ACCOOR SEE ACCOOR S
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                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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PROSITE; PS00433; PHOSPHOFRUCTOKINASE; 1.
Kinase; Transferase; Glycolysis; Multigene family; Allosteric enzyme;
Complete proteome.
SEQUENCE 342 AA; 36664 MW; CEEFC7B74092AB34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
          Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence of the model actinomycete Streptomyces coelicolor {\rm A3}\,(2)\,.\,^{\circ},
                                                                                                                                                                                                                              Nature 417:141-147(2002).
-!- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-
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0
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Klein P.S., Sun T.J., Saxe C.L. III, Kimmel A.R., Johnson R.L.,
Devreotes P.N.;
                                                                                                                                                                                                                                                                                                                                  -:- PATHWAY: KEY CONTROL STEP OF GLYCOLYSIS.
-:- SUBUNT: HOMOTETRAMER (BY SIMILARITY).
-:- SUBCELLULAR LOCATION: CYCOPIASMIC (By similarity).
-:- SIMILARITY: BELONGS TO THE PHOSPHOFRUCTOKINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
                                                                                                                                                                                                                                                                         fructose 1,6-bisphosphate.
-!- ENZYME REGULATION: ALLOSTERICALLY INHIBITED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JVN-1990 (Rel. 13, Created)
01-JNN-1990 (Rel. 13, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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Pred. No. 47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch)
MEDLINE=21996410; PubMed=12000953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000023; Ppfruckinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AL109661; CAB51967.1; -.
HSSP; P00512; 3PFK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00476; PHFRCTKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80.5%;
71.4%;
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                                                                                                                                                                                                                                                                                                                  PHOSPHOENOLPYRUVATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00365; PFK; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 GYDFTGF 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GYSFTGY 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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ID CAR1_DIC
AC P13773;
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Matches
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THE EXPRESSION OF A LARGE NUMBER OF DEVELOPMENTALLY REGULATED GENES, THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS.
-!- SUBCELLULAR LOCATION. Integral membrane protein.
-!- DEVELOPMENTAL STAGE: EXPRESSED PREDOMINANTLY DURING EARLY AGGREGATION AND AT LOW LEVELS DURING LATER STAGE.
-!- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.
-!- SIMILARITY: BELONGS TO FAMILY 5 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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PHOSPHORYLATION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00002; 7tm_2; 1.—
PRINTS; PR00247; GPCRCAMP.
PROSITE; PS50261; G_PROTEIN RECEP_F2 4; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Phosphorylation; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Methanococcus jannaschii.
Archaea; Buryarchaeota; Methanococci; Methanococales;
Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38C4561EE1CC9A69 CRC64;
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-2002 (Rel. 41, Last annotation update)
Putative Na (+)/H(+) exchanger MJ0057.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     426 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 53;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 (POTENTIAL)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEČUENCE FROM N.A.
STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASN-RICH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dictybb; DD02012; carA.
InterPro; IPR000848; GPCR_CAMP.
InterPro; IPR000832; GPCR_secretin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44312 MW;
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NCBI_TaxID=1097;
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INIT.MET
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TRANSMEM
TRANSMEM
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TRANSMEM
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CYB6_CHLTE
ID CYB6_CHL'
AC Q9F721;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
MEDLINE=96337999; PubMed=8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Stalavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Stott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kalley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Wosse C.R., Venter J.C.,
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND SEQUENCE OF 1-24.
Schuetz M., Zirngibl S., le Coutre J., Buettner M., Xie D.-L.,
Nelson N., Deutzmann R., Hauska G.;
"A transcription unit for the Rieske FeS-protein and cytochrome b in
Chlorobium limicola.";
Photosyn. Res. 39:163-174(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chlorobium limicola f.sp. thiosulfatophilum.
Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
Chlorobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPRO00676; NaH_Exchngr.
Pfam; PF00999; Na_H_Exchanger; 1.
Hypothetical protein; Transmembrane; Transport; Antiport; Sodium transport; Complete protecome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
PETB
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Pred. No. 58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.5%;
                                                                                                                                                                                                                                     Science 273:1058-1073(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Conservative
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Q592<u>9</u>7;
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FUNCTION: COMPONENT OF THE GREEN S-BACTERIA BC-COMPLEX WHICH CONSISTS OF THE RIESKE PROTEIN AND CYTOCHROME B SUBUNIT AND WHICH, APPEARS TO LACK A CYTOCHROME C1-EQUIVALENT. THIS COMPLEX HAS A COMPARATIVELY LOW REDOX POTENTIAL. COFFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY BOUND TO THE PROTEIN.
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STRAIN=TLS / ATCC 49652 / DSM 12025;

MEDLINE=20433268; PubNed=10976061;

MEDLINE=20433268; PubNed=10976061;

"Molecular evidence for the early evolution of photosynthesis.";

Science 289:1724-1730(2000)

-!- FUNCTION: COMPONENT OF THE GREEN S-BACTERIA BC-COMPLEX WHICH
CONSISTS OF THE RIESKE PROPEIN AND CYTOCHROME B SUBUNIT AND
WHICH, APPERAS TO LAGK A CYTOCHROME C1-EQUIVALENT. THIS

COMPLEX HAS A COMPARATIVELY LOW REDOX POTENTIAL (BY SIMILARITY).
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IRON 1 (HEME B562 AXIAL LIGAND)
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IRON 2 (HEME B566 AXIAL LIGAND)
SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000179; Cyt_b b6.
Pfam; PF0003; cytochrome b N; 1.
PROSITE; PS00192; CYTOCHROME B HEME; 1.
PROSITE; PS00133; CYTOCHROME B, PALSE NEG.
Electron transport; Respiratory chain; Transmembrane; Heme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 33; DB 1; Length 427; Pred. No. 58;
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CEE6F0AE1BC757D4 CRC64;
                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Cytochrome B-C complex cytochrome B subunit.
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71.4%;
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Best Local Similarity 71.4
Matches 5; Conservative
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Gaps

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Score 32; DB 1; Length 117; Pred. No. 25; 1; Mismatches 1; Indels

C530F829C906F69B CRC64;

IG HEAVY CHAIN V REGION 23. PRAMEMORK-1. COMPLEMENTARITY-DETERMINING-1. FRAMEMORK-2.

COMPLEMENTALITY-DETERMINING-2. FRAMEWORK-3.
BY SIMILARITY.

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mmunoglobulin V region; Signal.
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71.4%;
                                                                                                                   Query Match
Best Local Similarity 71.4%,
Lines 5; Conservative
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  SMART; SM00406; IGV; 1
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                                                                                                          117 AA;
                                                                                                                                                                   1 GYSFTGY 7
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                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6;
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SEQUENCE
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                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@iabb-sib.ch).
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COPACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 124:625-637(1981).

-!- MISCELLANEOUS: THIS GERMIINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES. THAT COULD ENCODE V RECIONS OF NPB ANTIBODIES. PIR, A02030; HVMS23.

HSSP; PO1810; 2FBJ.

InterPro; IPR00306; Ig_MHC.

InterPro; IPR003596; Ig_V.

Pfam; PF00047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Wusaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
MCBI_TaxID=10090;
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IRON 1 (HEME B562 AXIAL LIGAND) (BY
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SIMILARITY).
                                                                                                                                                                                                                                                                                              (HEME B562 AXIAL LIGAND)
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                                                                                                                      Query Match 80.5%; Score 33; DB 1; Length 427; Best Local Similarity 71.4%; Pred. No. 58; Matches 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                      87736B20F89167E3 CRC64;
          BOUND TO THE PROTEIN.
-!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
1g heavy chain V region 23 precursor.
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MEDLINE=81234548; PubMed=6788376;
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                                                                                                                    EMBL; AF287480; AAG12195.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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386
418
158
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                                                                                                                                                                                                                                                                                                258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
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Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K..
Baltimore D.;
                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
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PRAMEMORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEMORK-2.
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                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IIG heavy chain V region 3 precursor.
Mus musculus (Mouse).
117 AA
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BY SIMILARITY
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PP00047; Ig; 1.
SMART; SM0406; IGv; 1.
Immunoglobulin V region; Signal.
SIGNAL.
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C02034; HVMS45.
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117 AA;
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HV10_MOUSE
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Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
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COMPLEMENTARITY-DETERMINING-2.
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 Score 32; DB 1; Length 117;
Pred. No. 25;
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                                       Indels
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                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V region 102 precursor.
                                                                                                                                                                                            117 AA
                                      1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig_v.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv. 1.
Immunoglobulin V region; Signal.
78.0%;
71.4%;
                                      Conservative
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45 GYTFTSY 51
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45 GYTFTSY 51
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 Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                    GYSFTGY
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P01750;
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SEQUENCE
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HV09_MOUSE
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                                                                                   "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1971).
-!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
PIR, BO2034; HWS61.
HSSP: P01810; 2FBJ.
INTERPO: IPR003066; Ig_MHC.
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-!- MISCELLANBOUS: THIS GERMINDE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
Baltimore D.;
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MEDINE=81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IG HEAVY CHAIN V REGION 186-1.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
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Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
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BY SIMILARITY.
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SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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1117
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PIR; A02029; HVMSA1.
                    45 GYTFTSY 51
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                                                                                                                                                            NCBI_TaxID=10090;
 1 GYSFTGY
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P01747:
                                                                    HV52 MOUSE
P06327;
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HV03_MOUSE
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Matches
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Yancopoulos G.D., Alt F.W.;
"Developmentally controlled and tissue-specific expression of unrearranged VH gene segments.";
Cell 40:271-281(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IG HEAVY CHAIN V REGION VH558 B4.
                                                                               COMPLEMENTARITY-DETERMINING-2
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COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                           COMPLEMENTARITY-DETERMINING-1 FRAMEWORK-2.
                                                                                                                                78.0%; Score 32; DB 1; Length 117; 71.4%; Pred. No. 25; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.0%; Score 32; DB 1; Length 117; 71.4%; Pred. No. 25; ive 1; Mismatches 1; Indels
                                        IG HEAVY CHAIN V REGION 145. FRAMEWORK-1.
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                                                                                                              12921 MW; D37DE8A3F543E996 CRC64;
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                                                                                                                                                                                                                                                                          01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                               117 AA
                                                                                                                                                                                                                                                                                              Ig heavy chain V region VH558 B4 precursor.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY
                                                                                         FRAMEWORK-3
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InterPro,
InterPro,
Pfam, PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
Pfam; PF00047; ig; 1.
SMARY; SM00406; IGv; 1.
Imwunoglobulin V region; Signal.
SIGNAL 1 19
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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Conservative
                                                                                                                                          Local Similarity 71.4
les 5; Conservative
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45 GYTFTSY 51
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Matches 5; Conserv
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                                                                                                                                                                        1 GYSFTGY 7
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                                                                                                                                                                                                                                              HV49 MOUSE
P06328;
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NON TER
SEQUENCE
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SEQUENCE
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IG HEAVY CHAIN V REGION VH558 A1/A4.
FRAMIBWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
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MEDLINE=8509340; PubMed=2578321;
Yancopoulos G.D., Alt F.W.;
"Developmentally, controlled and tissue-specific expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPLEMENTARITY-DETERMINING-2
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                                                    01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
heavy chain V region VH558 Al/A4 precursor.
Mus musculus (Mouse).
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).
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117 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unrearranged VH gene segments.";
Cell 40:271-281(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1. Immunoglobulin V region; Signal.
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InterPro; IPR003006; 1g_MHC.
InterPro; IPR003596; 1g_v.
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nes 5, Conservative
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STANDARD;
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Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL (NPB ANTIBODIES).
                                                                                                                                                                                                                                                                                                                                                                                                                 Zakut R., Cohen J., Givol D.;
Nucleic Acids Res. 84839-4840(1980).
-!- MISCELLANBOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
FROM A MYELOMA THAT SECRETES IGG2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
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Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                     MEDLINE-81053741; PubMed-6253904; Zakut R., Cohen J., Givol D.; "Cloning and sequence of the CDNA corresponding to the variable region of immunoglobulin heavy chain MPC11."; Nucleic Acids Res. 8:3591-3601(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Heavy chain variable region contribution to the NPb family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78.0%; Score 32; DB 1; Length 121; 71.4%; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                              21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long a modified and this statement is not removed.
                                       121 AA.
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                                                                                                                                   Ig heavy chain V region MPC 11. Mus musculus (Mouse).
                                                                        21-JUL-1986 (Rel. 01, Created)
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HSSP; P01810; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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Matches
RESULT 20
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                                                                                        "The genetic basis of antibody production: the dominant anti-arsonate idiotype response of the strain A mouse.";
Eur. J. Immunol. 12:1023-1032(1982).
-!- MISCELLANBOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME JESCHENT, JH2.

SEGMENT, JH2.
PIR; A02028; HVMSG7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;

"A V region determinant (idiotope) expressed at high frequency in B
lymphocytes is encoded by a large set of antibody structural genes.";

BMBO J. 3:517-523(1984).

PIR; A02037; MHMS15.

HSSP; P01810; 2FBJ.

InterPro; IPR003006; Ig MHC.

InterPro; IPR003596; Ig W.

SMART; SM00406; IGv; 1.

Immunoglobulin V region.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Pred. No. 26;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78.0%; Score 32; DB 1; Length 120; 71.4%; Pred. No. 26;
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                                                                                                                                                                                                                                                                                                                                                                                            120 AA; 13307 MW; FF04E4A167B654AF CRC64;
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              SEQUENCE FROM N.A.
MEDLINE-83131846; Pubmed-6186498;
Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN'1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
01-UUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V region AC38 15.3.
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                                                                                                                                                                                                                                                    HSSP; P01789; 1MCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                   78.0%;
71.4%;
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                                                                              Marshak-Rothstein A.;
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120 AA;
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GYTFTSY 32
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tes 5; Conserv
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P06329;
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SEQUENCE
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SMART; SM00406; IGV; 1.
Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                     IG HEAVY CHAIN V REGION B1-8/186-2. FRAMEWORK-1.
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Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Somatic mutation in genes for the variable portion of the immunoglobulin heavy chain."; Science 216:309-311(1982).
                                                                                 COMPLEMENTARITY - DETERMINING - 1.
                                                                                                                           COMPLEMENTARITY - DETERMINING-2
                                                                                                                                                                                                                                                                                           Score 32; DB 1; Length 139;
Pred. No. 30;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                        15419 MW; 1B57DD4FD0C9F465 CRC64;
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Pred. No. 30;
1; Mismatches
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21-JUL-1986 (Rel. 01, Created)
2-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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JH2 SEGMENT
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  Signal.
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71.4%;
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71.4%;
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Best Local Similarity 71.4
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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Wmunoglobulin V
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HV02_MOUSE
ID _HV02_MOUSE
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SEQUENCE
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      (See http://www.isb-sib.ch/announce/
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-!- MISCELLANEOUS: THE B1-8 MU CHAIN MENA WAS CLONED FROM A HYBRIDOWA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky
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                                                                                                                                                                                                                                                        IG HEAVY CHAIN V REGION S43.
FRAMEWORK-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADD5881BF44B8EC9 CRC64;
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JH2 SEGMENT
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      entities requires a license agreement (
or send an email to license@isb-sib.ch)
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                             EMBL, J00539; AAA38172.1; -. PIR, AAC2038; G2MS43. HSSP, 001010; 2FBJ. InterPro; IPR0033006; Ig_MHC. InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; J00529; AAA38170.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 71.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 AA;
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Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1.

45 GYTFTSY

Length 140;

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                                                                                                                                                                                              -!- FUNCTION: MAY BE INVOLVED IN THE CONTROL OF THE CELL CYCLE AT THE GL/S (START) AND G2/M (MITOSIS) TRANSITIONS (BY SIMILARITY).
-!- SUBUNIT: INTERACTS WITH THE CDK2 AND THE CDC2 PROTEIN KINASES TO FORM A SERINE/THREONINE KINASE HOLGENZYME COMPLEX. THE CYCLIN SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=AM30 (770235) / Serotype B;
MEDLINE=95089703; PubMed=7997179;
WAN Ham M.S., van Alphen L., Mooi F.R., van Putten J.P.M.;
"The fimbrial gene cluster of Haemophilus influenzae type b.";
MOI. Microbiol. 13:673-684(1994).
-! FUNCTION: MAY BE A MINOR STRUCTURAL PROTEIN REQUIRED FOR PILUS
BIOGENESIS. MAY BE THE ADHESIVE COMPONENT IN THE PILI.
                                                                                                              "Molecular cloning and immunological analysis of goldfish cyclin A
                                                                                                                                                                                                                                                                                                                                                 SIMILARITY). SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Eagan / Serotype B;
MEDLINE=95012708; PubMed=7927773;
McCrea K.W., Watson W.J., Gilsdorf J.R., Marrs C.F.;
"Identification of hifb and hifb in the pilus gene cluster of Haemophilus influenzae type b strain Eagan.";
Infect. Immun. 62:4922-4928(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                       Katsu Y., Yamashita M., Hirai T., Tokumoto T., Kajiura H.,
Nagahama Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 32; DB 1; Length 391;
Pred. No. 80;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plam, PP02984; CYCLIN, SMART; SM00385; CYCLIN; 2. PROSITE; PS00292; CYCLINS; 1. PROSITE; PS00292; CYCLINS; 1. Call division; Mitosis.
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
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                     MEDLINE=95377548; PubMed=7649388;
                                                                                                                                             oocyte maturation.";
iol. 170:616-625(1995)
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83.3%;
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InterPro; IPR004367; Cyclin
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Pfam; PF02984; cyclin_C; 1.
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Quet Local Similarity 83.3.,
Best Local Similarity 63.3.
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HFEL HAEIN
ID HFEL HAE
AC P45994;
$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\fra
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Martin M.E., Efstathiou S., Craxton M., Macaulay H.A.;
"The DNA sequence of human herpesvirus-6: structure, coding content,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Carassius.
NCBI_TaxID=7957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Virology 209:39-51(1995).
-!- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS TOGETHER EBV BGLF3,
HVS-1 34, HSV-6 U67, AND HCMV UL95.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Human herpesvirus 6 is closely related to human cytomegalovirus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=9008013; PubMed=2152817;
Lawrence G.L., Chee M., Craxton M.A., Gompels U.A., Honess R.W.,
Barrell B.G.;
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Pred. No. 73;
0; Mismatches 1; Indels
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Roseolovirus.
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
CCNAI OR CCNA.
                                                                                                                                                               (Rel. 21, Created)
(Rel. 34, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                              353 AA.
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EMBL; X83413; CAA58359.1; -.
PIR; C36769; C36769.
InterPro; IPR004280; UL95.
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                                                                                                           STANDARD;
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                                                                                                                                                                                                                                                     Protein U67.
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                                                                                                                                                                                          01-OCT-1996
16-OCT-2001
                                                                                                     UL95 HSV6U
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IDENTIFICATION
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P39829;
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                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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A kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
A portise R., Brans A., Brans A., Brans A., Brans A., Brans B.C., Bron S.,
Brorise R., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
A Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
A Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
A Guiseppi G., Guy B.J., Hasono S., Hullo M.F., Itaya M., Jones L.,
Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
A Hee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
A Noone D., O'Reilly M., Porterelle D., Porwollik S., Prescott A.M.,
Prescean E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
A Rieger M., Rivolte C., Roche B., Rose M., Sadaie F.,
A Rieger M., Rivolte C., Roche B., Rose M., Sadaie F.,
A Rieger M., Rivolte C., Roche B., Rose M., Sadaie F.,
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MEDLINE=55219079; PubMed=7704254;
Ogawa K.-I., Akagawa E., Nakamura K., Yamane K.;
Ogevam K.-I., Akagawa E., Nakamura K., Yamane K.;
"Determination of a 21548 bp nucleotide sequence around the 24 degrees region of the Bacillus subtilis chromosome.";
Microbiology 141:269-275(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GARD BACSU STANDARD; PRT; 510 AA.
P42240; P42241;
01-NOV-1995 (Rel. 32, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable D-galactarate dehydratase (EC 4.2.1.42) (GalcD)...
                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 435;
                                                                                                                                                                                                                                                                                                                                           31 POTENTIAL.
435 MINOR FIMBRIAL SUBUNIT HIFE.
48851 MW, 420C733661DE7D67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
-!- SIMILARITY: TO B.PERTUSSIS FIMD AND E.COLI FIMH.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 32; DB
Pred. No. 89;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=168;
MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                         EMBL, Z33502; CAA83904.1; --
InterParc, IPR000259; Fimbrial.
Pfam, PF00419; Fimbrial; 1.
Fimbria; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                            78.0%;
                                                                                                                                                                                                                                   EMBL; U13254; AAA61542.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                    107 GYSFAGF 113
                                                                                                                                                                                                                                                                                                                                                                                              435 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GYSFTGY 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
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Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpetra P., Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vasarocti A., Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T., Winters P., Wingat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H.P., Zumstein B., Yoshikawa H.P., Jancthin A.; "The complete genome sequence of the Gram-positive bacterium Bacilus
                                                                                                                                                                                                                                                                                                                     Nature 390:249-256(1997)
-!- CATALYTIC ACTIVITY: D-galactarate = 5-dehydro-4-deoxy-D-glucarate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baird L., Georgopoulos C., and characterization of the Escherichia coli sohA gene, a suppressor of the htrA (degP) null phenotype."; J. Bacteriol. 172:1587-1594(1990).
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-!- SIMILARITY: BELONGS TO THE UXAA FAMILY.
-!- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 32; DB 1; Length 510;
Pred. No. le+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       510 AA; 54792 MW; C7283A007174CDE3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1995 (Rel. 31, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
D-galactarate dehydratase (EC 4.2.1.42) (GalcD)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D30808; BAA06472.1; ALT FRAME.
EMBL; D30808; BAA06473.1; ALT_FRAME.
EMBL; Z99105; CAB12045.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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71.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 71.41
Local 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SubtiList; BG11163; garD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 GYTFEGY 121
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STRAIN=K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GYSFTGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mau B., Shao Y.;
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us-10-007-790-5.rsp

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                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
"Two types of somatic recombination are necessary for the generation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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MANNAN ENDO-1,4-BETA-MANNOSIDASE
2 X 39 AA APPROXIMATE REPEATS.
AND XYNA, AND TO THOSE OF N.PATRICIARUM XYNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 32; DB 1; Length 569;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aydrolase; Glycosidase; Signal; Multigene family; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-ASN.
19277764E18328B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of complete immunoglobulin heavy-chain genes."; Nature 286:676-683(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 AA
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Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR002883; CBD_5.
Interpro; IPR00805; GlyCo hydro_26.
Interpro; IPR001230; Prenyl_site.
Pfam; PF02013; GDM_10; 2.
Pfam; PF02156; GlyCo hydro_26; 1.
PRINTS; PR00739; GLHYDRIASE26.
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SMART; SM00406; IGV; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64115 MW;
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85.7%;
                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X97520; CAA66134.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18
569
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477
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569 AA;
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GYSFTGY 7
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SEQUENCE
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HV44 MOUSE
   임
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                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20225875; PubMed=10762278;
Monterrubio R., Baldoma L., Obradors N., Aguilar J., Badia J.;
Monterrubio R., Baldoma L., Obradors N., Aguilar J., Badia J.;
M. common regulator for the operons encoding the enzymes involved in
D-galactarate, D-glucarate, and D-glycerate utilization in
Escherichia coli.,
J. Bacteriol. 182:2672-2674 (2000)
-:- CATALYTIC ACTIVITY: D-galactarate = 5-dehydro-4-deoxy-D-glucarate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Evidence that the Piromyces gene family encoding endo-1,4-mannanases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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SIMILARITY: THE 39 AA REPEATS ARE SIMILAR TO THOSE IN MANA, MANC
                                                                                                                                   MEDLINE=98447507; PubMed=9772162;
Hubbard B.K., Koch M., Palmer D.R., Babbitt P.C., Gerlt J.A.;
"Evolution of enzymatic activities in the enolase superfamily:
characterization of the (D)-glucarate/galactarate catabolic pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arose through gene duplication.";
FEMS Microbiol. Lett. 141:183-188(1996).
-!- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-beta-D-mannosidic linkages in mannans, galactomannans, glucomannans, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-UUL-1998 (Rel. 36, Last annotation update)
Mannan endo-1,4-beta-mannosidase C precursor (EC 3.2.1.78) (Beta-mannanase C) (1,4-beta-mannan mannanohydrolase C).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 32; DB 1; Length 523;
Pred. No. 1.1e+02;
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MEDLINE=96313314; PubMed=8768520;
Millward-Sadler S.J., Hall J., Black G.W., Hazlewood G.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
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Neocallimasticaceae, Piromyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            523 AA; 56401 MW; 919BCC8B49411BB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               569 AA
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                             Unpublished observations (DEC-1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M30178; -; NOT_ANNOTATED_CDS.
EcoGene; EG12522; gard.
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                                                                                                                                                                                                                                                                           in Escherichia coli.";
Biochemistry 37:14369-14375(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.0%;
71.4%;
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                                                                                                  CHARACTERIZATION.
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P55298;
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SEQUENCE
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AC PS5298 b
DT 01-0CT-10T DT 15-JUL-10T DT 15-JUL-10T DE MANDAN CO NEOCALL TR N 11 DAN CO NCBL TR N 11 DAN CO NCBL TR N 11 DAN RA MILIWAN RX MEDLINE RT EVIGET RT ACOSE t FENS MILIWAN CC FENS MILIWAN CO FENS MILIWAN CC FENS MILIWAN CO FENS MILIWAN CO
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                                                                 "MISCELLANBOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF WHICH OCCUR IN THE D AND J SEGMENTS.

-!- MISCELLANBOUS: THIS PROTEIN BINDS DEXTRAN.

PIR; A26242; MHMSJ5.

HSSP; PO1789; INCP.

InterPro; IPR003096; Ig_MHC.

InterPro; IPR003396; Ig_V.

Pfam; PF0047; ig; 1.

SMART; SMOO406; Ig_V.

SMART; SMOO406; Ig_V.

DISULPID 22 96 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
Schilling J., Clevinger B., Davie J.M., Hood L.;
"Amino acid sequence of homogeneous antibodies to dextran and DNA
rearrangements in heavy chain V-region gene segments.";
Nature 283:35-40(1980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=81245215; PubMed=6789211;
Givol D., Zakut R., Effron K., Rechavi G., Ram D., Cohen J.B.;
"Diversity of germ-line immunoglobulin VH genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h Similarity 71.4%; Pred. No. 38; 5; Conservative 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                   13024 MW; 292E2AF4BE447E41 CRC64;
                                                                                                                                                                                                                                                                                                                                                   Score 31; DB 1;
Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
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SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; J00488; AAA38519.1; -. PIR; AO2041; HVMS8A. HSSP, P01810; 2FBJ. InterPro; IPR0033006; Ig_MHC. InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                       75.6%;
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                                                                                                                                                                                                                                                                                                                                                                                            5; Conservative
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                                                                                                                                                                                                                                                                                                                   117 AA;
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Matches 5; Conserv
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Best Local Similarity
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P01758;
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SEQUENCE
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-83075344; PubMed=6816276;
Kehry M.R., Puhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
Hood L.E.;
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Pred. No. 38;
1; Mismatches 1; Indels
                   IG HEAVY CHAIN V REGION PJ14.
                                                                                                                                   1; Indels
   19
115 IG HEAVY CHAIN V REGION PO
115
12447 MW; 7569DD4A4843D500 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN HAS ALSO BEEN DETERMINED.
                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).
                                                                                          Score 31; DB 1
Pred. No. 38;
1; Mismatches
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71.4%;
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                                                                                                                                   5; Conservative
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GYTFTDY 32
                                                                                                                                                                                                        45 GFSLTGY 51
                                                           115 AA;
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Best Local Similarity
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Best Local Similarity
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P01757;
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P01756;
                   CHAIN
NON TER
SEQUENCE
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HV13 MOUSE
1D HV13 MOUSE
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DT 21-JUL.
DT 15-JUL.
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OC Mammal;
OC C Edwary
OC MARMEN;
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or send an email to license@isb-sib.ch).
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SMART; SM00406; IGV; 1.
Immunoglobulin V region; Signal.
SIGNAL
1 19 19 IG
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Best Local Similarity 71.4%;
Matches 5; Conservative
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                                                                                                           HSSP, P01772, 2FB4.
InterPro, IPR003006, Ig MHC.
InterPro, IPR003596; Ig V.
                                                                       EMBL; J00494; AAA38130.1;
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SGD; S0000771; YEL045C.
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                                                                                             PIR; A02042; HVMSB1.
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P32616;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                             Dildrop R., Bovens J., Slekevitz M., Beyreuther K., Rajewsky K.;
"A V region determinant (idiotope) expressed at high frequency in B
Lymphocytes is encoded by a large set of antibody structural genes.";
EMBO J. 3:517-523(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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MEDLINE-8222262; PubMed-6806821;
Krapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Simultaneous expression of immunoglobulin mu and delta heavy chains by a cloned B-cell lymphoma: a single copy of the VH gene is shared by two adjacent CH genes.";
                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mūs musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                01-JJN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Hobary chain V region AC38 205.12.
Mus musculus (Mouse).
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V region BCL1 precursor.
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J SEGMENT.
BY SIMILARITY.
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig, 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region.
                                                                                                                                   STANDARD;
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96
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| GYTFTDY 51
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HSSP; P01789; IMCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GYSFTGY 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HV15 MOUSE
P01759;
                                                                                                                             HV51 MOUSE
P06330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
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                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-S288C / AB972;
Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G., Hunicke-Smith S., Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V., Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                               .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-077-1993 (Rel. 27, Created)
01-077-1993 (Rel. 27, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
Hypothetical 16.5 kDa protein in GLY1-GDAl intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mulligan J.T., Dietrich F.S., Hennessey K.M., Sehl P., Komp Wei Y., Taylor P., Nakahara K., Roberts D., Davis R.W., Submitted (FEB-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75.6%; Score 31; DB 1; Length 141;
IG HEAVY CHAIN V REGION BCL1.
                                                                                                                                                                                                                                           Indels
                                     136 136
136 AA; 15078 MW; 6827CFBC6DB3F35E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 AA; 16468 MW; F6604AC5343A5D5C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; ATP-binding; Transmembrane. NP BIND 15 22 ATP (POTENTIAL). TRÂNSMEM 38 58 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 AA
                                                                                                                                                           Score 31; DB
Pred. No. 44;
                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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208
24197 |
                                                                                      Shih M., Lampi K.J.,
Submitted (AUG-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GYSFTGY 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P02522; 2BB2
                                                       SEQUENCE FROM N.A.
   NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; B
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDDMed=6774258; MEDINE=81012133; PubMed=6774258; Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.; Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.; "Two types of somatic recombination are necessary for the generation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- MISCELLANEOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A DIFFERENTIATED GENE ISOLATED FROM A MYELOMA THAT SECRETES IGG2B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus (Bovine).
Wakaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Murídae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75.6%; Score 31; DB 1; Length 144; 71.4%; Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15759 MW; 8E47A7CB3706D30A CRC64;
                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complete immunoglobulin heavy-chain genes."; cure 286:676-683(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 210 AA. 1919 1. 018790; Created) 15-JUL-1998 (Rel. 36, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 26-OCT-2011 (Rel. 40, Last annotation update) CRYBB3.
                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                   144 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain V region MOPC 141 precursor.
Pred. No. 46;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP, P01825, 7FAB.
InterPro, IPR003006, Ig_MHC.
InterPro, IPR003596, Ig_V.
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; V00768; CAA24149.1; -.
PIR; A02094; G2MS14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
   Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 AA;
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Matches 5; Conserv
                                                                                                                             |||||:
62 YSFTGF 67
                                                                                  2 YSFTGY 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                HV43 MOUSE .
P01819;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                            ELT. J. BIOCHEM. 139:467-479(1984).

-!- FUNCTION: CRYSTALLINS ARE THE DOMINANT STRUCTURAL COMPONENTS

OF THE VERTEBRATE EYE LENS.

-!- SUBJUILT: HOMO/HETEROJINER, OR COMPLEXES OF HIGHER ORDER. THE
STRUCTURE OF BETA-CRYSTALLIN OLIGOMERS SEEMS TO BE STABILIZED
THROUGH INTERACTIONS BETWEEN THE N-TERMINAL ARMS (BY SIMILARITY).

-!- DOMAIN: HAS A TWO-DOMAIN BETA-STRUCTURE, FOLDED INTO FOUR
VERY SIMILAR GREEK KEY MOTITES.

-!- SIMILARITY: BELONGS TO THE BETA/GAMMA-CRYSTALLIN FAMILY.
                                                                                                                               TISSUE=Lens cortex;
MEDLINE=84132667; PubMed=6698025;
MEDLINE=84132067; PubMed=6698025;
Berbers G.A.M., Hoekman W.A., Bloemendal H., de Jong W.W.,
Kleinschmidt T., Braunitzer G.;
"Homology between the primary structures of the major bovine beta-
crystallin chains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
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5; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
3
Shearer T.R., David L.L., to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
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L -> LG (IN REF. 2).
9DlC68B93C9966EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NPAFG -> HPNFA (IN REF. NE -> DD (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDSLL -> QDNLS (IN REF. LH -> IK (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SN -- NG (IN REF. 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C -> S (IN REF. 2).
S -> A (IN REF. 2).
R -> Q (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G -> GH (IN REF. 2)
H -> G (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONNECTING PEPTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C-TERMINAL ARM.
G -> GG (IN REF.
VI -> IV (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00247; XTALDG; 2.
PROSITE; PS00225; CRYSTALLIN BETAGAMMA; 4.
Eye lens protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (
or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOTIF 1.
MOTIF 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOTIF 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nterPro; IPR001064; Crystallin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00030; crystall; 2.
PRINTS; PR01367; BGCRYSTALLIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF013259; AAB67120.1; -. PIR; B27898; B27898.
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EMBL;
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAY SEQUENCE FROM N.A.

RAY MEDLINES-2005165 PubMed=10591208;

RAY MEDLINES-2005165 PubMed=10591208;

RAY DUNDAM I. A. MINECOUGH R.A. Almeda J.P., Babbage A.K.,

RAY Bailey C., Bailey J., Bailow K.E., Battes K.N., Beasley O.P.,

RAY BITG.C.P., Bailey J., Bailow K.E., Battes K.N., Beasley O.P.,

RAY BITG.C.P., Blakey S.E., Bridgemen A.M., Buck D., Charges J.,

RAY BITG.C.P., Blakey S.E., Bridgemen A.M., Buck D., Char Y., Clark G.,

RAY CORLOYD N.R., Colel G.G., COX A.V., Davis J., Dawson E.,

CORLOYD N.R., Coville G.J., COX A.V., Davis J., Dawson E.,

RAY BITG.C.P., Man Coville G.J., COX A.V., Davis J., Dawson E.,

RAY BITG.C.P., Fall-Tamlyn G., Hearhoct R.W., Hos., Holmes S.,

Hunt S.E., Jones M.C., Ershaw J., Kindberley A.M., King A.,

Hall R.E., Hall-Tamlyn G., Hearhoct R.W., Hos., Holmes S.,

Hunt S.E., Jones M.C., Evershaw J., Kindberley A.M., King A.,

Hall R.E., Jones M.C., Evershaw J., Kindberley A.M., King A.,

Hall R.E., Hall-Tamlyn G., Hearhoct R.W., Hos., Holwyd C., Liloyd D.M.,

RAY Martyn I.D., Mashredpil-Mohammadi M., Matthews L.H., McClay J.,

McClay J., McDaren S., McMurray A.A., Mille S.A., Mortimore B.J.,

RAY Martyn I.D., Mashredpil-Mohammadi M., Matthews L.H., McClay J.,

RAY Martyn I.D., Mashredpil-Mohammadi M., Matthews L.H., McClay J.,

RAY Martyn I.D., Mashredpil-Mohammadi M., Matthews L.H., McClay J.,

RAY Milliams L., Williams S.A., Milliams S.A., Smith M.L.,

Soderlund C., Spragon L., Steward C.A., Suleton J.E., Swann R.M.,

RAY Audin M., Wall M., Walliams S.A., Williams S., Rawasaki K., Sasaki T., Asakwa S., Kudoh J.,

RAY Minoshmas S., Kawasaki K., Sasaki T., Asakwa S., Kudoh J.,

RAY Minoshmas S., Kawasaki K., Sasaki T., Asakwa S., Kudoh J.,

RAY Minoshmas S., Links S., Links S., Loh P., Malla E., Mayner S., Born D.,

RAY Mang Q., Mang Y., Marg S., Links J., Milliams D., Paylin K., Milson R.,

RAY Mang Q., Mang Y., Marg S., Links S., Batterston R., Williams L.,

RAY Mang Q., Mang Y., Marg S., Links Saltes S., Bedelmann L.,

RAY Korf I., Bedell J.A., Hiller L., Mardis E., Wolldman P
                                                                                                                                                                                                                                                                                                                                                                                                                                     Different evolution rates within the lens-specific beta-crystallin
                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                              "Sequence analysis of betaA3, betaB3, and betaA4 crystallins completes the identification of the major proteins in young human
                                                                                                                                                                                                                                                    Lampi K.J., Ma Z., Shih M., Shearer T.R., Smith J.B., Smith D.L.,
David L.L.;
                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Lens;
BEDLINE=89279929; PubMed=2499686;
Aarts H.J.M., Jacobs E.H.M., van Willigen G., Lubsen N.H.,
Schoenmakers J.G.G.;
                                                                                                                                                                                                                      SEQUENCE OF 1-103 FROM N.A., AND MASS SPECTROMETRY
                                     CRB3 HUMAN STANDARD; PRT; 211 AA. P26998; Q92965; Q9UH09; 01-AUG-1992 (Rel. 23, Created) [-6-CT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Beta crystallin B3 (Beta-B3-crystallin).
                                                                                                                                                                                                                                                                                                                            Biol. Chem. 272:2268-2275(1997).
                                                                                                                                                                                                                                    MEDLINE=97152999; PubMed=8999933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . Mol. Evol. 28:313-321(1989).
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 66-211 FROM N.A.
                                                                                                                                                Homo sapiens (Human).
                                                                                                                               CRYBB3 OR CRYB3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       family.";
                         CRB3_HUMAN
                                                                                                                                                                                                                                                                                                                   lens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
         RESULT 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                               Nature 402:489-495(1999).

-!- FUNCTION: CRYSTALLINS ARE THE DOMINANT STRUCTURAL COMPONENTS OF THE VERTEBRATE EYE LENS.

-!- SUBUNIT: HOMO/HETERODIMER, OR COMPLEXES OF HIGHER ORDER. THE STRUCTURE OF BETA-CRYSTALLIN OLICOMERS SEEMS TO BE STRAILIZED THROUGH INVERACTIONS BETWERN THE N-TERMINAL ARMS (BY SIMILARITY).

-!- DOMAIN: HAS A TWO-DOMAIN BETA-STRUCTURE, FOLDED INTO FOUR VERY SIMILAR (BREEK KEY MOTIFS).

-!- MASS SPECTROMETRY: MM-24222; MM ERR=3; METHOD=Electrospray.

-!- SIMILARITY: BELONGS TO THE BETA/GAMMA-CRYSTALLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L., Tilahun Y., Wright H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -> L (IN REF. 2).
7557AAE9178FFAF1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D -> H (IN REF. 3)
E -> D (IN REF. 2)
                                                                         "The DNA sequence of human chromosome 22.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-TERMINAL ARM.
MOTIF 1.
MOTIF 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C-TERMINAL ARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update,
Beta crystallin B3 (Beta-B3-crystallin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TitterPro; IPR001064; Crystallin.
Pfam; PF00030; crystall; 2.
PRINTS; PR01367; BGCRYSTALLIN.
SMART; SM00247; XTALDS; 2.
BYEOSITE; PS00225; CRYSTALLIN BETAGAMMA; 4.
Bye lens protein; Repeat; Acetylation.
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.6%; Score 31; ilarity 71.4%; Pred. No. 6 Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOTIF 3.
MOTIF 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U71216; AAC50972.1; -. EMBL; X15144; CAA33242.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X15146; CAA33244.1; ALT_SEQ. 299916; CAB17042.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24230 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAA33243.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genew; HGNC:2400; CRYBB3.
MIM; 123630; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63
1113
1113
1155
1199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S10089; S10089.
HSSP; P02522; 2BB2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 GYEFPGY 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173
211 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X15146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X15145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRB3 MOUSE
Q9JJŪ9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                   "Sequence analysis of beta-A2-, beta-A4- and beta-B3-crystallin CDNA completes the identification of the members of this gene family in the
                                                                                                      Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: CRYSTALLINS ARE THE DOMINANT STRUCTURAL COMPONENTS

-!- FUNCTION: CRYSTALLINS ARE THE DOMINANT STRUCTURAL COMPONENTS

-!- SUBUNIT: HOWO/HETERODIMEN, OR COMPLEXES OF HIGHER ORDER. THE
STRUCTURE OF BETA-CRYSTALLIN OLIGOMERS SEEMS TO BE STABILIZED
THROUGH INTERACTIONS BETWEEN THE N-TERMINAL ARMS (BY SIMILARITY).

-!- DOMAIN: HAS A TWO-DOMAIN BETA-STRUCTURE, FOLDED INTO FOUR
VERY SIMILAR GREEK KEY MOTIFS.

-!- SIMILARITY: BELONGS TO THE BETA/GAMMA-CRYSTALLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 31, DB 1, Length 211;
Pred. No. 67;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACETYLATION (BY SIMILARITY)
N-TERMINAL ARM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOTIF 4.
C-TERMINAL ARM.
2F23F47987102196 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOTIF 1.
MOTIF 2.
CONNECTING PEPTIDE.
MOTIF 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; POZ522; 2BB2.

MGD; MGI:102717; Crybb3.

InterPro; IPR01064; Crystallin.

Pfam; PF00030; crystall; 2.

RRINTS; PR01367; BGCRYSTALLIN.

SMART; SM00247; XTALbg; 2.

RROSITE; PS00225; CRYSTALLIN BETAGAWWA; 4.

Eye lens protein; Repeat; Acetylation.

MOD_RES.

1 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24291 MW;
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Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156
200
211 AA;
[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
SEQUENCE
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Search completed: July 18, 2003, 15:07:15 Job time : 6.34 secs

160 GYEFPGY 166

8 8

1 GYSFTGY 7

Q91x94 mus musculu Q96imO homo sapien Q92130 mus musculu Q9f750 bacteroides O14979 homo sapien

Q96x81 sulfolobus

014979 homo sapien 098115 streptococc 064862 apple stem 098248 apple stem 0892f18 listeria mo 03331 listeria mo 092ey1 listeria in P71707 mycobacteri 08xui7 caenorhabdi 060159 schizosacch 08xui7 caenorhabdi 060159 schizosacch 08xui85 mycobacteri 085293 leishmania

Sequence:

Run on:

Searched:

Database

097mx7 clostridium (8r8e7 thermoanaer (99175 mus musculu (924r6 mus musculu (924r5 mus musculu (924r2 mus musculu (924p8 mus musculu

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Gaps

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Indels

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123 AA

PRELIMINARY;

Q8VIJ1 Q8VIJ1;

OBVIJ1 ID O

arabidopsis arabidopsis arabidopsis

RESULT 2

GYSFTGY

56

d

thermoplasm pyrococcus

Result Š. mus musculu mus musculu

097974 t 099706 f 0991081 m 099106 m 098209 m 098209 m 098229

Length 120;

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Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
"Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
"Definition of the BBL/GenBank/DDBJ databases.
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF307936; AAL09420.1;
InterPro; IPR003006; Ig_MHC.
NON_TER 1
NON_TER 1
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Pterin-mimicking anti-idiotope heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 AA; 13204 MW; DC4834ABIDE56F3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 41; DB.11;
100.0%; Pred. No. 1.7;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                  Q9Z130
Q9F750
O14979
                                                                                                                                                                        Q9S115
Q64962
Q9E948
Q8YED0
Q92F18
Q9EXF6
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Q92E00
P71707
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Q8VKS5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q97MX7
Q8R8E7
Q9JL75
Q924R6
Q924R5
Q924R2
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01-DEC-2001 (TrEMBLrel. 19, Last seq
                           Q91X94
Q96IM0
                                                                                                                                                                                                                                                                                                                                                                                Q9ZEY1
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                                                                                                                                                                                                                                                                                                                                                       033931
                                                                                                                                                PRELIMINARY;
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820
1023
1031
1645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ^
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NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GYSFTGY
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   SEQUENCE
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Matches
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Q920E8
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Q9u195 homo sapien
Q991c4 mus musculu
013572 saccharomyc
Q9anj6 bradyrhizob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8vijl mus musculu
O60994 leishmania
Q9ul94 homo sapien
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79.863 Million cell updates/sec
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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us-10-007-790-5.rspt

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Scristosoma japonicum (Blood fluke).
Bukaryota, Metazoa; Platyhelminthes; Trematoda, Digenea; Strigeidida;
Schistosomatoidea; Schistosomatidae; Schistosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 21, Last annotation update)
Monoclonal anti-idiotypic antibody NP30 heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SONG X.T., Feng Z.Q., Guan X.H.;
"Amplification, cloning and sequence analysis of the heavy chain variable region gene of monoclonal anti-idiotypic antibody NP30 of Schistosoma japonicum.";
Schistosoma japonicum.";
Submitted (JUM-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF282622; AAG01452.1;
                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                               Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                    MEDLINE-98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035020; AAD56256.1; -
HSSP; PO1810; 2FBJ.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig_V.
                          119 AA
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InterPro; IPR003600; Ig like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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SMART; SM00409; IG; 1.
SMART; SM00406; IGv; 1.
SMART; SM00410; IG_like; 1.
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                          PRELIMINARY;
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SMART; SM00406; IGv; 1.
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119 AA;
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26 GYTFTGY 32
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                    Wloch M.K., Alexander A.L., Pippen A.M., Pisetsky D.S., Gilkeson G.S., "Differences in V kappa gene utilization and VH CDR3 sequence among anti-DNA from C3H-1pr mice and lupus mice with nephritis."; Eur. J. Immunol. 26:2225-2233(1996).
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Shakarian A.M., Dwyer D.M.;
"Characterization and expression of a gene encoding the chitinase of Leishmania donovani.";
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Leishmania
                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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EMBL; AF009354; AAC17944.1; - 18/2.

InterPro; IPR001523; Glyco.hydro.18.

Ffam; PF00704; Glyco.hydro.18; 1.

ProDom; PD000471; Glyco.hydro.18; 1.

PROSITE; PS01095; CHITINASE.18; UNKNOWN.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC0037A806E9911E CRC64;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                           STRAIN=C3H/HEJ-LPR/LPR;
MEDLINE=96409289; Pubmed=8814271;
                                                                     Anti-DNA heavy chain (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13806 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1998 (TrEMBLrel.
01-AUG-1998 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00409; IG; 1
SMART; SM00406; IGV;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 GYSFTGY 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GYSFTGY 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GYSFTGY 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig;
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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CHI-1.
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SEQUENCE
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060994;
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MEDLINE=97313271; PubMed=9169875;

MEDLINE=97313271; PubMed=97313;

MEDLINE=97313271; PubMed=9169875;

MEDLINE=97313271; PubMed=9169875;

MEDLINE=97313271; PubMed=916975;

MEDLINE=97313271; PubMed=97313271;

MEDLINE=97313271; PubMed=916975;

MEDLINE=97313271; PubMed=97313271;

MEDLINE=97313271; PubMed=97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
Johnston M., Andrews S., Gattung S., Greco T., Kirsten J., Kucaba T.,
Favello A., Fulton L., Gattung S., Greco T., Kirsten J., Mucaba T.,
Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menezes S.,
Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L.,
Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Vaudin M.,
Wilson R., Waterston R.,
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                               Score 38; DB 11; Length 463;
Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fulton L.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
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Submitted (NOV-1995) to the EMBL/GenBank/DDBJ.databases
                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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                                                                                                                                                                                                                                                                                                                      92.7%;
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01-JAN-1998 (TrEMBLrel. 05,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GYSFTGY 7
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45 GYTFTGY
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                                                                                                     Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo,
NCBI_TaxID=9606;
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                   DB 5; Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92.7%; Score 38; DB 4; Length 125; 85.7%; Pred. No. 6.7;
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
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Last sequence update)
Last annotation update)
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EMBL; AF035019; AAD56255.1; -.
HSSP; PO1810; ZFBJ.
HSSP; PO1810; ZFBJ.
InterPro; IPR03006; Ig_MHC.
InterPro; IPR03596; Ig_V.
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                                                                                                  Mismatches
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                                   Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similar to RIKEN cDNA 1810060009 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
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HSSP; P01842; 7FAB.
Query Match
Best Local Similarity 85.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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26 GYTFTGY 32
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GYTFTGY 32
                                                                                                                                                         1 GYSFTGY 7
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QQUL95
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DD 01-M
DD MYOS
DD MYOS
DD MYOS
OC EUKR
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Mus musculus (Mouse)
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                                                                                                                                      13 GYMFTGY 19
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                                                                                                                                                                                                                                                                                     Pyrococcus abyssi
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NCBI_TaxID=29292;
                                                                                                                                                                                                                                                                                                                                                              STRAIN=ORSAY;
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Q9JL81;
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Q9JL81
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                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       "Potential symbiosis-specific genes uncovered by sequencing a 410-kb DNA region of the Bradyrhizobium japonicum chromosome."; J. Bacteriol, 183:1405-1412(2001). EBBL, AF322012; AAG60774.1; -SEQUENCE 239 AA; 27386 MW; 719BBS9C815165F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Bradyrhizobium group; Bradyrhizobium.
NCBI_TaxID=375;
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Gottfert M., Rothlisberger S., Kundig C., Beck C., Marty R.,
Hennecke H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.2%; Score 37; DB 2; Length 239; 85.7%; Pred, No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archaeà; Buryarchaeota; Thermoplasmata; Thermoplasmatales;
Thermoplasmataceae; Thermoplasma.
                                                                         Length 173;
                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
Jia Y., Cherry J.M.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U40829; AAB68295.1; -.
SGD, S0006544; YPRISOW.
SEQUENCE 173 AA; 19321 MW; DB830B5335F22DBI CRC64;
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Last annotation update)
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Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000)
EMBL; AP000995; BAB60238.1; -.
                                                                        90.2%; Score 37; DB 3;
85.7%; Pred. No. 15;
sive 1; Mismatches
                                                                                                                                                                                                              239 AA
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                                                                                                                                                                                                              PRT;
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STRAIN=GSS1 / DSM 4299 / JCM 9571;
MEDLINE=20570466; PubMed=11121031;
                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2001 (TrEMBLrel. 18, 01-0CT-2001 (TrEMBLrel. 18, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudouridylate synthase I.
                                                                                                                                                                                                                                                                                                   Bradyrhizobium japonicum.
                                                               Query Match
Best Local Similarity 85.
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                                                                                                                                                                                                               PRELIMINARY;
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Best Local Similarity
6; Conserva
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182 GFSFTGY 188
                                                                                                                                                  135 GFSFTGY 141
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                                                                                                                           1 GYSFTGY 7
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0979R4;
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                                                                                                                                                                                                                            09ANJ6
                                                                                                                                                                                                                Q9ANJ6
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Q9ANJ6
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MEDLINE=20468942; PubMed=10992488;
Malkiel S., Liao L., Cunningham M.W., Diamond B.;
m1-Cell-dependent antibody response to the dominant epitope of streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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                                                                                                                                       Length 246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               structure and evolution.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ248285; CAB49647.1;
Hypothetical protein; Complete proteome.
SEQUENCE 862 AA; 98273 MW; 722D1DEE2148603D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Anti-myosin immunoglobulin heavy chain variable region
                                                                                     246 AA; 28352 MW; 124AECE9BBED1218 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9V0Q6;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein PAB1881.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.8%; Score 36; DB 17;
85.7%; Pred. No. 1.4e+02;
                                                                                                                                     17;
                                                                                                                       87.8%; Pred. No. 5.,
85.7%; Pred. No. 5.,
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                                                                                                                                                                                                                                                                                                                                                                                                                          862 AA
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InterPro; IPR001406; PseudoU_synth_1.
Pfam; PF01416; PseudoU_synth_1; 1.
Complete proteome.
SEQUENCE 246 AA; 28352 MW: 124ARC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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Infect. Immun. 68:5803-5808 (2000)
EMBL; AF206025; AAF69323.1; -.
EMSP; PO1810; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                          Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 85.7
Matches 6; Conservative
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                            SEQUENCE FROM N.A.
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Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
Matis L.M., Evans M.J.;
Humanized porcine VCAM-specific monoclonal antibodies with chimeric
19G2/64 constant regions block human leukocyte binding to porcine
endothalial cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                         ol-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Anti-porcine VCAM mAb 2A2 heavy chain variable region (Fragment).
Rikaryoto. Vol.
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Lennard N., Quail M., Harris B., Rajandream M.A., Barrell B.G.
Mewes H.W., Lemcke K., Mayer K.F.X.;
                                                                                                                        85.4%; Score 35; DB 11; Length 114;
85.7%; Pred. No. 23;
iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85.4%; Score 35; DB 11; Length 117; 85.7%; Pred. No. 23; 1; Indels iive 0; Mismatches 1; Indels
                                                                                    114 AA; 12829 MW; 404885FDE6BA56F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 AA; 13122 MW; 4F65B193AFB77E5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2010 (TrEMBLrel. 19, Last annotation update)
Hypothetical 13.9 kDa protein (AT4929480/F17A13_300):
AT4G29480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U78799; AAD00291.1; -. HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 85.7
les 6; Conservative
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Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                 114
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                                                                                                                                                                                                                                                 18 GYSFTSY 24
                                                                                                                                                                                                        1 GYSFTGY 7
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                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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NON TER
SEQUENCE
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Q921C6
ID Q921C
AC Q921C
DT 01-MF
DT 0
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Q9M0D5
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Kim C.J., Chen H., Cheuk R., Koesema B., Meyers M.C., Banh J.,
Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                              Liu S.X., Sakano H., Pham P.K., Yamada K., Banh J., Etgu P., Lee J.M., Toriumi M., Yu G., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; "Full Length CDNA of gene T17A13 300/AT4929480 (G:7269847)"; submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
Yamada K., Liu S.X., Sakano H.L., Toriumi M., Yu G., Bowser L.,
Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
Kamaya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.
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Bowser L., Carninci P., Dale J.M., Gibson H.A., Goldsmith A.D.,
Hayashizaki Y., Ishida J., Jiang P. K., Jones T., Kamiya A.,
Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick Javis R.W., Theologis A., Ecker J.R.,
Javis R.W., Theologis A., Ecker J.R.,
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, ALIGISTS, CARJ706.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Theologis A.; "Full Length cDNA of gene F17A13 300/AT4g29480 (GI:7269847)."; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 34; DB 10; Length 122;
Pred, No. 38;
2; Mismatches 0; Indels
SEQUENCE FROM N.A.
EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Arabidopsis ORF clones.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Copia-like retroelement pol polyprotein.
AT2G19680 OR AT2G19680, F6F22.29.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 AA.
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122 AA; 13940 MW;
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SEQUENCE FROM N.A. Rotian K.-D., Mewes H.W., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D., Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D., Yamada K., M., Omodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Yu G., Yu S., Lan B., Lin J., Meyers M.C., Miranda M., Kawai J., Kim C., Koesema E., Lan B., Lin J., Meyers M.C., Miranda M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R., Theologis A., Shinozaki K., Davis R.W., Ecker J.R., "Full Length CDNA of gene AT4226210."; "Full Length CDNA of gene AT4226210."; "Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AL049171; CAB38950.1; "EMBL; AL161564; CAB7476.1; "EMBL; AL161564; CAB7476.1; "EMBL; ALL61564; CAB7476.1; "EMBL; ALG61564; CAB7476.1; "EMBL; ALG61564; CAB7476.1; "EMBL; ALG61564; CAB7476.1; "EMBL; AL161564; CAB7476.1; "EMBL; ALG61564; CAB7476.1; "EMBL; ALG61564; CAB7476.1; "EMBL; AL161564; CAB7476.1; "EMBL; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Goldsmith A.D., Lee J.M., Quach H.L., Tang C.C., Toriumi M., Yu G., Bowser L., Carninci P., Chen H.L., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin.Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinn zaki K., Davis R.W., Ecker J.R., Theologis A.; "Pull Length CDNA of gene Affag26210."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
             Mewes H.W., Mayer K.F.X., Schueller C., Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                      EU Arabidopsis sequencing project;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF370342; AAK44157.1; -. EMBL; AX063002; AAL34176.1; -.
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5; Conservative
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114 GFTFTGY 120
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Matches 5; Conserv
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                                                                                                        FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                     SEQUENCE
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                                                                                                                                                             SETALINE-CV. COLUMBIA,

STRAINE-CV. COLUMBIA,

MEDLINE-20081487; PubMed=10617197;

Lin X., Kaul S., Rounaley S.D., Shea T.P., Benito M.-I., Town C.D.,

Lin X., Kaul S., Rounaley S.D., Shea T.P., Benito M.-I., Town C.D.,

Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,

Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.S.,

Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,

Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,

Salzberg S.L., Fraser C.M., Venter J.C.,

Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NGUYGEN M., Karlin-Neumann G., Southwick A., Lam B., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J., Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., Bobmitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J., Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Sarou M., Seki M., Shinn P., Yamada K., Shinozaki K., Ecker J., Theologis A., Davis R.W.;
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Bevan M., Koetter P., Hempel S., Entian K.-D., Bancroft I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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01-MAR-2002 (TrEMBLrel. 20, Lar
Hypothetical 13.9 kDa protein.
125K17.20 OR AT4G26210.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 402:761-768(1999).
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| 114 GFTFTGY 120
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SEQUENCE FROM N.A.
STRAIN=JCM 10545 / 7;
PubMed=11572479;
Kawaarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                     .
0
                                                                                    82.9%; Score 34; DB 10; Length 122; 71.4%; Pred. No. 38;
                                                                                                                                                     Indels
Hypothetical protein.
SEQUENCE 122 AA; 13869 MW; DF854368DD4AF6AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) Hypothetical protein ST2629.
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Q9STR3

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110 098 TR3 09

Gaps

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Ouery Match 82.9%; Score 34; DB 4; Length 301; Best Local Similarity 71.4%; Pred. No. 1e+02; Matches 5; Conservative 1; Mismatches 1; Indels
               InterPro; IPR000504; RNA_rec_mot.
Pfam; PF00076; rrm; 2.
PR0SITE; PS50102; RRM; 2.
PR0SITE; PS0030; RRM NN_1; UNKNOWN_2.
Nucleocapaid; Ribonucleoprotein.
SEQUENCE 301 AA; 33589 MW; 6BF76C3AEB682BAD CRC64;
                                                                                                                                                                                                                                                                                             (TrEMBLrel. 10, (TrEMBLrel. 21.
    EMBL; BC007392; AAH07392.1;
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257 GYDYTGY 263
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Q9Z130;
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Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
Oshima T., Kikuchi H.;
                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                          091X94;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to heterogeneous nuclear ribonucleoprotein D (AU-rich
element RNA-binding protein 1, 37kD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34; DB 11; Length 257;
Pred. No. 87;
1; Mismatches 1; Indels
                                                                                                                                 82.9%; Score 34; DB 17; Length 128; 71.4%; Pred. No. 40; ive 1; Mismatches 1; Indels
                                      "Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodaii strain7.";
DNA Res. 8:123-140(2001).
EMBL; AP000990; BAB67747.1;
Hypothetical protein; Complete proteome.
SEQUENCE 128 AA; 15109 MW; 9D81AA58DA521885 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; EC011172; AAH11172.1; -.
MGD; MGI:101947; Hnrpd.
InterPro; IPR000504; RNA_rec_mot.
Pfam; PF00076; rrm; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50102; RRM; 2.
PROSITE; PS00030; RRM RNP 1; UNKNOWN 2.
Nucleocapid; Ribonucleoprotein.
SEQUENCE 257 AA; 29283 MW; 043CCC8A52329ACD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UTN-2002 (TrEMBLrel. 21, Last annotation update)
Heterogeneous nuclear ribonucleoprotein D-like.
                                                                                                                                                                                                                                                                               257 A.A.
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71.4%;
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Best Local Similarity 71.7
Best Local Si Conservative
                                                                                                                                             Best Local Similarity 71.4
Matches 5; Conservative
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TISSUE=SALIVARY GLAND;
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GYGYTGY 6
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10261M
AC 0961M
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DT 01-DE DT 01-DE DT 01-DE DC Bukar
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Q91X94
  SWRTTRAWS
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SEQUENCE FROM N.A.
MEDILINE=99207031; PubMed=9538234;
TSuchiya N., Kamei D., Takano A., Matsui T., Yamada M.;
TSuchiya N., Kamei D., Takano A., Matsui T., Yamada M.;
"Cloning and Characterization of a cDNA Encoding a Novel Heterogeneous
"Cloning and Characterization of a cDNA Encoding a Novel Heterogeneous
"Cloning and Characterization of a cDNA Encoding a Novel Heterogeneous
Nuclear Ribonucleoprotein-Like Protein and Its Expression in Myeloid
Nuclear Ribonucleoprotein-Like Protein and Its Expression in Myeloid
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDIJNE=20183688; Pubmed=10717477;
Akagi T., Kamei D., Tsuchiya N., Nishina Y., Horiguchi H., Matsui M.,
Kamma H., Yamada M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Molecular characterization of a mouse heterogeneous nuclear ribonucleoprotein D-like protein JKTBP and its tissue-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 301;
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                                                                                                      01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
JKTBP (Heterogeneous nuclear ribonucleoprotein D-like)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 AA; 33559 MW; 8AB2787FEB73311C CRC64;
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82.9%; Score 34; DB 11;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 1.
301 AA
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PROSITE; PS00030; RRM RNP_1; UNKNOWN_2.
Nucleocapsid; Ribonucleoprotein.
                                                                01-MAY-1999 (TrEMBLrel. 10, Created)
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InterPro; IPR000504; RNA_rec_mot.
Pfam; PF00076; rrm; 2.
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SEQUENCE FROM N.A.
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                                                                                                                                                    EMBL;
EMBL;
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Q9S115
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"Bacteroides fragilis NCTC3343 Produces at Least Three Distinct
capsular Polysaccharides: Cloning, Characterization, and Reassignment
of Polysaccharide B and C Biosynthesis Loci.";
Infect. Immun. 68:6176-6181(2000).
EMBL; AF285774; AAG26480.1;
-InterPro; IPR001296; Glycos_transf_1.
Transferase.
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01-AUG-1999 (TrEMBLrel. 11, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
JKTBPS (HARNP JKTBP) (A+U-rich element RNA binding factor) (Similar to beterogeneous nuclear ribonucleoprotein D-like).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                          Bacteria; CFB group; Bacteroidetes; Bacteroidales; Bacteroidaceae;
Bacteroides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Doi A., Takaoka Y., Yanagisawa K., Shiosaka T., Fujita S.;
Biochim. Biophys. Acta 0:0-0(1997).
[5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 403;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            403 AA; 46120 MW; E722DC5227EFBC13 CRC64;
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J. Biochem. 0:0-0(1998)
                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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85.7%; Pred. No. 1.4e+02;
iive 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=NCTC 9343;
MEDLINE=20490546; PubMed=11035722;
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                                                                                                                                                                                       Putative glycosyltransferase.
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                                  PRELIMINARY;
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                                                                                                                                                                                                                                                    Bacteroides fragilis.
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                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=817;
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Lange R., Wagner C., de Saizieu A.B., Flint N., Molnos J., Stieger M.,
Caspers P., Ranber M., Keck W., Anrein K.;
"Domain organization and molecular characterization of 13 two-
component systems identified by genome sequencing of S. pneumoniae.";
Gene 237:223-234(1999).
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Mitchell T.J., Keck W., Amrein K.E., Lange R.;
Mitchell T.J., Keck W., amrein K.E., Lange R.;
Mitchell T.J., Keck W., anterion of a novel Streptococcus pneumoniae
regulon controlled by an autoinduced peptide.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pneumoniae.
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
Streptococcaceae; Streptococcus.
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Reichmann P., Hakenbeck R.;
"A Peptide Inducible Signal Transduction System in Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O. Salzberg S.L., Lewis M.R., Radune D., Holtzapple B., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Histidine kinase (BLPH protein) (Sensor histidine kinase BLPH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                            to the EMBL/GenBank/DDBJ databases.
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Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50102; RRM; 3.
PROSITE; PS00030; RRM RNP 1; 2.
Nucleocapsid; Ribonucleoriorein.
SEQUENCE: 420 AA; 46437 WW; 00P631863859D0CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 34; DB 4; 1
Pred. No. 1.5e+02;
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                                                                                                                                                                                                                                   HSSP; P09651; 1UP1.
InterPro; IPR000504; RNA_rec_mot
Pfam; PF00076; rrm; 2.
                                                                                                                                                           EMBL, AB017018; BAR75240.1; --
EMBL, BC011714; AAH11714.1; --
HSSP; P09651; 1UP1.
Strausberg R.;
Submitted (JUL-2001) to the EMI
EMBL; AB017019; BAA75241.1; -.
EMBL; AB017018; BAA75239.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HK13 OR IH OR BLPH OR SP0527.
                                                                                                                D89092; BAA24361.1; -. D89678; BAA22860.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.9%;
71.4%;
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Bost Local Similarity 71.4%,
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STRAIN=16M / ATCC 23456 / BIOTYPE 1;
MEDLINE=20020109; PubMed=11756688;
DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T., Ivanova N., Anderson I., Bhattacharyva A., Lykidis A., Reznik G., Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E., Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., Haselkorn R., Kyrpides N., Overbeek R.;
The genome sequence of the facultative intracellular pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yoshida K., "Genome heterogeneity of apple stem pitting virus in apple trees."; chimitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                              oshikawa N., Matsuda H., Oda Y., Isogai M., Takahashi T., Ito T.,
                                                                                                                                                               RNA polymerase.
Apple stem pitting virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Foveavirus.
NCBL_TaxID=35350;
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Brucellaceae; Brucella.
NCBI_TaxID=29459;
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SEQUENCE 2185 AA; 247591 MW; 76DB4BB6FC202029 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).

EMBL, AR005628; AAL53129.1;

Interpro; IPR000819; Peptidase M17.

Pfam; PF0083; Peptidase M17; 1.

PRINTS; PR00481; LAMNOPPTDASE.

PROSITE; PS00631; CYTOSOL_AP; 1.

Hydrolase; Aminopeptidase; Complete proteome.

SEQUENCE 460 AA; 48742 MW; B7559FB05F185412 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OL-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 33; DB 16;
Pred. No. 2.6e+02;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       460 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytosol aminopeptidase (EC 3.4.11.1).
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InterPro; IPR001788; RNA dep RNApol2.
InterPro; IPR000606; Viral helicasel
                                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR005123; 20G-FeII_Oxy.
InterPro; IPR003323; OTU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF03171; 20G-PeII_OXy; 1.
Pfam; PF02338; OTU; 1.
Pfam; PF00978; RNA dep RNApol2; 1.
Pfam; PF01443; Viral_helicase1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUN-2000) to the EME
EMBL; AB045371; BAB15950.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80.5%;
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Best Local Similarity 85.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brucella melitensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 732 GYSYTGF 738
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Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEROPS; C23.001;
                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=IF38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BMEI1948.
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Q8YED0
                   ACCOOR DE REPARENTE DE LA PACE DEL PACE DE LA PACE DE L
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EMBL; D21829; BAA04853.1; -...

MEROPS; C23.001; -...
McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K., Holt L.B., Loftus B.J., Yang F., Smith H.O., Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.; "Complete genome sequence of a virulent isolate of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Apple stem pitting virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Foveavirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82.9%; Score 34; DB 16; Length 446; 100.0%; Pred. No. 1.6e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51824 MW; D8CBCD28F5DF274C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfan; PF02518; HATPase c; 1.
PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
Kinase; Complete proteome.
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InterPro; IPR003123; Ord.
InterPro; IPR001788; RNA_dep_RNApol2.
InterPro; IPR0016066; Viral_helicasel.
Pfam; PF03171; 20G-FeII_Oxy; 1.
Pfam; PF03187; Ord; 1.
Pfam; PF00378; RNA_dep_RNApol2; 1.
Pfam; PF00443; Viral_helicasel; 1.
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InterPro; IPR003594; ATPbind ATPase.
InterPro; IPR001064; Crystallin.
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                                                                                                                                                                                  Science 293:498-506(2001).
EMBL; AJ006401; CAB54587.1; -.
EMBL; AJ78419; CAC18581.1; -.
EMBL; AJ76410; CAC03516.1; -.
EMBL; AB007964; AAK74685.1; -.
TIGR; SP0527; -.
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RNA-directed RNA polymerase.
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Best Local Similarity 100....
Fac 6; Conservative
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732 GYSYTGF 738
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Best Local Similarity
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                                                                                                                                                           pneumoniae.
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INTERPRO; IPR001611; LRR.
INTERPRO; IPR001592; LRR_out.
Pfam; PP00560; LRR; 7.
                                                                                                EMBL; AJ012385; CAC20635.1; -
                                                                                                                              InterPro; IPR001611; LRR.
InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
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Similarity 71.4%;
5; Conservative ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-JUN-2001 (TrEMBLrel. 17,
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
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033931
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Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L.; Dussurget O.,
Entian K.-D., Fshhi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Darbouche A., Zechel S., Chakraborty T., Domann E.; Interia "Identification of a new leucine-rich protein operon in Listeria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
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Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
Listeriaceae; Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Listeria innocua.
Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
Listeriaceae; Listeria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     505 AA; 54909 MW; BCEE8B477E3678CC CRC64;
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Last annotation update)
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Last annotation update)
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TIGRPAMs; TIGR01167; LPXTG anchor; 1.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Comparative genomics of Listeria species.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
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InterPro; IPR01899; Gram pos_anchor.
InterPro; IPR01611; LRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Internalin like protein (LPXTG motif)
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                                                                                                                                                                                                                                                                                                                                                             Created)
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STRAIN=CLIP 11262 / SEROVAR 6A;
PubMed=11679669;
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01-MAR-2001 (TrEMBLrel. 16,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 19, (TrEMBLrel. 21,
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                                                                                                                                                                                                                                                                                       PRELIMINARY;
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Best Local Similarity
Local 5; Conserve
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395 GYTFTGW 401
                                                                                                    111 GYSFTRY 117
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SEQUENCE 505 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1642;
                                     GYSFTGY
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01-JUN-2002
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                                                                                                                                                                                                                RESULT 27
Q92F18
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Dramsi S., Dehoux P., Lebrun M., Goossens P.L., Cossart P., "Identification of four new members of the internalin multigene family of Listeria monocytogenes EGD.";
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products InlF, InlD,
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0
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Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales; Listeriaceae; Listeria.
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Pred. No. 3.1e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                80.5%; Score 33; DB 2; Length 548; 71.4%; Pred. No. 3.1e+02; ive 2; Mismatches 0; Indels
monocytogenes EGD: characterization of the gene products
and InlE and arrangement of the corresponding genes.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                     Pfam; PF00560; LRR; 7. SMART; SM00370; LRR; 5. SMART; SM00369; LRR TYP; 4. SEQUENCE 548 AA; 58552 MW; B0A192B18A414AEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEAN; PF00560; LRR; 7.
SMART; SM00370; LRR; 2.
SEQUENCE 548 AA; 58631 MW; 4A36A8112C564872 CRC64;
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Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
A Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
A Baquero F., Berche P., Bloecker H., Brandt P., Chatxaborty T.,
Charbit A., Chetcuani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
B Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Gebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Krhi M., Kunst F., Kurspkat G.,
Nordella S., Matournam A., Mara Vicente J., Ng E., Nedjari H.,
A Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
Comparative genomics of Listeria species.",
Escience 294:849-852(2001).
EMBL: ALS96165; CAC95893.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
Listeriaceae; Listeria.
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01-NOV-1998 (TYEMBLrel. 08, Created)
01-NOV-1998 (TYEMBLrel. 08, Last sequence update)
01-UN-2002 (TYEMBLrel. 21, Last annotation update)
Probable penicillin-binding proteins 1A/1B (PBP1).
PONA OR RV0050 OR MTCY21.13.
                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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71.4%; Pred. No. 3.4e+02;
ive 2; Mismatches 0;
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TIGRPAMS, TIGR01167, LPXTG anchor; 1.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
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01-DEC-2001 (TrEMBLrel. 19, Last sequ
01-UTN-2002 (TrEMBLrel. 21, Last anno
Internalin like protein (LPXTG motif)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Listilist; LIN00661; -.
InterPro; IPR001899; Gram pos_anchor.
InterPro; IPR001611; LRR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=CLIP 11262 / SEROVAR 6A;
PubMed=11679669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis
                                                                                                                                                                                                                 PRELIMINARY;
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                                                           395 GYTFTGW 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              490 GYTFTGW 496
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Matches 5; Conserv
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SEQUENCE 596 AA
                                                                                                                                                                                                                                                                                                                                                                                                Listeria innocua.
                                1 GYSFTGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1642;
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                                                                                                                                                           RESULT 32
Q92E00
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M MEDLINE=21537279; PubMed=11679669;

A Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

Baquero F., Berche P., Blocker H., Brandt P., Chakraborty T.,

A Charbit A., Checuani F., Couve E., de Daruvar A., Dehoux P.,

Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

Butian K.-D., Fishi H., Garcia-del Portillo F., Garrido P.,

A Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

A Madueno E., Maitournam A., Mata Vicente J., No E., Nedjari H.,

A Nordeiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Remmel B., Rose M., Schlueter T., Simose N., Tierrez A.,

Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,

T. Comparative genomics of Listeria species.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                 Raffelsbauer D., Bubert A., Engelbrecht F., Scheinpflug J., Simm P. Hess J., Kaufmann S.H.E., Goebel W., "The gene cluster infC2E of Listeria monocytogenes contains additional new internalin genes and is important for virulence in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
Listeriacee; Listeria.
NCBI_TaxID=1639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.5%; Score 33; DB 16; Length 548; 71.4%; Pred. No. 3.1e+02; Live 2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00560; LRR; 7.
SEQUENCE 567 AA; 61326 MW; F52C836CE8F3C4BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            548 AA; 58681 MW; 3EE34A05CAA1B88F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of Listeria monocytogenes EGD.";
Infect. Immun. 65:1615-1625(1997).
EMBL; U77368; AAB67970.1;
InterPro; IPRO01611; LRR.
                                                                                                                                                                                 Mol. Gen. Genet. 260:144-158(1998)
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MEDLINE=97270455; PubMed=9125538;
STRAIN=EGD;
MEDLINE=99077282; PubMed=9862466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 294:849-852(2001).
EMBL; AJ007319; CAA07457.1; -.
EMBL; AL591974; CAD00790.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001611; LRR.
InterPro; IPR001592; LRR_out.
Pfam; PF00560; LRR; 7.
SMART; SM00370; LRR; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ListiList; LMO00263; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||:|||:
GYTFTGW 382
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Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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SEQUENCE 548 AA
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Matches

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033932; 033932

RESULT 31 033932 ö

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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAINE-CDC 1551 / OSHKOSH;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W.;
"Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Actinomycetales, Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBL_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lyne M., Rajandream M.A., Barrell B.G., Lucas M., Gaillardin C.,
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AL023859; CAA19579.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000644; CBS_domain.
InterPro; IPR001807; Cl-channel_volt.
Pfam; PF00571; CBS; Cl-channel_volt.
Pfam; PF00554; voltage_CLC; 1.
PRINTS; PR00762; CLCHANNEL.
SMART; SM0116; CBS; 1.
SEQUENCE 812 AA; 90562 MW; B0BAAA8CBD8F672D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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85977 MW; CA94D5D830332B1C CRC64;
                                                                                                                                                                                                                                                                                           Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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Last annotation update)
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Best Local Similarity 71.4%; Pred. No. 4.8e+02;
Matches 5; Conservative 1; Mismatches 1;
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                                                                                                                          812 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                          Created)
                                                                                                                          PRT;
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InterPro; IPR001460; Transpeptdse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fam; PF00912; Transglycosyl; 1.
fam; PF00905; Transpeptidase; 1.
                                                                                                                                                                     01-AUG-1998 (TrEMBLrel. 07, 01-AUG-1998 (TrEMBLrel. 07, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-JUN-2002 (TrEMBLrel. 21,
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                                                                                                                          PRELIMINARY;
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649 GYDFSGY 655
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SEQUENCE 820 AA;
     689 GYSYVGY 695
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NCBI_TaxID=4896;
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                                                                                                                                                                                                                                                Chloride channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GYSFTGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=972H-;
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01-AUG-1998
                                                                                                                     060159
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                                                                        RESULT 35
060159
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Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         wall; Transmembrane; Complete proteome. ACYLATED BY PENICILLIN (BY SIMILARITY).
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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
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                                                                                                                                                                                              complete genome sequence.";
Nature 393:337-544[1998]
Nature 393:337-544[1998]
-!- FUNCTION: CELL WALL FORMATION.
-!- PATHWAY: FINAL STAGES IN PEPTIDOGLYCAN SYNTHESIS.
-!- SHECELLULAR LOCATION: MEMBRANE ASSOCIATED (BY SIMILARITY).
-!- SIMILARITY: TO OTHER BACTERIAL CLASS IA PENICILLIN-BINDING
-!- PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

80.5%; Score 33; DB 16; Length 678;
Best Local Similarity 71.4%; Pred. No. 4e+02;
Matches 5; Conservative 2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
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PRINTS; PR00160; GLUTAREDOXIN.
SEQUENCE 797 AA; 90812 MW; 43CS8B2B64394698 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01040BA6C347B0E2 CRC64;
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Last annotation update)
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Peptidoglycan synthesis; Cell wall; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 797 AA
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InterPro, IPR001264; GT_51.
InterPro, IPR001460; Transpeptdse.
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Pfam, PF00912, Transglycosyl, 1.
Pfam, PF00905, Transpeptidase; 1.
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MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z82082; CAB04966.1; --
HSSP; P37687; 1FOV.
                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z80775; CAB02529.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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678 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 GFSFTGF 86
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Q9XUI7 RESULT, 34

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calcium pump are linked to virulence in Leishmania mexicana amazonesis
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Clostridiales; Clostridiaceae; Clostridium.
NCBI_TaxID=1488;
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Pred. No. 6.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07B51CE3C51B142B CRC64;
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Last annotation update)
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Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1645 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             00154; ATPASE E1 E2; UNKNOWN 1
1031 AA; 113097 MW; 07B51CE30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=21359325; PubMed=11466286;
                                                                                                                                                                                                  Interpro; IPR001757; ATPase_E1-E2.
Interpro; IPR004014; Cation_ATPase.
Interpro; IPR00661; H/K Na/K ATPase.
Interpro; IPR001454; HIgmase/hydrlase.
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TTE2057.
Thermoanaerobacter tengcongensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                    J. Biol. Chem. 272:9464-9473(1997).
EMBL: U70540; AAC47505.1; -.
HSSP; P04191; 1EUL.
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                                                                                                                                                                                                                                                                                                                            Pfam; PF00689; Cation ATPase C; 1. Pfam; PF00690; Cation ATPase N; 1. Pfam; PF01122; E1-E2 ATPase; 1. Pfam; PF00702; Hydrolase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Bacteriol. 183:4823-4838(2001)
EMBL; AE007519; AAK78049.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.7%;
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Best Local Similarity 85.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2001 (TrEMBLrel. 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0119; CATATPASE, PROSITE; PS00154; ATPASE ED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clostridium acetobutylicum
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CAC0063.
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Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Leishmania.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
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STRAIN=RAY/DA/LV78;
STRAIN=RAY/DA/LV78;
MEDLINE=97238888 PubMed=9083086;
Lu H.G., Zhong L., Chang K.P., Docampo R.;
"Intracellular Ca2+ pool content and signaling and expression of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=FRIEDLIN;
Thens A.C., Murphy L., Quail M., Harris D., Oliver K., Lawson D.,
Rajandream M.A., Barrell B.G.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
Smith D.F.;
                               80.5%; Score 33; DB 16; Length 820; 71.4%; Pred. No. 4.9e+02; Live 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33; DB 5; Length 1023;
Pred. No. 6.2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "A physical map of the Leishmania major Friedlin genome."; Genome Res. 8:135-145(1998).
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A; 111719 MW; D0B451CECAF3F67E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Probable organelle-type calcium ATPase.
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Last annotation update)
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EMBL, AL389994, CRC44909.11, -.
InterPro; IPR001757, ATPase_ B1-E2.
InterPro; IPR004014, Cation_ATPase.
InterPro; IPR001654; H/K Na/K ATPase.
InterPro; IPR001454; H1gnase/Nydrlase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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Pfam; PF00690; Cation ATPase N; 1.
Pfam; PF00122; E1-E2 ATPase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04, 01-JUN-2002 (TrEMBLrel. 21,
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                                                                                                 Conservative
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222 GFSFTGF 228
Query Match
Best Local Similarity
-hea 5; Conserv?
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Leishmania major.
                                                                                                                                                                   GYSFTGY
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009489
AC 00948
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DT 01-JU
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Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
NCBI_TaxID=119072;
                                                                                                                                         0; Gaps
                             Query Match

78.0%; Score 32; DB 16; Length 61;
Best Local Similarity 71.4%; Pred. No. 43;
Matches 5; Conservative 1; Mismatches 1; Indels
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Search completed: July 18, 2003, 15:09:41 Job time : 29.06 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                               July 18, 2003, 15:01:44; Search time 16.9 Seconds (without alignments) 39.423 Million cell updates/sec
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| SIDS2/gcgdata/geneseqp-embl/AA198.DAT:
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA199.DAT:
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                              protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Sequence:
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SUMMARIES			uc	IP3 recogn	IP3 recogn	nan diagno	ide with t	01007 prot	Membrane-bound pro	fusion pro	01007 poly	creted pro	luman metastasis-a
			Description	Murine P	Murine P	Novel hu	Polypept	Human PR	Membrane	Albumin	Human PR	Human se	Human me
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			ΙD	AAY87658	AAY87655	ABG15138	AAW85739	AAB33441	AAY66679	AAE12413	AAU12387	AAB74735	AAB35462
	oko	Query		21	21	22	50	21	21	22	22	22	22
			Length		124	197	346	346	346	346	346	346	346
			Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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Claim 8; Page 13; 15pp; Japanese.

RO1007 RO1007 Ibumin ngiogen RO1007 uman di	in #899 brain de #816 peptid secret de #783 in #672 brain	Human bone marrow Peptide #6557 enco Peptide #8060 enco Human peptide enco Novel central nerv Novel human enzyme Cone snail O-supe Cone snail O-supe SEN virus protein	Human secreted pro- Human polypeptide Human foetal prote Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Novel central nerv Novel unan enzyme Novel central nerv K. aestuarii carbo K. aestuarii carbo	
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PIP3; phosphatidylinositol-3,4,5-triphosphate; variable region; CDR2; immunogen; antibody; heavy chain; complementarity determining region. Murine PIP3 recognizing Mab variable region heavy chain CDR2 region. A monoclonal antibody recognizing phosphatidylinositol-3,4,5-triphosphate (FUKU/) FUKUI Y. (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK AAY87658 standard; Protein; 5 AA. 98JP-0252921 98JP-0252921 11-AUG-2000 (first entry) WPI; 2000-353334/31. JP2000083664-A. 07-SEP-1998; 07-SEP-1998; 28-MAR-2000. AAY87658; Mus sp. RESULT 1 AAY87658 

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This invention describes a novel antibody specifically recognizing phosphatidylinositol-3.4,5-triphosphate (PIP3). The antibody of the invention is used in immunogenic compositions in which a dead Salmonella genus microbe is used as an adjuvant and mixed with PIP3. The antibody can be used in an immunoassay contraining a step in which the above antibody or its variable region is reacted with PIP3 present in a sample and the bond based on their immunological reaction. The method can determine PIP3 easily in a high sensitivity. This sequence represents the mutine PIP3 recognizing monoclonal antibody variable region heavy chain complementarity determining region, CDR2 described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel antibody specifically recognizing phosphatidylinositol-3,4,5-triphosphate (PIP3). The antibody of the invention is used in immunogenic compositions in which a dead Salmonella genus microbe is used as an adjuvant and mixed with PIP3. The antibody can be used in an immunoassay containing a step in which the above antibody or its variable region is reacted with PIP3 present in a sample and the bond based on their immunological reaction. The method can determine PIP3 seasily in a high sensitivity. This sequence represents the murine PIP3 recognizing monoclonal antibody variable region heavy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunogen; antibody; heavy chain.
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The invention relates to isolated polymulaterize (1) and polymerase chain reaction (FCR) primers, oligomers, and for chromosome polymerase chain reaction (FCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques of recommal activity of (II) of to to treat disease states involving (II) is useful for generating antibodies against it, detecting or quantitating a polymeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polymeptide and polymucleotide sequences have applications in capponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and continuous acid sequences of the invention.

Catagnostic amino acid sequences of the invention.

Catagnostic amino acid sequences of the invention.

Catagnostic amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                              Human, chromosome mapping, gene mapping; gene therapy, forensic, food supplement, medical imaging; diagnostic, genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to isolated polynucleotide (I) and
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100.0%; Pred. No. 2.4e+02;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                         Novel human diagnostic protein #15129.
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                                                                                                                                       ABG15138 standard; Protein; 197
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23-AUG-2000; 2000US-0649167.
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Matches 5; Conservative
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                                      52 SCYNA 56
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160 SCYNA 164

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bank is described. The protein is identified by the presence of a hydrophobic N-terminal secretory signal region, knowledge of the protein is identified by the presence of a protein by the problem. The terminal secretory signal region, knowledge of the protein function is not required, as in e.g. methods of expression cloning. The cDNAs encode proteins comprising transmembrane domains of and can be used as probes for gene diagnosis and gene sources for gene therapy. Abnormalities of Membrane proteins are associated with a number of hitherto-cryptogenic diseases. e.g. cystic fibrosis. Polynuclectides and proteins of the invention can be used in research; as nutritional supplements; for cell proliferation; cell differentiation or cytokine activity or to induce the production of cytokines; for immune stimulating or suppressing activity; for tissue growth activity; for haemostatic and thrombolytic activity, for receptor/ligand activity; for themotactic/chemokinetic activity; for haemostatic and thrombolytic activity for receptor/ligand activity; for anti-inflammatory activity or for tumour inhibition activity. A search of a protein database revealed no proteins having an allogy with this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane protein, transmembrane domain, translocation protein, endoplasmic reticulum; sec61 alpha subunit, research; probe; diagnosis; gene therapy; nutritional supplement; cytokine proliferation; cell proliferation; cell differentiation; haemactopiesis regulation; tissue growth; activin; inhibin; chemotactic activity; chemotinesis; haemostasis; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibition;
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                                                                                                                                                                                                                      AAW85739 standard; Protein; 346 AA
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dermatological; antiarthitic; antitheumatic; immunosuppressive; haemostatic; antithreumatic; immunosuppressive; haemostatic; antithroid; antidabetic; nootropic; neuroprotective; antianaemic; hepatotropic; virucide; antisposiatic; antiallergic; antiathmatic; systemic lugus erythematosus; rheumatoid arthritis; osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis; idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis; autoimmune haemolytic anaemia; diabetes mellitus; autoimmune haemolytic anaemia; diabetes mellitus; demyelinating disease; hepatobiliary disease; Whipple's disease; inflammatory bowel disease; lumune-mediated skin disease; allergic disease; immune-mediated skin disease;
                                                                                                             cardiant;
                                                                                                             immune related disease; diagnosis; antiinflammatory;
                                                                                   Human PRO1007 protein UNQ491'SEQ ID NO:146.
                                                                                                                                                                                                                                                                                graft rejection; graft-versus-host-disease
          AAB33441 standard; Protein; 346 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NDC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO anti-PRO antibodies, agonists and antisonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, osteoarthritis, idiopathic inflammatory myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune mediated renal disease, demyelinating diseases of the central and peripheral nervous systems, hepatobiliary diseases inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, cautoimmune or immune-mediated skin diseases, allergic diseases, immunological diseases of the lung, and transplantation associated diseases including graft rejection and graft-versus-host-disease. AACSS337 to AACSS337 to AACSS337 represent PCR primers and hybridisation probes used the isolation of human PRO polymucleotide and protein sequences given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                          Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus
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                                                                                                                       Henzel W;
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                                                                                                                    P, Goddard A, Gurney AL, Hebert C, H. an J, Pennica D, Shelton DL, Smith.V; Watanabe CK, Wood WI, Yan M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY66679 standard; protein; 346 AA
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98US-0087609.
98US-0087759.
                                                                                                                                              Pan J,
18-FEB-2000; 2000WO-US04342.
22-FEB-2000; 2000WO-US04414.
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Matches 5; Conservative
                                                                                                                                                                           Stewart TA, Tumas D,
                                                                     (GETH ) GENENTECH INC.
                                                                                                                                              Lu Y,
                                                                                                                                                                                                                         WPI; 2000-572271/53
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                                                                                                                       Ashkenazi AJ,
Kabakoff RC,
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02-JUN-1998;
02-JUN-1998;
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ID AAY6
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AC AAY6
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DT 05-7
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DY 05-7
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DY Nem
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KW Mem
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KW Mem
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KW Mem
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COS Horr
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polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors, TIE Iligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapphing and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by recombinant techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, albumin, HA, immune system disorder; transplant rejection; blood related disorder; myocardial infarction; glomerulonephritis; hyperproliferative disorder; childhood acute myeloid leukaemia; renal cell carcinoma; cardiovascular disorder; vulnerary; melanoma; arrhythmia; respiratory disorder; non-allergic rhinitis; antileukaemic; neurological disease; Alzheimer's disease; endocrine disorder; measles; phecoytochroma; reproductive system disorder; neuroprotective; syphilis; infectious disease; gastrointestinal disorder; neuroprotective; syphilis; irritable bowel syndrome; HIV; human immunodeficancy virus infection; cytostatic; antiinflammatory; gene therapy; immunosuppressive; cardiant; antiarthritic; antirheumatic; renal disorder; antimicrobial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Albumin fusion proteins comprising a therapeutic protein and albumin, useful in the treating metastatic renal cell carcinoma, metastatic melanoma, malignant melanoma, renal cell carcinoma, HIV (human
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                                                                                                                                                                                                                                                                                                                 100.0%; Score 30; DB 21; Length 346; 100.0%; Pred. No. 4e+02;
     The invention provides membrane-bound PRO polypeptides and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE12413 standard; Protein; 346 AA.
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21-DEC-2000; 2000US-256931P.
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Matches 5; Conservative
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                                                                                                                                                                                                                                                                                 346 AA;
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AAE12413
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98US-0091360.
98US-0091544.
98US-0091478.
                                                       98US-0091486.
98US-0091519.
98US-0091626.
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98US-0095301.
98US-0095302.
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98US-0095916.
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                                                                                                         acute myeloid leukaemia, metastatic renal cell carcinoma, metastatic menanoma, malignant melanoma, renal cell carcinoma, renal disorders (e.g. glomerulonephritis), cardiovascular disorders (e.g. arrhythmias), respiratory disorders (e.g. non-allergic rhinitis), neurological diseases (e.g. Alzhaimer's diseases), endocrine disorders (e.g. pheocytochroma), reproductive system disorders (e.g. syphilis), infectious diseases (e.g. measles), gastrointestinal disorders (e.g. irritable bowel syndrome), HIV (human immunodeficiency virus) infection and wound healing. Nucleic acids encoding albumin fusion protein is used in gene therapy. The present sequence is a human protein related
invention relates to human albumin (HA) fusion proteins and their
                                                                                                                                                                                                                                                                                                                                                               Gaps
             corresponding nucleic acid sequences. Therapeutic proteins fused to albumin or its fragments have an extended shelf-life. The albumin fusion proteins are useful in the treatment, prevention, diagnosis, and/or detection of diseases, disases uch as immune system disorders (e.g. transplant rejection), blood related disorders (e.g. myocardial infarction), hyperproliferative disorders (e.g. childhood
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Best Local Si Conservative
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                                                                                                                                                                                                                                                                                                  346 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
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ANU12172-AAV12446 represent novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bloactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumours by constrong the proliferation of chondrocytes, the proliferation of chondrocytes, the proliferation of chondrocytes, the proliferation of inner ear utricular supporting cells or cartilade, the release of proteoglycans from cartilade, the proliferation of inner ear utricular supporting cells or C T-lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide contends in assays to identify be contended in assays to identify and contended in a 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; secreted protein; diagnosis; immunomodulatory; antisclerotic; dermatological; immunosupressive; antinflammatory; anti-HIV; immunostimulant; cytostatic; cardiant; vascular; anti-angiogenic; ophthalmological; neuroprotectant; nootropic; anticonvulsant; vaccine; antialzahmer; antiparkinsonian; antimarcobial; vulnerary; gene therapy; immune disorder; hyperproliferative disorder; cardiovascular disease; cancer; angiogenic disorder; neurological disorder; infectious disease;
                                                                                                                                                                                                                                                                   Gao W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antisense RNA/DNA,
                                                                                                                                                                                                                                        Filvaroff E, Ga
                                                                                                                                                                                                                                                                 ssini M, Deforge L, Desnoyers L, Filvaroff E, G.
Goddard A, Godowski PJ, Gurney AL, Sherwood S;
art TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted protein sequence encoded by gene 3 SEQ ID NO:44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRO polypeptides can be used to generate probes, antisense RNA/
transgenic or knock out animals and can be used in gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 12; Fig 432; 813pp; English
                                                                                                   2000WO-US14941.
2000WO-US15264.
2000WO-US30873.
                                                                                2000WO-US14042
                                                 2000WO-US13705
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                                                                                                                                                                                                                                                                   Baker KP, Beresini M,
                                                                                                                                                                                                                                                                                                     ME, Goddard
Stewart TA,
                                                                                                                                                                                                               (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-408281/43.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAS21459.
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                                                                                                      30-MAY-2000;
02-JUN-2000;
                                                                                                                                                          10-NOV-2000;
                                                                                                                                                                                                                                                                                          Gerritsen ME,
Smith V, Ste
                                                 17-MAY-2000;
                                                                                22-MAY-2000;
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                           30-MAR-2000;
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The present invention provides the protein and coding sequences of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human and rat metastasis-associated antigen C4.4A. The protein is expressed rarely in the adult, except on metastasising cancer cells. Because of this, the sequences are useful in cancer diagnosis and treatment of cell proliferation diseases. The present sequence is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; secreted and transmembrane protein; PRO; cytostatic; cell death; cancer; chromosomal mapping; gene mapping; tissue typing; diagnostic assay.
                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid encoding rat or human metastasis-associated antigen C4.4A for treating cell proliferative disorder associated with a metastasizing tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 30; DB 22; Length 346; 100.0%; Pred. No. 4e+02; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human PRO1007 (UNQ491) protein sequence SEQ ID NO:197.
                                                                                                                                                                                                         (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
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                                                                                                                                                                                                                                                             Wuerfel J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig 2; 63pp; English.
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99US-0143048.
99US-0144758.
99US-0145698.
99US-0146222.
                                                                                                         29-SEP-2000; 2000WO-EP09567
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Best Local Similarity 100.00
Entra 5; Conservative
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                                                                                                                                                                                                                                                           Zoeller M, Roesel M,
                                                                                                                                                                                                                                                                                                          WPI; 2001-258133/26.
N-PSDB; AAF58882.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human C4.4A antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 SCYNA 164
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       WO200123553-A2.
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                                                                                                                                                         39-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF81787 to AAF81817 encode the human secreted proteins given in AAB74733 to AAB74772. Human secreted proteins can have activities based on the tissues and cells they are expressed in. Example of activities include: immunomodulatory; antisclerotic; dermatological; immunosuppressive; antisclerotic; dermatological; immunosuppressive; antisclerotic; ophthalmological; neuroprotectant; noctropic; canticorvulaant; antialzhehimers; antiparkinsonian; antimicrobial; and vulnerary. Human secreted proteins can be used in gene therapy and vulnerary. Human secreted protein ucleotide sequences (NAM1) and proteins (PEPI) may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. For example, NAM1 and PEPI may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patients genome the artifict that affect the activity of proteins by expressing in a patients genome the activity of proteins by expressing in a patients genome the activity of proteins by expressing in a patients genome the activity of proteins by expressing in a patients genome the activity of proteins proteins and proteins or deletions in a patients genome the activity of proteins proteins proteins and proteins proteins and proteins proteins proteins proteins and proteins and proteins proteins proteins proteins proteins proteins and proteins proteins proteins and proteins protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hyperproliferative disorders (e.g. cancers), cardiovascular diseases, angiogenic disorders, indections diseases and/or for promoting wound healing, regeneration and /or chemotaxis, AAF81778 to AAF81786 and AAB74732 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to supplement the patients own production of polypeptides. Disorders that may be prevented, diagnosed and/or treated include immune disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding 25 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                       rence KA, Fiscella M, Wei P, Baker KP;
Komatsoulis GA, Moore PA, Soppet DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 30; DB 22; Length 346; 100.0%; Pred. No. 4e+02;
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wound healing; regeneration; chemotaxis; chromosome 19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; Page 462-463; 485pp; English.
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Young PE, Komatsou
                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                   16-AUG-2000; 2000WO-US22325.
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Beet Local Similarity 100.uv
S; Conservative
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N-PSDB; AAF81789.
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                                                                                                    WO200112775-A2
                                                                                                                                                                                                                                                      17-AUG-1999;
                                                  Homo sapiens
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Birse CE,
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99WO-US28313 99WO-US28301

01-DEC-1999

Homo sapiens

RESULT 10 AAB35462

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The present sequence is one of twenty eight novel PRO polypeptides. The PRO polypeptides and their agonists, including antibodies, peptides, and small molecule agonists, may be used to treat various tumours, e.g., cancers such as breast cancer, ovarian cancer, renal cancer, colorectal cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer, central nervous system cancer, melanoma or leukaemia. They are also useful for treating other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders, and inflammatory, angiogenic and immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Twenty eight nucleic acids encoding PRO polypeptides which are useful for treating various tumors, e.g. breast cancer, and other inflammatory, angiogenic and immunological disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 30; DB 22; Length 346; 100.0%; Pred. No. 4e+02; ive 0; Mismatches 0; Indels
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Watanabe CK, Wood WI;
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30-MAR-2000; 2000WO-US08439
17-MAY-2000; 2000WO-US13705
                                                                                                                                                                                                   99WO-US20594.
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                                                                                                                                                                                                                                                                                                                                                                  2000WO-US03565
                                                         30-MAY-2000; 2000WO-US14941
                                                                                                                                                             99US-0144758
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Best Local Similarity luv.
5, Conservative
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16-DEC-1999;
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                   07-DEC-2000
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                                                                                                                                          23-JUN-1
                                                                                                                                                                                                                                             30-NOV-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteins. The PRO proteins have cytostatic activity. The PRO proteins can be used for targeted delivery of bioactive molecules, such as toxins, radiolabels or antibodies, that cause cell death. PRO mucleotide sequences, and their fragments, can be used as hybridisation probes, in chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AFA44270 to AFA44470 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAR44087 to AAR44269 and AAB65180 to PREPERSON PRO PROJYMUCLEOTIGE and protein sequences given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, PRO, cytostatic, nootropic, neuroprotective, respiratory general,
antiinflammatory, antiangiogenic, immunosuppressive, immunostimulant,
PRO agonist, cancer, inflammatory disorder, immunological disorder.
                                                                                                                                                                                                                                                                                                                            Godowski PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                 Paoni NF;
Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present invention describes human secreted and transmembrane PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRO polynucleotides used to produce polypeptides used to target bioactive molecules such as toxins, radiolabels or antibodies, to specific cells, to cause targeted cell death -
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                                                                                                                                                                                                                                                                                                     Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12; Fig 125; 935pp; English
                                                                          11-FEB-2000; 2000MO-US033652.
18-FEB-2000; 2000MO-US04341.
22-FEB-2000; 2000MO-US04414.
24-FEB-2000; 2000MO-US04914.
24-FEB-2000; 2000MO-US05004.
                                                                                                                                                                                02-MAR-2000; 2000WO-US05841.
99WO-US30095,
                                      2000WO-US00219.
2000WO-US00376.
                                                                                                                                                                                                                          20-MAR-2000; 2000WO-US07377
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                                                                                                                                                                                                                                                                   (GETH ) GENENTECH INC.
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N, Fong S,
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N-PSDB; AAF44162.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            346 AA;
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16-DEC-1999;
20-DEC-1999;
05-JAN-2000;
06-JAN-2000;
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Zhang Z;
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AAB50958
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Henzel W, Kabakoff RC;

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One hundred and eighty seven nucleic acids encoding PRO polypeptides,
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L, Hillan KJ, Marsters SA, Pan J,
CK, Williams PM, Wood WI, Ye W;
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2001US-0854208.
2001US-0854280.
                                                                                              09-JUL-2001; 2001WO-US21735
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JF, Watanabe CK,
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BAKER K P.
FERRARA N.
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GERRITSEN M E.
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GURNEY A L.
HILLAN K J.
MARSTERS S A.
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STEPHAN J F.
WATANABE C K.
WILLIAMS P M.
   antiarteriosclerotic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ABL95625
                                                WO200208284-A2
                                                                                                                                                                                                                                                                                                   10-NOV-2000;
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                                                                       31-JAN-2002
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(STEP/)
(WATA/)
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                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to albumin fusion proteins comprising a albumin, HaA). The protein X and human albumin (HA, also known as human serum albumin, HsA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and diagnosing disorders such as cancer, reproductive disorders, disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes), haematopoietic disorders, neural disorders (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease, encephalomyellitis, meningitis, schizophrenia), and connective disorders (e.g. osteoporosis, arthritis) ABG63326-ABG65518 represent albumin
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                                                                                                                                                                                                                                                                                                                                              New fusion protein for treating disease e.g. diabetes comprises an albumin fused to a therapeutic protein -
        Albumin fusion protein; therapeutic protein X; human albumin; HA; human serum albumin; HSA; cancer; reproductive disorder; disorder; disorder; immune disorder; endocrine disorder; haematopoietic disorder; neural disorder; connective disorder; cytostatic; antinfertility; antinflammatory; antiulcer; immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic; neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB95487 standard; Protein; 346 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (e.g. osteoporosis, assertion. fusion proteins of the invention.
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                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                      25-APR-2000; 2000US-199384P.
21-DEC-2000; 2000US-256931P.
                                                                                                                                                                                                   12-APR-2001; 2001WO-US11988.
                                                                                                                                                                                                                            .2-APR-2000; 2000US-229358P.
                                                                                              osteopathic; antiarthritic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0.
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SCYNA 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       346 AA;
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                                                                                                                                                      WO200177137-A1
                                                                                                                     Homo sapiens
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                                                                                                                                                                              18-OCT-2001
                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                 Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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Paoni NF;

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160 SCYNA 164
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                                                   05-APR-2001;
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10-MAY-2001;
                                                                                                                                  01-JUN-2001;
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                                 14-MAR-2001;
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                                                                                                                                                                         Baker KP,
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                                                          PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma healing. The present sequence is a PRO protein of the invention.
                                                                                                                                                                                                                                                                                                                                                    Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; rheumatoid arthritis; mycardial infarction; thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping.
                                                   present invention provides the protein and coding sequences of human
useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal
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                                                                                                                                                             100.0%; Score 30; DB 23; Length 346; 100.0%; Pred. No. 4e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                   Human PRO1007 protein sequence SEQ ID NO:130.
                                                                                                                                                                                                                                                                        ABB84881 standard; Protein; 346 AA,
                              Claim 11; Fig 130; 567pp; English
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2000US-220624P.
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2000WO-US23522.
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                                                                                                                                                                                   Conservative
                                                                                                                                                  346 AA;
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08-NOV-2000;
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                           Sequence
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ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to ABB85003. The PRO proteins and polymucleotides have cardiant, cytostatic, antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polymucleotides, proteins, agoniets and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular rheumatoid arthritis, angina, mypertension, arterial restenoiss, rheumatoid arthritis, angina, mypoardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polymucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABL88259 to ABL88267 represent primers and probes used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Paoni NF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gerber H, Gerritsen ME, Goddard A;
L, Hillan KJ, Marsters SA, Pan J,
CK, Williams PM, Wood WI, Ye W;
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2001US-0802706.
2001US-0808689.
2001US-0816744.
2001US-0828366.
2001US-0854208.
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2001WO-US17443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GETH ) GENENTECH INC.
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N-PSDB; ABL88136.
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Best Local Similarity
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measuring human gene expression in sample derived from human foetal liver. The single exon nucleic acid probes may be used from predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein #8990 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                   Claim 27; SEQ ID NO 36736; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, gene expression, heart, microarray, vascular system;
cardiovascular disease, hypertension, cardiac arrhythmia,
                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a single exon nucleic acid
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80.0%; Pred. No. 1.1e+02;
iive 1; Mismatches 0;
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2000US-0608408.
2000US-0632366.
                                                                                                                                                 04-OCT-2000; 2000GB-0024263.
                      2000US-0180312
2000US-0207456
                                                                                    03-AUG-2000; 2000US-0632366
21-SEP-2000; 2000US-0234687
                                                                                                                         2000US-0236359
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2000US-0236359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                                                                                                                                   Hanzel DK,
                                                                                                                                                                                                                                                                             WPI; 2001-483447/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                              27-SEP-2000;
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27-SEP-2000;
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                                                                  30-JUN-2000;
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    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques for identifying expressed genes. (I) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of stress expressing (II). (I) and (II) are useful in medical imaging of stres expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic amino acid sequences of data and products dependent on DNA and diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fip. wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide #11607 encoded by human foetal liver single exon probe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention relates to isolated polynucleotide (I) and
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                                                                                 31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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N-PSDB; AAS79324.
                                                                                                                                                                                       Drmanac RT, Liu C,
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                                                                                                                                             HYSE-) HYSEQ INC
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11-OCT-2001
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ABB44101
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Length 20;

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                                                                                              measuring human gene expression in a sample derived from human heart (see ARA12135. ARA141305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays.
                                                                                                                                   By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                      Human brain expressed single exon probe encoded protein SEQ ID NO: 37228.
                                      Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                        Gaps
                                                                                      present invention relates to single exon nucleic acid probes for
                                                                                                                                                                                                                                                                                                                                                                                                                         Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
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Pred. No. 1.1e+02;
1; Mismatches 0; Indels
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                                                                 Claim 15; SEQ ID No 28761; 530pp; English.
DR;
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Rank
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Chen W,
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                                                                                                                                                                                                                                   90.0%;
80.0%;
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2000US-0234687.
2000US-0236359.
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2000US-0608408.
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                                                                                                                                                                                                                                            Local Similarity 80.0
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Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-483446/52
                   WPI; 2001-488899/53
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                                                                                                                                                                                                                                                                                                                                                                                                                                              epilepsy; cancer.
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SCYNS 8
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21-SEP-2000;
27-SEP-2000;
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Penn SG,
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                                                                                      The
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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide #8167 encoded by probe for measuring cervical gene expression.
                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probe; human; microarray; gene expression; cervical epithelial cell;
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Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                            90.08;
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21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
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2000US-0608408
                                                                                                                                                                                            the probes of the invention
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                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included
                                                                                                                                                                                                                                                                                                               Human peptide encoded by genome-derived single exon probe SEQ ID 36526
                                                                                                                                                                                                                                                                                                                                              Human; single exon probe; asthma; lung cancer; CODD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tubercous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histlocytosis; lymphangioleiomyomcosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples -
                                       Gaps
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0
   Length 20;
                                     0; Indels
   Score 27; DB 22;
Pred. No. 1.1e+02;
                                       Mismatches
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   90.08;
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27-SEP-2000; 2000US-236359P.
04-OCT-2000; 2000GB-0024263;
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2000US-0608408
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                                                                                                                                                                                                                                                                           (first entry)
Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nyaline membrane disease
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                                                                        1 SCYNA 5
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                                                                                                SCYNS
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in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several. tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes of the exons should frames (ORF). The probes are used for gene probesopen reading frames (ORF). The probes are used for gene probesopen neading frames (ORF). The study of lung diseases such as asthma, lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease. (COPP), interstitial lung disease (ILD), familial idiopathic pulmonary fibroais, neurofibromatosis, tubercous sclerosis, Gaucher's disease. Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcioldosis, pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                             encoded by a single exon probe of the invention is a peptide/protein Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form at directly from WIPO at
                                                                                                                                                                                                                                                                                                                  haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a peptide/protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiucer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; food additive; preservative; chromosome identification; cancer; female reproductive system disorder; immune disorder; wound healing; cardiovascular disorder; neurological disease; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; secreted protein; diagnosis; cytostatic; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human secreted protein sequence encoded by gene 2 SEQ ID NO:62.
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Pred. No. 1.1e+02;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB39403 standard; Protein; 30 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-2000; 2000WO-US07724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JAN-2000; 2000US-0174850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
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N-PSDB; AAC74338.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SCYNA 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 SCYNS 8
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acid probes useful for

probe for

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measuring human gene expression in a sample derived from human foetal.

liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly, from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                  Claim 27; SEQ ID NO 32963; 639pp + sequence listing; English.
                                                                                                                                                         The invention relates to a single exon nucleic acid
                                                       Human genome-derived single exon nucleic acid F
analyzing gene expression in human fetal liver
                    WPI; 2001-483447/52
                                                                                                                                                                                                                                                                                                                                                              Sequence
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    8
                                                                                                                                                                                                                               and certs una genes are expressed in branger of activities include:
antiallerati; immunosuppressive; noctropic; neuroprotective; antivital;
antiallerati; immunosuppressive; noctropic; antiinflammatory; antiulcer;
culnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; and
cardiant. The polymucleotides and polypeptides are useful for preventing,
crabbits, goats, horses, cats, dogs, chickens or sheep. The polypeptides
can also be used as a food additive or preservative to increase or
chromosome identification. They are also useful as probes for diagnosing
a disorder related to the female reproductive system, particularly breast
and/or ovary cancer. They are also useful in the gene therapy of breast
and ovarian cancer. Secreted protein nucleic acids, proteins,
and ovarian cancer. Secreted protein nucleic acids, proteins,
creatment and prevention of: (a) cancer; (b) immune disorders; (c)
cratiovascular disorders; (d) wound healing; (e) neurological diseases;
and (f) infectious diseases such as viral, bacterial, fungal and
parasitic infections. AAC74228 to AAC74326 and AAB33401 represent
sequences used in the exemplification of the present invention.
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                                                                                                                The polynucleotide sequences given in AAC74337 to AAC74386 encode the human secreted proteins given in AAB39402 to AAB3948 represent human secreted polypoptide sequences and proteins homologous to them, which are given in the exemplification of the present invention. Human secreted proteins have activities based on the tissues and cells the genes are expressed in Example of activities include:
Fifty nucleic acid molecules encoding human secreted proteins, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                               Claim 11, Page 357, 391pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB40328 standard; Peptide; 54 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Penn SG, Hanzel DK, Chen W,
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Matches '4; Conservative
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19 NCYNA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-FEB-2000;
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27-SEP-2000
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                                                                                                                                                                                                                                              Protein #6723 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single exon nucleic acid probes for analyzing gene expression in human hearts -
                                                Gaps
                                                ö
                                                                                                                                                                                                                                                                     Human, gene expression; heart; microarray; vascular system;
cardiovascular disease; hypertension; cardiac arrhythmia;
                       Length 54;
                       Score 27; DB 22; L. Pred. No. 2.7e+02; 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 15; SEQ ID No 26494; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen W, Rank DR;
                                                                                                                                                                  ABB24724 standard; Protein; 54 AA.
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                        90.0%;
80.0%;
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27-SEP-2000; 2000US-0236359
04-OCT-2000; 2000GB-0024263
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2000US-0608408
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                                                                                                                                                                                                                                                                                                congenital heart disease.
                                                   4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-488899/53
                     Query Match
Best Local Similarity
Matches 4; Conserv
54 AA;
                                                                          1 SCYNA 5
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                                                                                                  5 SCYNS
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80.08;

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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                         AAM73838;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                      Human brain expressed single exon probe encoded protein SEQ ID NO: 33234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                              Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
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                                                                                                                                        Score 27; DB 22; Length 54;
Pred. No. 2.7e+02;
1; Mismatches 0; Indels
                                                                                             at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                          90.08;
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                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                4; Conservative
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                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                   54 AA;
                                                                                                                                                                                                  SCYNS 9
                                                                                                                                                                                     SCYNA 5
                                                                                                                                                                                                                                                                                                                                                                                      epilepsy; cancer
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                           AAM61129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            brains
                                                                                                                                                              Matches
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90.0%; Score 27; DB 22; Length 54;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 Human bone marrow expressed probe encoded protein SEQ ID NO: 34144.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; bone marrow expressed exon; gene expression analysis; probe;
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Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.0%; Score 27; DB 22;
80.0%; Pred. No. 2.7e+02;
iive 1; Mismatches 0;
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                                         1; Mismatches
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                                                                                                                                                                                                                                                          AAM73838 standard; Protein; 54 AA.
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30-JUN-2000; 2000US-0608408.
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21-SEP-2000; 2000US-0234687
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                                         4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-488900/53
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Matches 4; Conserv
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                                                                                        1 SCYNA 5
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26-MAY-2000;
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The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human peptide encoded by genome-derived single exon probe SEQ ID 33392.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; single exon probe; asthma; lung cancer; COPD; ILD;
chronic Obstructive pulmonary disease; interstitial lung disease;
familial idiopathic pulmonary fibrosis; neurofibromatosis;
tuberous sclerosis; daucher's disease; Niemann-Pick disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta -
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Pred. No. 2.7e+02;
Timmatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 27; SEQ ID No 34292; 654pp; English
                                                                                                                                                                                                                                                                                                                                                                                                            Rank DR
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2000US-207456P.
2000US-0608408.
2000US-0632366.
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04-OCT-2000; 2000GB-0024263.
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                                                            30-JAN-2001; 2001WO-US00663
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21-SEP-2000; 2000US-0234687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   numan genetic disorders.
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Best Local Similarity
Matches 4; Conserv
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30-JUN-2000;
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26-MAY-2000;
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09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                            Penn SG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to human single exon nucleic acid probes (SERP): see AAIIO08-AAIIS459). The present sequence is a petide encoded by one such probe. The SERPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                 Peptide #6557 encoded by probe for measuring cervical gene expression.
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                                                                                       Probe; human; microarray; gene expression; cervical epithelial cell;
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2000US-0207456.
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2000US-0236359.
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Best Local Similarity
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21-SEP-2000;
27-SEP-2000;
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                                                                                                                                                                                 Homo sapiens
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Gaps

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Length 54;

05-JUN-2002 (first entry)

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a collection or detectably tabeled nucleic acids delived tions named a warmy identifying exons in a eukaryotic genome, comprising

(a) algorithmically predicting at least one exon from genomic sequences

(b) algorithmically predicting at least one exon from genomic sequences

of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from enkaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon cypression of the exons in the tissues and/or cell types using hybridisation to a single exon meroarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases

CC (COPD), interstital lung disease (ILD), familial idiopathic pulmonary disease, neurodipromary placency, plannan-Pick disease, Hermansky-pudlak syndrome, sarcoidosis, pulmonary hasman-pick disease, Hermannaky-pudlak syndrome, sarcoidosis, pulmonary hasman-pick disease.
                                                                                                                                                                                                                                                                                                                           haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis, pulmonary pulmonary histiocytosis, lymphangioleiomyomtosis, pulmonary alveolar protesinesis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a peptide/protein Note: The sequence data for this patent did not form part of the printed specification.
                                                                                                                                                                                                                      Spatially-addressable set of single exon nucleic acid probes, used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                                                           measure gene expression in human lung samples
                                                                                                                                                                                                                                                                                    Claim 27; SEQ ID No 33392; 634pp; English
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                                                                                                                                    Chen W, Rank DR;
                                                                                         (MOLE-) MOLECULAR DYNAMICS INC
21-SEP-2000; 2000US-234687P.
27-SEP-2000; 2000US-236359P.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                Penn SG, Hanzel DK,
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Best Local Similarity
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hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; ischaemia; andiogenesis; nervous system disorder; Alzheimer's disease; AIDS; ocular disorder; acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; diabetes; cancer; leukaemia; neovascularisation; respiratory disorder; renal disorder; kidney failure; blood disorder; myocardial infarction; wound healing; cell proliferation; skin aging; food additive; food preservative; gene therapy.
                                      Central nervous system; CNS; autoimmune disease; rheumatoid arthritis
                   Novel central nervous system protein #406.
                                                                                                                                                                                                        17-JAN-2001; 2001WO-US01332
                                                                                                                                                                                                                                                                  000US-0189874
                                                                                                                                                                                                                                                                            2000US-0190076
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                                                                                                                                                                  WO200155318-A2
                                                                                                                                               Homo sapiens.
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                                                                                                                                                                                                                                                                             17-MAR-2000;
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                                                                                                                                                                                     02-AUG-2001
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2000US-0232080

08-SEP-2000;

AAU87496 standard; Protein; 83 AA.

RESULT 30

AAU87496;

AAU87496 ID AAU8 XX AC AAU8

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Gaps

; 0

Conservative

Matches

SCYNS 9 SCYNA 5 4;

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2000US-0249300
                                                2000US-0249211
                                         NOV-2000;
                              01-NOV-2000
                                 08-NOV-2000
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The invention describes an isolated nucleic acid molecule (I) encoding a covel central nervous system protein. (I) and polypeptides (III) encoded to novel central nervous system protein. (I) and polypeptides (III) encoded a pathological condition. Disorders which are disgnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. angiogenesis, nervous system disorders e.g. Alzheimer's disease and amglochtic lateral sclerosis, infections caused by bacteria, viruses c.g. capquired immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. deprinced immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. described infection, gastrointestinal disorders e.g. dysphagia, adenocarcinomas and irritable bowel syndrome, reproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes can disorders e.g. corners involving neovascularisation e.g. malignancies, respiractory disorders e.g. nonallergic rhinitis, renal disorders e.g. respiractory disorders e.g. nonallergic rhinitis, renal disorders e.g. centerkiney failure and blood related disorders e.g. myocardial conference transplantenon, for supporting cell culture of epithelial cell proliferation, to prevent skin aging due to subburn, to maintain organs before transplantened. for supporting end conference conference conference and seed as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 9; SEQ ID No 1014; 837pp; English.
                                                                                               2000US-0251479.
2000US-0251856.
2000US-0251868.
2000US-0251869.
2000US-0251869.
                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC
                                                       2000US-0251988
2000US-0256719
                                                                                                                                                                                                           2000US-0251990
2000US-0254097
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N-PSDB; ABK43826.
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                                                                                                    06-DEC-2000;
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Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase; ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder;

Novel human enzyme polypeptide #358.

17-DEC-2001 AAU23272;

AAU23272 standard; Protein; 83 AA

RESULT 31 AAU23272

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2000US-0235834.
2000US-0235835.
2000US-0236327.
2000US-023636367.
2000US-0236369.
2000US-0236370.
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2000US-0237040.
2000US-0239935.
2000US-0239937.
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2000US-0250160.
2000US-0250391.
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2000US-0241785
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2000US-0249213
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                                                                                                          29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-CST-2000; 20-CST-2000; 20-CS
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13-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
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08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
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    inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; cytostatic; anti arthritic; nephrotropic; anticoagulant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-AUG-2000; 2000US-0225759.
14-AUG-2000; 2000US-0225759.
12-AUG-2000; 2000US-0225759.
22-AUG-2000; 2000US-0226868.
22-AUG-2000; 2000US-0226868.
23-AUG-2000; 2000US-0227182.
23-AUG-2000; 2000US-0229343.
01-SEP-2000; 2000US-02293134.
08-SEP-2000; 2000US-0231243.
08-SEP-2000; 2000US-0231244.
08-SEP-2000; 2000US-0231413.
08-SEP-2000; 2000US-0231413.
08-SEP-2000; 2000US-0231413.
08-SEP-2000; 2000US-02313939.
14-SEP-2000; 2000US-0231399.
                                                                                                                                                                                                14-FEB-2000; 2000US-0194664.
24-FEB-2000; 2000US-0184664.
26-MAR-2000; 2000US-0184664.
17-MAR-2000; 2000US-018076.
18-AFR-2000; 2000US-0190076.
19-AFR-2000; 2000US-0190076.
19-AFR-2000; 2000US-02018123.
19-MAY-2000; 2000US-02018186.
30-UN-2000; 2000US-021686.
30-UN-2000; 2000US-0216647.
07-UUL-2000; 2000US-0216647.
07-UUL-2000; 2000US-0216647.
11-UUL-2000; 2000US-0216647.
                                                                                                                                                         2001WO-US01239
                                                                                            WO200155301-A2
                                                             Homo sapiens
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21-SEP-2000;
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14-AUG-2000;
14-AUG-2000;
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14-AUG-2000
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                                                                                                                                                                                                    The present invention relates to the isolation of novel human enzyme polypeptides, and the CDNA (AAS40785-AAS41684) and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of mannodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. athhitis), neurological disorders (e.g. AIDS) autoimmune disorders (e.g. athhitis), neurological disorders (e.g. AIDS) autoimmune disorders (e.g. athhitis), neurological disorders (e.g. athhitis), neurological disorders (e.g. atherosclerosis), concerts (e.g. athma), cardiovascular disorders (e.g. atherosclerosis), concerts (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), concerts (e.g. athains) and infectious disorders (e.g. Influenza). The polynucleotides of the invention can also be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                    Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   demyelinating disease, multiple sclerosis, Huntingdon's disease, neuropathy, carpal tunnel syndrome, cardiovascular disorder; congestive heart failure, cancer, immunosuppression, epilepsy;
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Pred. No. 4e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O-superfamily conotoxin propeptide, M6.8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cone snail; O-superfamily conotoxin; sodium channel;
                                                                                                                                                                                 Claim 11; SEQ ID No 1268; 1180pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU05900 standard; Peptide; 83 AA
                                                            Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      asthma; ischaemia; stroke; pain.
                                   (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.0%;
11-DEC-2000; 2000US-0254097.
05-JAN-2001; 2001US-0259678.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                           Barash SC,
                                                                                    WPI; 2001-465566/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37 NCYNA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SCYNA 5
                                                                                               N-PSDB; AAS41142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cone snail
                                                                                                                                                                                                                                                                                                                                                                                           invention.
                                                           Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU05900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                           diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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The sequence is a cone snail O-superfamily conotoxin propeptide.

The peptides are useful for regulating the flow of sodium through sodium channels in an individual and the treatment or prevention of disorders associated with voltage gated ion channel disorders, including demyelinating diseases i.e. multiple sclerosis, optic neurowelitis, disseminated encephalomyelitis, adrenoleukodystrophy, acute transverse myelitis, progressive multifocal leukoencephalopathy, sub acute realerosing panecephalomyelitis (SSPB), metachromatic leukodystrophy, polizaeus-Merzbacher disease, spinal cord injury, botulinum toxin poisoning, Huntington's, compression, entrapment neuropathies i.e. ulnar nerve palsy, and carpal tunnel syndrome, cardiovascular disorders, hypersylvaemia, immunosuppression, cocaine addiction, cancer, cognitive dysfunction, neurotransmitter disorders cardiotic Lambert syndrome) and reversal of curare and other neuromuscular blocking drugs. The neurological disorder is a sailure, preferably one associated with applesy. The neurological disorder is neurotoxic injury associated with stroke, cerebrovascular accident, pression or spinal cond trauma, myocardial infarct, physical reaums.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s, suffocation, perinatal asphyxia or hypoglycaemic events. Th is pain i.e. migraine, acute pain, persistent pain, nociceptive pain. The disorder is inflammation or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to a pain
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                                                                                                                                                                                                                                                                                                                                                                                                                                            New O-superfamily polypeptides useful for treating voltage gated ion channel disorders, including demyelinating diseases i.e. multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cardiovascular disorder. A conotoxin peptide of is useful to alleviate pain in a mammal in pain or about to be subjected to a pai causing event, and to treat disorders associated with radical depolarisation of excitable membranes by activating a KATP channel, disorders include cardiac, ocular and cerebral ischaemia and asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cone snail; O-superfamily conotoxin; sodium channel; demyelinating disease; multiple sclerosis; Huntingdon; s disease; neuropathy; carpal syndrome; cardiovascular disorder; congestive heart failure; cancer; immunosuppression; epilepsy;
                                                                                                                                                                                                                                       Watkins M, Hillyard DR, McIntosh JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Pred. No. 4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 15; Page 53; 277pp; English.
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26-JUN-2000; 2000US-0214263.
20-JUL-2000; 2000US-0219440.
                                                                27-OCT-2000; 2000US-0243412.
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                                                                                                                                                                                                                                       BM, Cartier GE,
, Jones RM;
                                                                                                                                    UTAH ) UNIV UTAH RES
                                                                                                                                                                    COGN-) COGNETIX INC
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Best Local Similarity
Matches 4; Conserv
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53 ACYNA 57
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                                   20-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neuropathic
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                                                                                                                                                                                                                                                                           Layer RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sclerosis
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us-10-007-790-6.rag

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The present invention is concerned with the sequence of the genome of the SEN virus (SENV), and the proteins encoded by it. SENV is thought to be the cause of hepatopathies which are not linked to the presence of the hepatitis A, B and B viruses in man. The genome and proteins of this virus can be used in gene therapy and vaccination against the virus, which also causes disorders of the gastrointestinal tract, including Crohn's disease and lupus erythematosus, inflammatory diseases, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping.
                                                                                                                                            SEN virus; SENV; gastrointestinal tract disorder; inflammatory disease; proliferative disorder; hepatopathy; hepatitis; viral infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids representing the genome of the SEN virus (SENV) and encoded proteins, useful for treatment of hepatopathies, inflammatory diseases and proliferative disorders such as cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 27; DB 21; Length 80
Pred. No. 4.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                      SEN virus protein fragment SEQ ID NO: 82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted protein, SEQ ID NO: 5586.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proliferative disorders such as cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 336-337; 392pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mantero GL
Olivero P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG01505 standard; Protein; 90 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.08;
                                                                                                                                                                                                                                                                                                                                                                                                                     99IT-MI00923.
                                                                                                                                                                                                                                                                                                                                                                                                 98IT-MI02437
                                                                                                                                                                                                                                                                                                                                                              99WO-EP08566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99EP-0113932
                                                             12-OCT-2000 (first entry)
                                                                                                                                                                                          vaccination; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fiordalisi G,
Vaglini L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DIÁS-) DIASORIN SRL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-376551/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 SCYNS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SCYNA 5
                                                                                                                                                                                                                                 Hepatitis virus
                                                                                                                                                                                                                                                                        WO200028039-A2
                                                                                                                                                                                                                                                                                                                                                            09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primi D, Fi.
Bonelli F,
                                                                                                                                                                                                                                                                                                                                                                                                   .0-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                         30-APR-1999;
                                                                                                                                                                                                                                                                                                                  18-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                               L4-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                        AAB11527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 35
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    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BX SX K K K E X L X Y X I I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence is a cone snail O-superfamily conotoxin propeptide.

The peptides are useful for regulating the flow of sodium through sodium channels in an individual and the treatment or prevention of disorders associated with voltage gated ion channel disorders, including demyelinating diseases i.e. multiple sclerosis, optic neuromyelitis, diseaminated encephalomyelitis, adrenoleukodystrophy, acute transverse myelitis, progressive multifocal leukoencephalopathy, sub acute sclerosing panecephalomyelitis (SSPB), metachromatic leukodystrophy, Pelizaeus Merzbacher disease, spinal cord injury, botulinum toxin poisoning, Huntington's, compression, entrapment neuropathies i.e. ulnar nerve palsy, and carpal tunnel syndrome, cardiovascular discorders, i.e. cardiac arrhythmias and congestive heart failure, reactive gliosis, hyperglycaemia, immunosuppression, cocaine addiction, cancer, cognitive dysfunction, neurotransmitter disorders is addiction, lambert syndrome) and reversal of curare and other neuromuscular blocking drugs. The neurological disorder is a neurotoxic injury is associated with stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, corder is pain i.e. midraine, contrained acute pain, persistent pain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disorder is pain i.e. migraine, acute pain, persistent pain, neuropathic pain, nociceptive pain. The disorder is inflammation or a cardiovascular disorder. A conotoxin peptide of is useful to alleviate pain in a mammal in pain or about to be subjected to a pain causing event, and to treat disorders associated with radical depolarisation of excitable membranes by activating a KATP channel, the disorders include cardiac, ocular and cerebral ischaemia and asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New O-superfamily polypeptides useful for treating voltage gated ion channel disorders, including demyelinating diseases i.e. multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                             Watkins M, Hillyard DR, McIntosh JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Pred. No. 4.1e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 15; Page 52; 277pp; English.
asthma; ischaemia; stroke; pain.
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                                                                                                                                                                                                       30-DEC-1999; 99US-0173754.
26-JUN-2000; 2000US-0214263.
20-JUL-2000; 2000US-0219440.
27-OCT-2000; 2000US-0243412.
                                                                                                                                                               28-DEC-2000; 2000WO-US35431
                                                                                                                                                                                                                                                                                                              (UTAH ) UNIV UTAH RES FOUND
                                                                                                                                                                                                                                                                                                                                                                           Cartier GE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
                                                                                                                                                                                                                                                                                                                                                                       A BM, Carr
                                                                                                                                                                                                                                                                                                                                    (COGN-) COGNETIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-418352/44.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-418352/
N-PSDB; AAS10937
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                                                                                 WO200149312-A2
                                       Conus magus
                                                                                                                      12-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                           Olivera BM,
Layer RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sclerosis
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Sottini A; Bonelli M;

GL, Mattioli S,
P, Dal Corso A,

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Gaps

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EP1033401-A2

AAB11527 standard; Protein; 88 AA.

RESULT 34 AAB11527

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Matches

Length 88;

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Liu C,
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                                                                                                                                                                                                                                       inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-AUG-2001.
                                                                             disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM06481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yeung G,
Liu C, A
Tang YT,
                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 37
                                                                                                                                                                                                                                                                                                                                                                                                                                AAM06481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; cytokine; cell proliferation; cell differentiation; gene therapy; accine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                       The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                       New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                         Score 27; DB 21; Length 90;
Pred. No. 4.3e+02;
1; Mismatches 0; Indels
                                                                                                  Giordano J;
                                                                                                                                                                                                     Claim 13; SEQ ID 5586; 71pp + CD-ROM; English
                                                                                                  Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human polypeptide SEQ ID NO 27296.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA013404 standard; Protein; 94 AA.
                                                                                                                                                                                                                                                                                                                                                                                                         90.0%;
                              21-FEB-2000; 2000EP-0200610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0515126.
2000US-0577409.
                                                      99US-0122487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                  Dumas Milne Edwards J,
                                                                                                                     WPI; 2000-500381/45.
N-PSDB; AAC01511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||||:
SCYNS 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                     90 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SCYNA 5
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                                                                            (GEST ) GENSET
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18-MAY-2000;
                                                    26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-SEP-2001.
         06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAO13404;
                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polyneptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haemacopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, foetal protein, cytostatic, immunosuppressive, immunostimulant, nootropic, neuroprotective, thrombolytic, osteopathic, antiinflammatory, gene therapy, antisense therapy, cancer, immune disorder, growth disorder, osteoporosis, thrombolytic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT;
                                                                                                                                                                            Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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                                                                                                                                                                                                                                                                                                                          Claim 20; SEQ ID NO 27296; 1399pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 27; DB 22;
Pred. No. 4.5e+02;
1; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nervous system disorder; inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human foetal protein, SEQ ID NO: 212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM06481 standard; Protein; 96 AA.
Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-JAN-2000; 2000US-0491404.
15-SEP-2000; 2000US-0663870.
06-NOV-2000; 2000US-0707351.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-465571/50.
N-PSDB; AAH94156.
                                                                   WPI; 2001-514838/56.
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Best Local Similarity
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71 ACYNA 75
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990S-0134370.
990S-0134768.
990S-0134941.
990S-0135124.
990S-0135629.
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990S - 0140354
990S - 0140354
990S - 0140921
990S - 0140921
990S - 0142055
990S - 0142055
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990S - 0142055
990S - 0142077
990S - 0142077
990S - 0142077
990S - 0142077
990S - 0144085
990S - 0144333
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99US-0139750.
99US-0139763.
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99US-0136782.
99US-0137222.
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99US-0137724.
99US-0138094.
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99US-0138847.
99US-0139119.
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99US-0145086.
99US-0145088.
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99US-0145192.
99US-0145145.
99US-0145218.
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10-JUN-1
14-JUN-1
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04-JUN-1
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Novel fetal proteins useful for the treatment and diagnosis of diseases associated with dysfunction of the protein e.g. cancers, immune disorders, growth disorders, thrombolytic disorders, nervous system disorders and inflammation -
                                                                                  The invention relates to novel foetal polypeptides encoded by polynucleotides comprising one of 477 sequences fully defined in the specification. The foetal polynucleotides and polypeptides are useful in the treatment and diagnosis of diseases such as cancers, immune disorders, growth disorders (e.g. osteoporosis), thrombolytic disorders, nervous system disorders and inflammation. The present an expressed sequence is a polypeptide encoded by a cDNA assembled using an expressed sequence tage (EST) found to be expressed in human foetal tissue cDNA libraries.
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                                                               Claim 10; Page 257; 715pp; English,
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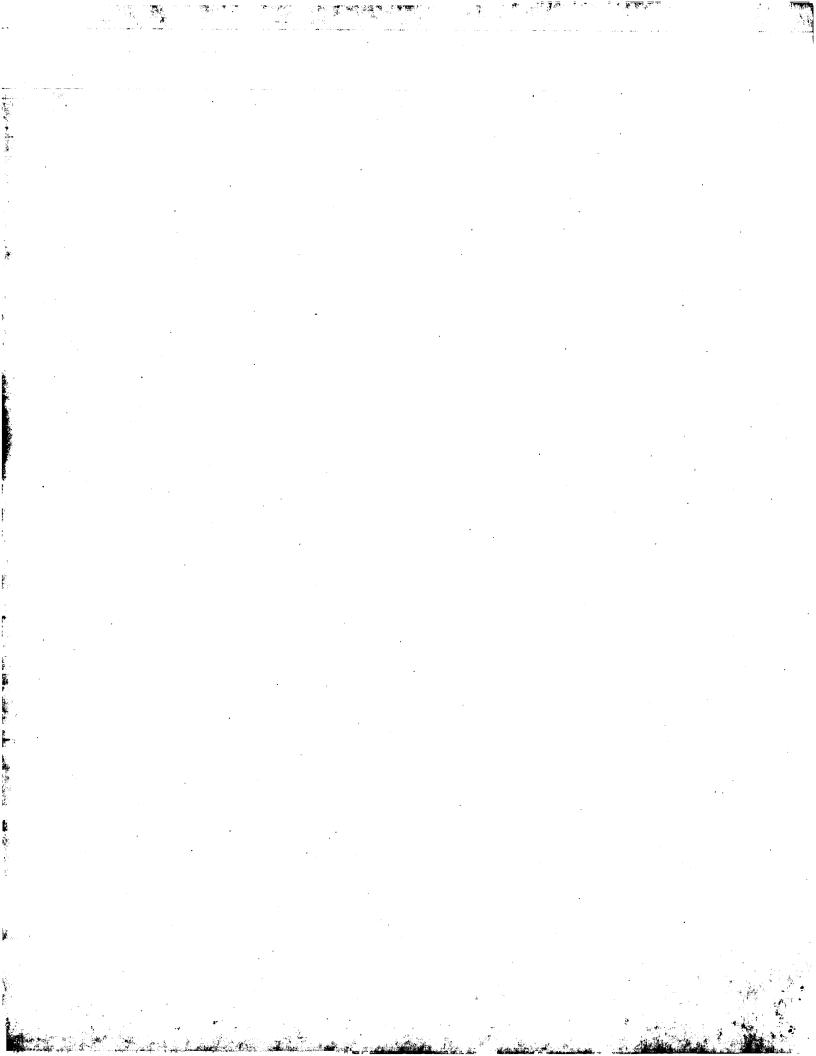
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Sequence 11,
               Patent No.
Seguence 2
Seguence 1
                                                                                                                                                                                  Sequence
Sequence
Sequence
Sequence
 Sequence
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Fatent No. 6348580
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REPERENCE:
CURRENT APPLICATION NUMBER: US/09/257,069
CURRENT APPLICATION NUMBER: US/09/257,069
CURRENT APPLICATION NUMBER: US/09/257,069
FILE REPERENCE: M3-008-US
CURRENT APPLICATION NUMBER: US/09/257,069
FILE REPERENCE: M3-008-US
CURRENT APPLICATION NUMBER: US/09/257,069
FRIOR FILING DATE: 1998-09-07
NUMBER OF SEQ ID NOS: 10
                                          US-08-867-087B-13
US-08-867-087B-13
US-08-816-605-9
US-09-006-353A-11
US-09-150-864A-8
US-09-130-864A-8
US-09-134-001C-3187
US-09-134-001C-3187
US-09-134-001C-3736
US-09-134-001C-3736
                                                                                                                                                                                                                                                US-08-442-043A-16
US-08-117-083-61
US-08-331-625A-43
US-08-888-366-8
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APPLICANT: D'Andrea, Alan D.
APPLICANT: Zhu, Yuan
TITLE OF INVENTION: Deubiquitinating Enzymes That Regulate
TITLE OF INVENTION: Deubiquitinating Enzymes That Regulate
TITLE OF INVENTION: Cell Growth
FILE REFERENCE: DFCI-435p2A2
CURRENT APPLICATION NUMBER: US/09/019,095A
CURRENT TILING DATE: 1998-02-05
PRIOR APPLICATION NUMBER: PCT/US96/12884
PRIOR APPLICATION NUMBER: US 60/002,066
PRIOR APPLICATION NUMBER: US 60/019,787
PRIOR FILING DATE: 1995-08-09
PRIOR FILING DATE: 1996-06-14
NUMBER OF SEQ ID NOS: 51
SEQ ID NO 23
LENGTH: 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 242;
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- APPLICANT: Hillman, Jennifer
- APPLICANT: Hillman, Jennifer
- APPLICANT: Glang, Hong Wolfe
- TITLE OF INVENTION: NOVEL HUMAN TUMOR-ASSOCIATED ANTIGEN
- NUMBER OF SEQUENCES: 4
- CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 27; DB 4; I
Pred. No. 2.3e+02;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,148
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Incyte Pharmaceuticals, Inc.
3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08808148
Patent No. 6020478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: PETELECOMMUNICATION INFORMATION TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 80.0%;
Matches 4; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Consensus
US-09-019-095A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 31/2 CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :||||
22 NCYNA 26
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APPLICANT: Peles, Elior
TITLE OF INVENTION: CASPR/190, A FUNCTIONAL LIGAND FOR RPTP-BETA AND THE
TITLE OF INVENTION: AXONAL CELL RECOGNITION MOLECULE CONTACTIN
FILE REFERENCE: 7683-111
CURRENT PILLING DATE: 1997-03-26
EARLIER APPLICATION NUMBER: 60/014,199
EARLIER PILLING DATE: 1996-03-27
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PLENG PATE: 2.0
SEQ ID NO 11
LENGTH: 158
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Patent No. 6465210

GENERAL INFORMATION:
APPLICANT: Peles, Elior
TITLE OF INVENTION: CASPR/190, A FUNCTIONAL LIGAND FOR RPTP-BETA AND THE
TITLE OF INVENTION: AXONAL CELL RECOGNITION MOLECULE CONTACTIN
FILE REFERENCE: 7683-111
CURRENT APPLICATION NUMBER: US/08/826,134A
CURRENT FILING DATE: 1997-03-26
FEARLIER PEPLING DATE: 1996-03-27
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
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                    DB 4; Length 124; 32;
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Pred. No. 1.5e+02;
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                                                             0; Indels
                                                               0; Mismatches
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                      100.0%; Score 30; 100.0%; Pred. No.
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                                                                                                                                                                                                                                      ; Sequence 11, Application US/08826134A; Patent No. 6465210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.0%;
Query Match
Best Local Similarity 100.00
-hea 5; Conservative
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; LENGTH: 158
; TYPE: PT
; ORGANISM: Rattus norvegicus
US-08-826-134-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 80.0
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Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-826-134-11
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52 SCYNA 56
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95 SCYNS 99
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GENERAL INFORMATION:

APPLICANT: Kimcto, No. 6312933ihiro

APPLICANT: Kimcto, No. 6312933ihiro

APPLICANT: Kimcto, No. 631293ihiro

APPLICANT: Yamamoto, Hiroaki

APPLICANT: Witeuhashi, Kazuya

TITLE OF INVENTION: BOXEL CARBONYL REDUCTASE, METHOD FOR PRODUCING ALCOHOL USING SAII

TITLE OF INVENTION: BOXEME

FILE REFERENCE: 06501-050001

CURRENT APPLICATION NUMBER: US/09/468,738A

CURRENT FILING DATE: 1999-12-21

PRIOR APPLICATION NUMBER: JP 1999-171160

PRIOR APPLICATION NUMBER: JP 1999-17116

PRIOR PILING DATE: 1999-06-17

PRIOR PILING DATE: 1999-06-17

PRIOR PILING DATE: 1999-12-21

NUMBER OF SEQ ID NOS: 29

SOFTWARE: PatentIN Ver. 2.0, reformatted using WordPerfect 5.1

LENGTH 296
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APPLICANT: Kamoto, Hiroaki
APPLICANT: Mimoto, Hiroaki
APPLICANTON: ENZYME
TITLE OF INVENTION: ENZYME
FILE REPERBING: 06501-050001
CURRENT APPLICATION NUMBER: US/09/940,019
CURRENT FILING DATE: 2001-08-27
FRIOR PRILOR DATE: 1999-06-17
PRIOR FILING DATE: 1999-06-17
PRIOR FILING DATE: 1999-06-17
PRIOR FILING DATE: 1998-12-21
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0, reformatted using WordPerfect 5.1
SEQ ID NO 23
LENOTH: 296
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Pred. No. 2.8e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                  Score 27; DB 4; Length 292;
Pred. No. 2.8e+02;
                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 23, Application US/09468738A Patent No. 6312933
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Patent No. 6416986
GENERAL INFORMATION:
                                                                     TYPE: PRT ORGANISM: Kluyveromyces aestuarii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Kluyveromyces aestuarii
                                                                                                                                                                                                  90.0%;
80.0%;
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Best Local Similarity
Matches 4; Conserv
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Matches 4; Conserv
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196 TCYNA 200
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192 TCYNA 196
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US-09-468-738A-23
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      SEQ ID NO 2
LENGTH: 292
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Facent No. 6312933

GENERAL INFORMATION:

APPLICANT: Kimoco, No. 6312933ihiro

APPLICANT: Kimoco, No. 6312933ihiro

APPLICANT: Mitanbashi, Kazuya

TITLE OF INVENTION: NOVEL CARBONYL REDUCTASE, METHOD FOR PRODUCING SAID ENZYME, DNA

TITLE OF INVENTION: NOVEL CARBONYL REDUCTASE, METHOD FOR PRODUCING ALCOHOL USING SAI

TITLE OF INVENTION: BNZYME

TITLE OF INVENTION BNZYME

FILE REFERENCE: 06501-05001

CURRENT APPLICATION NUMBER: JP 1999-12-21

PRIOR FILING DATE: 1999-06-17

PRIOR FILING DATE: 1998-12-21

NUMBER OF SEQ ID NOS: 29

SOFTHARE: PATENTING DATE: JP 1998-363130

NUMBER OF SEQ ID NOS: 29

SOFTHARE: PATENTING DATE: JP 1998-12-21

NUMBER OF SEQ ID NOS: 29
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APPLICANT: Kinoto, No. 6416986ihiro
APPLICANT: Kinoto, Hiroaki
APPLICANT: Yamamoto, Hiroaki
APPLICANT: Wisuhashi, Kazukaki, Kazuka
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Pred. No. 2.8e+02;
1; Mismatches 0;
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Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
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US-09-940-019-2
; Sequence 2, Application US/09940019
; Patent No. 6416986
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Kluyveromyces aestuarii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.0<del>%</del>;
80.08;
                                                                                                                                                                                                                                                                                           90.0%;
LENGTH: 281 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 80.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIBRARY: GenBank
CLONE: 755242
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192 TCYNA 196
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US-09-468-738A-2
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LENGTH: 292
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US-08-808-148-4
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Sequence 4, Application US/08826134A
Patent No. 6465210
GENERAL INFORMATION
GENERAL INFORMATION
TITLE OF INVENTION: CASPR/190, A FUNCTIONAL LIGAND FOR RPTP-BETA AND THE
TITLE OF INVENTION: AXONAL CELL RECOGNITION MOLECULE CONTACTIN
CURRENT APPLICATION NUMBER: US/08/826,134A
CURRENT FILING DATE: 1997-03-26
EARLIER FILING DATE: 1997-03-26
EARLIER FILING DATE: 1996-03-27
NUMBER OF SEQ ID NOS: 32
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                                                                                                                                            COMPUTER: READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Patent BM PC compatible
COMPUTER: Patent BM PC compatible
COMPUTER: Patent BM PC compatible
COMPUTER: Patent BM PC COMPUTER: BM PC COMPUTER: DATE:
CURRENT APPLICATION NUMBER: US/08/687,080
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/592,126
FILING DATE: 26-JAN-1996
ATTORNEY AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 38,615
TELEPHONE: (415) 324-0860
INFORMATION FOR SED ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 645 amino acids
TYPE: amino acids
TYPE: maino acids
TYPE: Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 27; DB 4;
Pred. No. 1.2e+03;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 27; DB 2;
Pred. No. 6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                   ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INDIVIDUAL ISOLATE: G18.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.0%;
80.0%;
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4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-08-826-134-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 4
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Best Local Similarity 80.0
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 4; Conserv
                                                                         Palo Alto
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                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE
                                                                                                                                  94306
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                                                                                                                COUNTRY:
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US-08-826-134-4
                                                                           CITY:
STATE:
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                                                                                                Gaps
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                                                                                                                                                                                                                                                        Sequence 144, Application US/08592126
Patent No. 5831091
GENERAL INFORMATION:
APPLICANT: Gregory Dolganov
TITLE OF INVENTION: Transcripts Encoding Immunomodulatory
TITLE OF INVENTION: Polypeptides
NUMBER OF SEQUENCES: 151
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350
CITY: Palo Alto
                                                         Length 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; . Length 645;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,126
                                                                           2.8e+02;
                                                         Score 27; DB 4;
Pred. No. 2.8e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-080
TELEPHONE: (415) 324-080
INFORMATION FOR SEQ ID NO: 144:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.0%; Score 27;
80.0%; Pred. No.
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; ORGANISM: Kluyveromyces aestuarii
US-09-940-019-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: G18.pep
                                                     90.0%;
80.0%;
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amino acid
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Best Local Similarity 80.0.
                                                                         Best Local Similarity 80.0
Matches 4; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                     196 TCYNA 200
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                                                                                                                                  1 SCYNA 5
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                                                                                                                                                                                                                                               US-08-592-126-144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: C. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-687-080-47
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                                                         Query Match
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SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                     APPLICANT: Peles, Elior
TITLE OF INVENTION: CASPR/190, A FUNCTIONAL LIGAND FOR RPTP-BETA AND THE
TITLE OF INVENTION: AXONAL CELL RECOGNITION MOLECULE CONTACTIN
FILE REFERENCE: 7683-111
CURRENT APPLICATION NUMBER: US/08/826,134A
CURRENT FILING DATE: 1997-03-26
BARLIER APPLICATION NUMBER: 60/014,199
BARLIER PILING DATE: 1996-03-27
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 1384;
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Patent No. 5814478

GENERAL INFORMATION:

TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS

TITLE OF INVENTION: AND LIGANDS

NUMBER OF SEQUENCES: 32

CORRESPONDENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: Regeneron Pharmaceuticals, Inc.

STATE: NY

STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.0%; Score 27;
80.0%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASISEQ Version 2.0
SOFTWARE: PASISEQ VERSION 2.0
APPLICATION NUMBER: US/08/644,271
FILING DATE: 10-MAY-1996
                                                                                                                                              Sequence 2, Application US/08826134A
Patent No. 6465210
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PELECOMMUNICATION INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Cobert, Robert J
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 80.0 Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      676 SCYNS 680
                                          ||||:
SCYNS 681
              SCYNA 5
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US-08-644-271-30
                                                                                                          RESULT 14
US-08-826-134-2
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LENGTH: 13
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Sequence 34, Application US/09077955A

Sequence 34, Application US/09077955A

FREEDT NO. 6413740.

APPLICANT: Valenzuela et al., David M.

TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS

FILE REFERENCE: REG195-B-PCT-US

CURRENT APPLICATION NUMBER: US/09/077,955A

CURRENT FILING DATE: 1998-09-10

EARLIER PPLICATION NUMBER: 08/44,271

EARLIER FILING DATE: 1996-05-10

EARLIER FILING DATE: 1996-12-15

NUMBER OF SEQ ID NOS: 36
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Pred. No. 1.7e+03;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                DB 2; Length 1940;
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APPLICANT: Miller, Timothy J.
APPLICANT: Klepfer, Sharon
APPLICANT: Reed, Albert Paul
APPLICANT: Reed, Albert Paul
APPLICANT: Jones, Elaine V.
TITLE OF INVENTION: Canine Coronavirus S Gene and Uses
TITLE OF INVENTION: Therefor
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: RaithKline Beecham Corporation - Corporate
ADDRESSEE: Patents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                   Score 27;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 33, Application US/08331625A Patent No. 6057436
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                                                                                                                                                                                                                                   90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.0%;
                                    TOPOLOGY: linear
MOLECULE TYPE: protein
MOLECULE TYPE: protein
MAME/KEY: Rat Agrin
LOCATION: 1...1940
JS-08-644-271-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 34
                                                                                                                                                                                                                                Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 90.0
Best Local Similarity 80.0
Matches 4; Conservative
                        single
TYPE: amino acid
STRANDEDNESS: siz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-077-955-34
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86.7%; Score 26; DB 100.0%; Pred. No. 23; Live 0; Mismatches
                                                                       FILING DATE: 13-MAY-1991
APPLICATION NUMBER: US 07/613,066
FILING DATE: 14-MOV-1990
ATTORNEY/AGENT INFORMATION:
                            FILING DATE: <Unknown>
APPLICATION NUMBER: US 07/698,927
                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
ON NUMBER: 08/331,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/256,747C
FILING DATE: 06-OCT-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/08256747C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: (
                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
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CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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ADDRESSEE: SmithKline Beecham Corporation - Corporate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Canine Coronavirus S Gene and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 26; DB 3; Length 14;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,625A
                                                                                                                                                                                           APPLICATION NUMBER: US/08/31,025A
FILING DATE:
CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/680,194
FILING DATE: 08-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/698,927
FILING DATE: 13-MAY-1991
PRIOR APPLICATION NUMBER: US 07/613,066
FILING DATE: 14-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: SCANECK, PARTICIA A.
REGISTRATION NUMBER: 33,777
REFERENCE/DOCKET NUMBER: SBC H85010-1
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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APPLICATION NUMBER: US/09/494,151
FILING DATE: 28-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 33, Application US/09494151
Patent No. 6372224
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Miller, Timothy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Klepfer, Sharon
Reed, Albert Paul
Jones, Elaine V.
                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: King of Prussia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (215) 270-5015
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
3Y: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCYN 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-494-151-33
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APPLICANT: CHONG, Pele
APPLICANT: GILLAM, Shirley
APPLICANT: OU, Dawei
APPLICANT: TINGLE, Aubrey
TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR A RUBELLA VACCINE
NUMBER OF SEQUENCES: 78
                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 14; 23;
                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Sim & McBurney
6th Floor 701, 330 University Avenue
NAME: Schreck, Patricia A.
REGISTRATION NUMBER: 33,777
REGISTRATION NUMBER: 38,777
RELECONMUNICATION INFORMATION:
TELECONMUNICATION INFORMATION:
TELEFAX: (215) 270-5016
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 aming acids
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Sequence 64, Application US/08867087B

Patent No. 5990386

GENERAL INPORMATION:
APPLICANT: An. GYNHeung

TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT
TITLE OF INVENTION: AND APICAL DOMINANCE IN PLANTS

NUMBER OF SEQUENCES: 70

CORRESPONDENCE ADDRESS:
ADDRESSEE: Klarquist Sparkman Campbell Leigh & ADDRESSEE: Whinston, LLP

STREET: One World Trade Center
STREET: 121 S.w. Salmon Street
STREET: Silte 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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                                                                                                                                           CONTINITY UNITED SCACES OF AMERICA ZIP: 97204
COMPUTER READABLE FORM: S1/2 inch COMPUTER: IBM PC compatible OPERATING SYSTEM: MS DOS SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/867,087B FILING DATE: Une 2, 1997
CLASSIFTCATION DATA: 0.5 08/32,449
FILING DATE: October 14, 1994
APPLICATION NUMBER: U.S. 08/485,981
FILING DATE: Une 7, 1995
ATTORNEY/AGENT INFORMATION: NAME: DOW, Alan. E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 12.
STREET: SUITE 150.
STREET: Suite 150.
CITY: Portland
STRTE: Oregon
COUNTRY: United States of America
71P: 97204
71P: 97204
71P: 97204
71P: 97204
71P: 97204
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/323,449
                                                                                                                                  United States of America
STREET: 121 S.W. Salmon Street STREET: Suite 1600 CITY: Portland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
COMPUTER: MordPerfect 5.1
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/867,01
FILING DATE: June 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 amino acid residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 35,123
REFERENCE/DOCKET NUMBER: 4630-
TELECOMINICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 226-9446
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                  COUNTRY:
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                                                                                                                                                                                                                                                                                                                                       APPLICANT: CHONG, Pele
APPLICANT: GLLLAM, Shirley
APPLICANT: OU, Dawei
APPLICANT: TINGLE, Aubrey
TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR A RUBELLA VACCINE
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 63, Application US/08867087B

Sequence 63, Application US/08867087B

Patent No. 5990386

GENERAL INFORMATION:
APPLICANT: An, Gynheung

TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT

TITLE OF INVENTION: AND APICAL DOMINANCE IN PLANTS

NUMBER OF SEQUENCES: 70

CORRESPONDENCE ADDRESS:
ADDRESSEE: Whinston, LLP

STREET: One World Trade Center
                                                Score 26; DB 3; Length 26; Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CHRRENT APPLICATION DATA: APPLICATION NUMBER: US/08/834,130A FILING DATE: 14-APR-1997 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/ACENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REERENCE/DOCKET NUMBER: 1038-686 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1153
TELEPHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                      US-08-834-130A-68; Sequence 68, Application US/08834130A; Patent No. 6180758; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                            86.7%; Scc.
100.0%; Pre
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100.0%; Pic
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                                         Query Match
Best Local Similarity 100.
Matches 4; Conservative
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ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 4; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Sim
STREET: 6th Flo
CITY: Toronto
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                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
APPLICANT: Wang, Chang Yi
APPLICANT: Shen, Ming
TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR
TITLE OF INVENTION: FOOT-AND-MOUTH DISEASE
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
                                                                                                                                        100.0%; Prec. ....
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APPLICATION NUMBER: US/09/100,600A
FILING DATE: 20-Jun-1998
CLASSIFICATION: 424
ATTORNEY AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 129,133
REFERENCE/DOCKET NUMBER: 1151-4156
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
                                                                                                                      86.7%; Score 26;
                                                                                                                                                                                                                                                                                                                                                   Sequence 76, Application US/09100600A
Patent No. 6107021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 29, Application US/09494151
; Patent No. 6372224
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Miller, Timothy J. Klepfer, Sharon Reed, Albert Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZUP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 345 Park Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 47 amino acids
                                                                                                                                                                 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 212-751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                   TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Word 97
                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                 34 SCYN 37
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                                                                                                                                                                                                          1 SCYN 4
                                                                               US-08-331-625A-29
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                                                                                                                                                                                                                                                                                                                               US-09-100-600A-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: NY COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 25
US-09-494-151-29
                                                                                                                                                                 Matches
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Patent No. 6057436

GENERAL INFORMATION:
APPLICANT: Miles, Timothy J.
APPLICANT: Klepfer, Sharon
APPLICANT: Reed, Albert Paul
APPLICANT: NUMBER OF SEQUENCES: 59
CORRESPONDENCE ALBERS: 59
CORRESPONDENCE ALBERS:
ADDRESSEE: ShithKline Beecham Corporation - Corporate
ADDRESSEE: Patents
                                                                                                                                                                                                                                                                                                                                                       86.7%; Score 26; DB 2; Length 34; 100.0%; Pred. No. 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,625A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                       NAME: Dow, Alan. E.
REGISTRATION NUMBER: 35,123
REFERENCE/DOCKET NUMBER: 4630-47071
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 226-7391
TELEFAX: (503) 226-7346
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Schreck, Patricia A.
REGISTRATION NUNBER: 33,777
REFERENCE/DOCKET NUMBER: SBC H85010-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/880,194
FILING DATE: 08-WAY-1992
PRIOR APPLICATION NUMBER: US 07/698,927
FILING DATE: 13-WAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/613,066
FILING DATE: 14-NOV-1990
ATTORNEY/AGENT INFORMATION:
FILING DATE: October 14, 1994
APPLICATION NUMBER: U.S. 08/485,981
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                 LENGTH: 34 amino acid residues
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 1946-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 709 Swedeland Road
King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (215) 270-5015
                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                         2 CYNA 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 23
US-08-331-625A-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                         Query Match
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NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation - Corporate
Patents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Canine Coronavirus S Gene and Therefor
                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,625A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/09/494,151
FILING DATE: 28-Jan-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/331,625
                                                                                                                                                            CLASSIFICATION: 435
CLASSIFICATION: 435
APPLICATION DATA:
APPLICATION NUMBER: US 07/880,194
FILING DATE: 08-MAX-1992
REIGN APPLICATION NUMBER: US 07/699,927
FILING DATE: 13-MAX-1991
RIOR APPLICATION NUMBER: US 07/613,066
APPLICATION NUMBER: US 07/613,066
FILING DATE: 14-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Schreck, Patricia A.
REGISTRALION NUMBER: SSC H85010-
REFERENCE/DOCKET NUMBER: SBC H85010-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09494151
Patent No. 6372224
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Miller, Timothy J. Klepfer, Sharon Reed, Albert Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jones, Elaine V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: King of Prussia STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5015
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.7%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown
MOLECULE TYPE: protein
    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-494-151-4
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                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation - Corporate
Patents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:

APPLICANT: Miller, Timothy J.

APPLICANT: Reed, Albert Paul
APPLICANT: Reed, Albert Paul
APPLICANT: Gene and Uses;
TITLE OF INVENTION: Canine V.

TITLE OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation - Corporate
ADDRESSEE: Patente
                     Coronavirus S Gene and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/494,151
FILING DATE: 28-Jan-2000
CLASSIFICATION: <unversion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Schreck, Patricia A.
REGISTRATION NUMBER: 33, 777
REFERENCE/DOCKET NUMBER: SBC H85010-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
74;
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/331,625
FILING DATE: «UNKNOWN»
APPLICATION NUMBER: US 07/698,927
FILING DATE: 13-MAY-1991
APPLICATION NUMBER: US 07/613,066
FILING DATE: 14-NOV-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                            ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
, SEQUENCE DESCRIPTION: SEQ ID NO: 29: US-09-494-151-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 26;
Pred. No.
                                                                                                                                         STREET: 709 Swedeland Road CITY: King of Prussia STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08331625A
Patent No. 6057436
Jones, Elaine V.
TITLE OF INVENTION: Canine Co
Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 47 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Patents
ADDRESSEE: Patents
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 19406-2799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 SCYN 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SCYN 4
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US-08-331-625A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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Patent No. 5874240
GENERAL INFORMATION:
APPLICANT: Ni, Jiang
APPLICANT: Ni, Jiang
APPLICANT: Ni, Jiang
APPLICANT: Gentz, Reiner
TITLE OF INVENTION: Human 4-IBB Receptor Splicing Variant
NUMBERSPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 148;
                                                                                                                                                                                       Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 5180813

** APPLICANT: Stinski, Mark F.

** TITLE OF INVENTION: EARLY ENVELOPE GLYCOPROFEIN OF HUMAN; CYTOMEGALOVIRUS (HMCV) AND MONOCLONAL ANTIBODIES TO THE
                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86.7%; Score 26; DB 6; Len
... Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/816.605
                                                                                                                                                                                                           1.7e+02;
                                                                                                                                                                                       Score 26; DB 2;
Pred. No. 1.7e+0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Human Genome Sciences, Inc. 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-MAR-1997
13-MAR-1997
13-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/328,227
FILING DATE: 24-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                           100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                        LENGTH: 114 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                         Query Match 86.7
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLYCOPROTEINS
HUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 9410
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 SCYN 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                       46 SCYN 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: MC
COUNTRY:
                                                                                                                                                     US-08-888-366-8
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                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO:2
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Patent No. 5972656

GENERAL INFORMATION:
APPLICANT: Lopez, Osvaldo
APPLICANT: Wylie, Dwane E.
APPLICANT: Wagner, Fred W.
ITITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,366
FILING DATE: 03-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/187,407
FILING DATE: 07-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,542
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,542
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,299
FILING DATE: «Unknown»

APPLICATION NUMBER: US 07/698,927
FILING DATE: 13-MAY-1991
APPLICATION NUMBER: US 07/613,066
FILING DATE: 14-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Schreck, Patricia A..
REFERENCE/DOCKET NUMBER: 33,777
FEEECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      86.7%; Scor.
100.0%; Pred. No. co.
                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown;
MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-494-151-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Carter, Charles G.
REGISTAATION NUMBER: 35,093
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/493,299
FILING DATE: 14-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/324,392
FILING DATE: 14-MAR-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                         TELEPHONE: (215) 270-5015
TELEFAX: (215) 270-5090
                                                                                                                                                                                                             TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 4; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SCYN 4
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US-08-888-366-8
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US-08-236-918A-8
; Sequence 8, Application US/08236918A
; Patent No. 5674704
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Patent No. 5874240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 255 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                     GENERAL INFORMATION:
    73 CYNA 76
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TELEFAX: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-236-918A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13, Application US/08867087B
Fatent No. 5990386
GENERAL INFORMATION:
APPLICANT An, Gynheung
TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT
TITLE OF INVENTION: AND APICAL DOMINANCE IN PLANTS
NUMBER OF SEQUENCE: 70
CORRESPONDENCE: 70
CORRESPONDENCE: Marquist Sparkman Campbell Leigh & ADDRESSEE: Minatorn, Lip
STREET: One World Trade Center
STREET: Suite 1600
CITY: Portland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.7%; Score 26; DB 2; Length 250; 100.0%; Pred. No. 3.7e+02;
                                                                                                                                                                                                               Length 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                               DB 2; L6
                                                                                                                                                                                                     86.7%; Score 100.0%; Pred. No. 3.3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTRY: United States of America CLOMPUTRY: United States of America 21P: 97204

COMPUTER READBLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch COMPUTER: IBM PC compatible OPERATING SYSTEM: MS DOS SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,087B FILING DATE: June 2, 1997

CLASSIFICATION: 800

RIGHT APPLICATION BATA:
APPLICATION NUMBER: U.S. 08/323,449

FILING DATE: October 14, 1994
APPLICATION NUMBER: U.S. 08/485,981
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Alan. E.
REGISTRATION NUMBER: 35,123
REFERENCE/DOCKET NUMBER: 35,123

REFERENCE/DOCKET NUMBER: 35,123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 250 amino acid residues amino acid
TELECOMMUNICATION INFORMATION
                TELEPHONE: 301-309-8504
TELEFAX: 301-309-8512
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 13
                                                                                            LENGTH: 219 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                               , MOLECULE TYPE: protein US-08-816-605-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oregon
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US-08-867-087B-13
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Gaps
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APPLICANT: Ni, Jiang
APPLICANT: Vi, Guo-Liang
APPLICANT: Yi, Guo-Liang
APPLICANT: Gentz, Reiner
TITLE OF INVENTION: Human 4-1BB Receptor Splicing Variant
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86.7%; Score 26; DB 1; Length 255; 100.0%; Pred. No. 3.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                           B: Kathryn A. Anderson, Immunex Corporation
51 University Street
APPLICANT: Aderson, Mark R.
APPLICANT: Goodwin, Raymond G.
APPLICANT: Smith, Craig A.
TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: Seattle
CITY: Seattle
CITY: Washington
                                                                                                                                                                                                                                                                        STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple 7.5.3
SOFTWARE: Microsoft Word, Version #6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/236,918A
FILING DATE: 06-May-1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/060,843
FILING DATE: 07-May-1993
CLASSIFICATION NUMBER: US 08/060,843
FILING DATE: 07-May-1993
CLASSIFICATION NUMBER: US 28/060,843
FILING DATE: 07-May-1993
CLASSIFICATION NUMBER: US 28/050,843
FELECOMMUNICATION NUMBER: 32,172
REGISTRATION NUMBER: 32,172
REGISTRATION NUMBER: 2801-B
TELECOMMUNICATION NUMBER: 2801-B
TELECOMMUNICATION NUMBER: 2801-B
TELEPHONE: (206) 557,430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: MD COUNTRY: USA
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GENERAL INFORMATION:
APPLICANT: Alderson, Mark R.
APPLICANT: Alderson, Mark R.
APPLICANT: Goodwin, Kaymond G.
APPLICANT: Smith, Craig A.
APPLICANT: Smith, Craig A.
TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand and Human Receptor TITLE OF INVENTION: That Binds Thereto
TITLE REPERENCE: 2801-B
CURRENT APPLICATION NUMBER: US/09/150,864A
CURRENT APPLICATION NUMBER: 09/060,843
FRIOR FILING DATE: 1993-05-07
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 255
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                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09007097A

Patent No. 6303121

BAREAL INFORMATION:
APPLICANT: KWANION:
FILE OF INVENTION: METHOD OF USING HUMAN RECEPTOR PROTEIN 4-1BB

FILE REPERENCE: 740.011012

CURRENT APPLICATION HUMBER: US/09/007,097A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 255;
                                                                                                           86.7%; Score 26; DB 4; Length 255; 100.0%; Pred. No. 3.8e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT , ORGANISM: Homo sapiens (clone: hu4-1BB) US-09-150-864A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-150-864A-8
; Sequence 8, Application US/09150864A
; Patent No. 6355779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.7%;
100.0%;
                                                                                                              Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                               ; MOLECULE TYPE: protein US-09-006-353A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 4; Conserv
      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 SCYN 7
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US-09-007-097-2
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Pred. No. 3.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: WEI, YING-FEI
APPLICANT: YU, GUO-LIANG
APPLICANT: GENTZ, REINER
APPLICANT: GENTZ, REINER
APPLICANT: GENTZ, REINER
APLICANT: TIVER
TIVE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN CENTER
STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPTRE: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,605
FILING DATE: 13-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: 36,373
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFPHONE: 301-309-8504
TELEFPKX: 301-309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIE. 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/006,353A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 34
US-09-006-353A-11
; Sequence 11, Application US/09006353A
; Patent No. 6261801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF341
TELECOMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 255 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-816-605-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: WEI, Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
SD
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SCYN 7
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COUNTRY:
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Sequence 3736, Application US/09134001C

Patent No. 6380370
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: UNMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: S674
SEQ ID NO 3736
LENGTH: 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-134-001C-3187
US-09-134-001C-3187
Sequence 3187, Application US/09134001C
Factor No. 6380370
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: DEPLERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: UNMBER: US/09/134,001C
TITLE OF INVENTION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
FRIOR APPLICATION NUMBER: US 60/064,964
FRIOR APPLICATION NUMBER: US 60/055,779
FRIOR FILING DATE: 1997-11-08
FRIOR APPLICATION NUMBER: US 60/055,779
NUMBER OF SEQ ID NOS: S674
SEQ ID NO 3187
LENGTH: 270
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                                                                                                                                                                                                                            Length 255;
                                                                                                                                                                                                                          DB 5; Le
3.8e+02;
                                                                                                                                                                                                                          Score 26; DB 5
s; Pred. No. 3.86
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                               86.7%; 8
100.0%;
                                                                                255 amino acids
TELEFAX: 607-273-2609
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
TEMORET
                                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 86.7
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                   , MOLECULE TYPE: protein
PCT-US96-03965-8
                                                                                                           amino acid
                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                             LENGTH:
                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US96-03965-8
Sequence 8, Application PC/TUS9603965
GENERAL INFORMATION:
APPLICANT: Kwon, Byoung Se
APPLICANT: Kang, Chang-Yuil
TITLE OF INVENTION: Monoclonal antibody against human
TITLE OF INVENTION: receptor 4-1BB
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                          Sequence 11, Application US/09573986

Patent No. 6455040

GENERAL INPORMATION:
APPLICANT: Wei, Jian
APPLICANT: Ruben, Steven
APPLICANT: Gentz, Reiner
APPLICANT: 2000-05

TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
FILE REFERENCE: 1468.126004

CURRENT APPLICATION NUMBER: US/09/573,986

CURRENT FILING DATE: 2000-05-18

NUMBER OF SEQ ID NOS: 27

SEQ ID NO 11

SEQ ID NO 11

LENGTH: 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/03965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Barnard, Brown & Michaels
STREET: 306 East State Street, Suite 220
CITY: Ithaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE: 16-SEP-193
PRIOR APPLICATION NUMBER: US 08/012,269
FILING DATE: 01-FEB-1933
PRIOR APPLICATION NUMBER: US 07/922,996
FILING DATE: 30-UUL-1992
PRIOR APPLICATION NUMBER: US 07/922,996
FILING DATE: 30-UUL-1992
APPLICATION NUMBER: US 07/927,977
FILING DATE: 07-NOV-1988
FILING DATE: 07-NOV-1988
FILING DATE: NFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Michaels, Christopher A
REGISTRATION NUMBER: 34,390
REFERENCE/DOCKET NUMBER: KWOS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 607-273-1711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 14850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-09-573-986-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCYN 7
     RESULT 37
US-09-573-986-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
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0; Gaps

Search completed: July 18, 2003, 15:11:48 Job time : 6.8 secs

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Sequence

197, 197, 197,

Sequence

Sequence Sequence

US-09-990-444-197
US-09-991-181-197
US-09-990-436-197
US-09-990-436-197
US-09-997-653-197
US-09-997-653-197
US-09-997-653-197
US-09-997-666-197
US-09-997-666-197
US-09-990-438-197
US-09-990-438-197
US-09-990-437-197
US-09-990-437-197
US-09-991-157-197

Sequence

Sequence Sequence

197, 197,

Sequence

Sequence Sequence Sequence Sequence

197,

197,

Sequence | Sequence |

Sequence Sequence

197.

Sequence Sequence Sequence Sequence

Sequence

US-09-997-628-197 US-09-997-683-197 US-09-989-729A-197 US-09-997-349-197

ALIGNMENTS

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197,

Sequence

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APPLICANT: Wood, William I...,
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PICS8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/989,862
CURRENT FILING DATE: 2001-11-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 197, Application US/0998962
Publication No. US20030130182A1
MEMERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Grimaldi, J. Christopher
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumars, Daniel
Watanabe, Colin K.
Williams, P. Mickey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fong, Sherman
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ferrara, Napoleone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Baker, Kevin P.
Botstein, David
Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kljavin,Ivar J.
Napier,Mary A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Godowski, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pan, James
US-09-989-862-197
 APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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APPLICANT:
APPLICANT:
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                                                                                                  July 18, 2003, 15:09:56; Search time 12.9 Seconds (without alignments) 46.031 Million cell updates/sec
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1: \( \text{cgn2} \bigcde{6} \\ \text{prodata/1/pubpaa/PCT_NEW_PUB.pep:*} \)

2: \( \text{cgn2} \bigcde{6} \\ \text{prodata/1/pubpaa/PCT_NEW_PUB.pep:*} \)

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5: \( \text{cgn2} \bigcde{6} \\ \text{prodata/1/pubpaa/PCT08} \\ \text{PUB.COMB. pep:*} \)

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US-09-991-163-197
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                                                                      protein search, using sw model
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PRIOR PELING DATE: 1998-66-16
PRIOR PELICATION NUMBER: 60/08538
PRIOR PELING DATE: 1998-66-17
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PRIOR PELICATION NUMBER: 60/08959
PRIOR PELING DATE: 1998-06-17
PRIOR PELICATION NUMBER: 60/089601
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PRIOR PELING DATE: 1998-06-24
PRIOR PELICATION NUMBER: 60/09045
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PRIOR PELING DATE: 1998-06-24
PRIOR PELICATION NUMBER: 60/09055

APPLICATION NUMBER: 60/091360

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PRIOR PILLING DATE: 1998-06-05
PRIOR PELLING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR APPLICATION NUMBER: 60/08873
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PRIOR PELLING DATE: 1998-06-10
PRIOR PELLING DATE: 1998-06-11
                                                                                                             PRIOR FILING DATE: 1998-04-28

PRIOR APPLICATION NUMBER: 66/084600

PRIOR APPLICATION NUMBER: 66/087106

PRIOR FILING DATE: 1998-05-28

PRIOR FILING DATE: 1998-05-28

PRIOR FILING DATE: 1998-05-28

PRIOR FILING DATE: 1998-06-02

PRIOR FILING DATE: 1998-06-02

PRIOR PELICATION NUMBER: 66/08759

PRIOR FILING DATE: 1998-06-02

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PRIOR PILING DATE: 1998-06-04

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PRIOR APPLICATION NUMBER: 60/088026

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PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
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PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P273011663
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CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR PLING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
                                                                                                                                         A APPLICATION NUMBER: 00/031349

R APPLICATION NUMBER: 60/091519

R FILING DATE: 1998-07-02

R RILING DATE: 1998-07-02

R APPLICATION NUMBER: 60/091635

R APPLICATION NUMBER: 60/091633

R FILING DATE: 1998-07-02

R APPLICATION NUMBER: 60/091633

R FILING DATE: 1998-07-02

R APPLICATION NUMBER: 60/091982

R FILING DATE: 1998-07-07

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APPLICATION NUMBER: 60/066770
FILING DATE: 1997-11-24
APPLICATION NUMBER: 60/075945
FILING DATE: 1998-02-25
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FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091544
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Ferrara, Napoleone
       FILING DATE: 1998-07-01
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Paoni, Nicholas F.
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Goddard, Audrey
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Best Local Similarity 100.
Matches 5; Conservative
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Botstein, David
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REFLICATION NUMBER: 60/089948
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RETLING DATE: 1998-06-19
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RETLING DATE: 1998-06-19
RETLING DATE: 1998-06-22
RAPPLICATION NUMBER: 60/090246
RETLING DATE: 1998-06-22
RAPPLICATION NUMBER: 60/090254
RETLING DATE: 1998-06-22
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RETLING DATE: 1998-06-22
RETLING DATE: 1998-06-22
RETLING DATE: 1998-06-23
RETLING DATE: 1998-06-23
RETLING DATE: 1998-06-23
RETLING DATE: 1998-06-23
                                                                                                       R PILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089653

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089801

R APPLICATION NUMBER: 60/089907

R APPLICATION NUMBER: 60/089908

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APPLICATION NUMBER: 60/090535
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APPLICATION NUMBER: 60/091519
FILING DATE: 1998-07-02
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089599
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089600
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APPLICATION NUMBER: 60/090429
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090431
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APPLICATION NUMBER: 60/090435
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APPLICATION NUMBER: 60/090444
FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/090540
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APPLICATION NUMBER: 60/090542
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APPLICATION NUMBER: 60/090557
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APPLICATION NUMBER: 60/090676
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APPLICATION NUMBER: 60/090678
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APPLICATION NUMBER: 60/090695
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APPLICATION NUMBER: 60/090696
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APPLICATION NUMBER: 60/090862
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PRILOR PR
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PPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/989,723
CURRENT FILING DATE: 2001-11-19
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-07
PRIOR PELING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
PRIOR PLING DATE: 1998-07-07
PRIOR PLING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/09182
PRIOR FILING DATE: 1998-07-07
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PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
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; Sequence 197, Application US/09989723
; Patent No. US20020072092A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
APPLICANT: Baker,Kevin P.
; APPLICANT: Baker,Kevin P.
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PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
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PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-29
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APPLICATION NUMBER: 60/084600
FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/087106
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Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A
Tumas, Daniel
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Gerritsen, Mary E.
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Best Local Similarity 100.
Matches 5; Conservative
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Napier, Mary A.
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Eaton, Dan L.
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98-05-28 BER: 60/087607 98-06-02 BER: 60/087609 98-06-02		1 1998-06-04 1998-06-04 1998-06-04 1998-06-04 1998-06-05 1998-06-05 1998-06-05 1998-06-05 1998-06-05 NUMBER: 60/088212 1998-06-05 NUMBER: 60/08855 1998-06-05 1998-06-05 1998-06-06 1998-06-06 NUMBER: 60/088734 1998-06-10 NUMBER: 60/088738 1998-06-10 NUMBER: 60/088738 1998-06-10 NUMBER: 60/088738	2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	BER: 60/089514 98-06-16 98-06-16 98-06-17 98-06-17 98-06-17 98-06-17 BER: 60/089598 98-06-17 BER: 60/089600 98-06-17 BER: 60/089653 98-06-17
PRIOR FILING DATE: 1998- PRIOR APPLICATION NUMBER PRIOR FILING DATE: 1998- PRIOR APPLICATION NUMBER PRIOR FILING DATE: 1998-	APPLICATION PULLING DATE: PILLING DATE: PILLING DATE: PILLING DATE: PILLING DATE: APPLICATION PI	PRIOK FLIING DATE: 1998-0 PRIOR APPLICATION NUMBER: PRIOR PILING DATE: 1998-0	APPLICATION TELLING DATE: APPLICATION FILLING DATE: APPLICATION FILLING DATE: APPLICATION APPLICATION FILLING DATE: APPLIC	FILING DATE: 19 PELICATION NUM FILING DATE: 19 APPLICATION NUM FILING DATE: 19
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PRIOR APPLICATION NUMBER: 60/083901
PRIOR APPLICATION NUMBER: 60/083907
PRIOR PILING DATE: 1938-06-18
PRIOR FILING DATE: 1938-06-19
PRIOR FILING DATE: 1938-06-19
PRIOR FLING DATE: 1938-06-19
PRIOR FLING DATE: 1938-06-19
PRIOR FLING DATE: 1938-06-19
PRIOR FLING DATE: 1938-06-19
PRIOR PLING DATE: 1938-06-19
PRIOR APPLICATION NUMBER: 60/090254
PRIOR APPLICATION NUMBER: 60/090254
PRIOR PLING DATE: 1938-06-20
PRIOR APPLICATION NUMBER: 60/090349
PRIOR PLING DATE: 1938-06-21
PRIOR APPLICATION NUMBER: 60/090349
PRIOR PLING DATE: 1938-06-24
PRIOR PLING DATE: 1938-06-25
PRIOR PLING DATE: 1938-07-02

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PRIOR FILING DATE: 1998-06-09
PRIOR PLING DATE: 1998-06-09
PRIOR PLING DATE: 1998-06-10
PRIOR PLING DATE: 1998-06-10
PRIOR PLING DATE: 1998-06-10
PRIOR FILING DATE: 1998-06-10
PRIOR FILING DATE: 1998-06-10
PRIOR PLING DATE: 1998-06-11
PRIOR PLING DATE: 1998-06-12
PRIOR PLING DATE: 1998-06-16
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PRIOR FILING DATE: 1998-06-04
PRIOR PILING DATE: 1998-06-05
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APPLICATION UNDHER: 60/089538
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089598
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APPLICATION NUMBER: 60/089599
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APPLICATION NUMBER: 60/089600
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APPLICATION NUMBER: 60/089653
FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089947
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CURRENT APPLICATION NUMBER: US/09/989,279
CURRENT FILING DATE: 2001-11-19
RIOR APPLICATION NUMBER: 60/06250
PRIOR PILING DATE: 1997-06-16
PRIOR PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06531
PRIOR PILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/06531
PRIOR PILING DATE: 1997-11-24
PRIOR PILING DATE: 1997-11-24
PRIOR PILING DATE: 1998-03-25
PRIOR PILING DATE: 1998-03-25
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PRIOR PILING DATE: 1998-04-28
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US-09-989-279-197
i Sequence 197, Application US/09989279
j Patent No. US20020072496A1
j CENERAL INFORMATION:
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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APPLICATION NUMBER: 60/08/106
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Grimaldi, J.Christopher
Gurney, Austin L.
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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TITLE OF INVENTION: Zenin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERBNCE: P2730PLC65
CURRENT APPLICATION NUMBER: US/09/989,727
CURRENT APPLICATION NUMBER: US/09/989
PRIOR PILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/06250
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-11-12
PRIOR PLING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-24
PRIOR PILING DATE: 1997-11-24
PRIOR PILING DATE: 1998-03-20
PRIOR PILING DATE: 1998-05-28
                                                                                                                                                Sequence 197, Application US/09989727
Patent No. US20020072497A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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APPLICATION NUMBER: 60/087609
FILING DATE: 1998-06-02
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FILING DATE: 1998-06-02
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Gurney,Austin L.
Kljavin,Ivar J.
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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R APPLICATION NUMBER: 60/089948
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R FILING DATE: 1998-06-19
R APPLICATION NUMBER: 60/08952
R APPLICATION NUMBER: 60/090246
R FILING DATE: 1998-06-22
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R APPLICATION NUMBER: 60/090254
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APPLICATION NUMBER: 60/090542
FILING DATE: 1998-06-7
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APPLICATION NUMBER: 60/090694
FILING DATE: 1998-06-25
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FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090696
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APPLICATION NUMBER: 60/090862
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APPLICATION NUMBER: 60/091360
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APPLICATION UNMBER: 60/091519
FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091626
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FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091978
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APPLICATION NUMBER: 60/090349
FILING DATE: 1998-06-23
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FILING DATE: 1998-06-23
APPLICATION NUMBER: 60/090429
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APPLICATION NUMBER: 60/090431
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APPLICATION NUMBER: 60/090435
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APPLICATION NUMBER: 60/090444
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APPLICATION NUMBER: 60/090445
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APPLICATION NUMBER: 60/090535
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APPLICATION NUMBER: 60/090557
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APPLICATION NUMBER: 60/090690
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APPLICATION NUMBER: 60/091478
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APPLICATION NUMBER: 60/091544
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PRIOR APPLICATION NUMBER: 60/088025 PRIOR FILING DATE: 1998-06-04 PRIOR APPLICATION NUMBER: 60/088026

0; Gaps

Query Match
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels

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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088810
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APPLICATION UNMBER: 60/089538
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089598
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APPLICATION NUMBER: 60/089599
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089600
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FILING DATE: 1998-06-22
                            FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088029
                                                                                                                                                           APPLICATION NUMBER: 60/088033
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088326
FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/088212
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APPLICATION NUMBER: 60/088217
FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088655
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APPLICATION NUMBER: 60/088826
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APPLICATION NUMBER: 60/088858
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PLICATION NUMBER: 60/089514
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APPLICATION NUMBER: 60/089532
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FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/08824
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FILING DATE: 1998-06-11
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                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/088167
                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/088202
                                                                                                                                                                                                                                                                                                1998-06-05
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PRIOR PRIOR
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| PRICE APPLICATION DATE: 1998-06-25
| PRICE APPLICATION NUMBER: 60/090254
| PRICE APPLICATION NUMBER: 60/090154
| PRICE APPLICATION NUMBER: 60/090155
| PRICE APPLICATION NUMBER: 60/090131
| PRICE APPLICATION NUMBER: 60/090135
| PRICE APPLICATION NUMBER: 60/090135
| PRICE APPLICATION NUMBER: 60/090145
| PRICE APPLICATION NUMBER: 60/090146
| PRICE APPLICATION NUMBER: 60/0901478
| PRICE APPLICATION NUMBER: 60/091146
| PRICE PLINE DATE: 1998-6-20-00
| PRICE PLINE DATE: 1998-0-00
| PRICE PLINE DATE: 1998-0-000
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Matches 5; Conservative 0; Mis Qy 1 SCYNA 5 Db 160 SCYNA 164

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R FILING DATE: 1998-06-05

R APPLICATION NUMBER: 60/089212

R APPLICATION NUMBER: 60/089217

R APPLICATION NUMBER: 60/088217

R FILING DATE: 1998-06-05

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R FILING DATE: 1998-06-09

R FILING DATE: 1998-06-09
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R APPLICATION NUMBER: 60/089600
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089653
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089801
                                             APPLICATION NUMBER: 60/088326
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088167
APPLICATION NUMBER: 60/088202
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APPLICATION NUMBER: 60/088810
FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/089532
FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089908
FILING DATE: 1998-06-18
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APPLICATION NUMBER: 60/090349
FILING DATE: 1998-06-23
APPLICATION NUMBER: 60/090355
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APPLICATION WINBER: 60/088738
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088742
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FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/088826
FILING DATE: 1998-06-10
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FILING DATE: 1998-06-11
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FILING DATE: 1998-06-11
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FILING DATE: 1998-06-17
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FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/089948
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APPLICATION NUMBER: 60/089952
FILING DATE: 1998-06-19
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FILING DATE: 1998-06-22
     APPLICATION NUMBER: 60/088033
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APPLICATION NUMBER: 60/089440
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APPLICATION NUMBER: 60/089512
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APPLICATION NUMBER: 60/089514
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                                 .998-06-04
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C70
CURRENT APPLICATION NUMBER: US/09/989,731
CURRENT APPLICATION NUMBER: 06/049787
PRIOR PILING DATE: 1997-06-1
PRIOR APPLICATION NUMBER: 60/06250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR PAPPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
                      Sequence 197, Application US/09989731
Patent No. US20020103125A1
GENERAL INFORMATION:
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APPLICATION UNDBER: 60/066770
FILING DATE: 1997-11-24
APPLICATION NUMBER: 60/075945
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APPLICATION NUMBER: 60/083322
FILING DATE: 1998-04-28
APPLICATION NUMBER: 60/084600
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APPLICATION NUMBER: 60/087609
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APPLICATION UNDBER: 60/087759
FILING DATE: 1988-06-02
APPLICATION NUMBER: 60/087827
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APPLICATION UNDBER: 60/088021
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088025
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APPLICATION NUMBER: 60/088026
FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/088030
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APPLICATION NUMBER: 60/087607
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                                                                                                                                                                                                                                                                                                                                                                     Grimaldi, J. Christopher
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                                                                               Eaton, Dan L.
Ferrara, Napoleone
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                                                                                                                                                                                                                                                                                             Gerritsen, Mary E.
Goddard, Audrey
                                                                                                                                                                                                                                                Fong, Sherman
Gerber, Hanspeter
                                                                                              APPLICANT: Ashkenazi,Avi J.
APPLICANT: Baker,Kevin P.
APPLICANT: Botstein,David
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Napier, Mary A.
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pan, James
US-09-989-731-197
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Zhang, Zening and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic CURRENT APPLICATION NUMBER: 105/04589,732

CURRENT APPLICATION NUMBER: 60/04280

PRIOR FILING DATE: 1997-06-15

PRIOR PLING DATE: 1997-10-17

PRIOR PLING DATE: 1997-10-17

PRIOR PLING DATE: 1997-06-25

PRIOR PLING DATE: 1998-06-25

PRIOR PLING DATE: 1998-06-26

PRIOR APPLICATION NUMBER: 60/0810

PRIOR PRIOR PRIING DATE: 1998-06-02

PRIOR PLING DATE: 1998-06-02

PRIOR PLING DATE: 1998-06-03

PRIOR PLING DATE: 1998-06-03

PRIOR PLING DATE: 1998-06-03

PRIOR PLING DATE: 1998-06-03

PRIOR PLING DATE: 1998-06-04

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FILING DATE: 1998-06-04
                                                                                                                                               Godowski, Paul J.
Grimaldi, J.Christopher
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                    Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                                                                                                                                       Roy, Margaret Ann
Stewart, Timothy A
Tumas, Daniel
                                        errara, Napoleone
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                                                                                 Gerber, Hanspeter
Gerritsen, Mary E
                                                                                                                                                                                                                     Kljavin, Ivar J.
                                                                                                                                                                                                                                     Napier, Mary A.
                                                                                                                               Goddard, Audrey
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3R FILING DATE: 1998-07-01
3R FILING DATE: 1998-07-02
3R FILING DATE: 1998-07-01
40R FILING DATE: 1998-07-01
40R FILING DATE: 1998-07-01
40R APPLICATION NUMBER: 60/091519
40R APPLICATION NUMBER: 60/091519
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                                                                             R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090435
R APPLICATION NUMBER: 60/090444
R FILING DATE: 1998-06-24
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R APPLICATION NUMBER: 60/090542

R APPLICATION NUMBER: 60/090557

R APPLICATION NUMBER: 60/090557

R APPLICATION NUMBER: 60/090676

R APPLICATION NUMBER: 60/090676

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R APPLICATION NUMBER: 60/090696
R FILING DATE: 1998-06-25
R APPLICATION NUMBER: 60/090862
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FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091978
APPLICATION NUMBER: 60/091982
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APPLICATION NUMBER: 60/091626
FILING DATE: 1998-07-02
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APPLICATION NUMBER: 60/092182
FILING DATE: 1998-07-09
                  ION NUMBER: 60/090429
                                        FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090431
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APPLICATION NUMBER: 60/090535
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APPLICATION NUMBER: 60/090540
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FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090695
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1998-06-23
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Best Local Similarity 100.
Matches 5; Conservative
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APPLICATION NUMBER: 60/088167. FILING DATE: 1998-06-05

FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088202

PRIOR PRIOR PRIOR /

Sequence 197, Application US/09989732
Patent No. US20020123463A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David

LICATION NUMBER: 60/088326

1998-06-04 TUMBER: 60/ 1998-06-04

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R FILING DATE: 1998-06-05
R APPLICATION NUMBER: 60/088655
R FILING DATE: 1998-06-09
R APPLICATION NUMBER: 60/088734
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088738
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088742
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088742
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R APPLICATION NUMBER: 60/089907
R FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089908
R FILING DATE: 1998-06-18
R APPLICATION NUMBER: 60/089947
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R APPLICATION UNMBER: 60/088826
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088858
R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/08861
R FILING DATE: 1998-06-11
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R APPLICATION NUMBER: 60/090254
R FILING DATE: 1998-06-22
R APPLICATION NUMBER: 60/090349
R FILING DATE: 1998-06-23
R APPLICATION NUMBER: 60/090355
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APPLICATION NUMBER: 60/089105
FILING DATE: 1998-06-12
APPLICATION NUMBER: 60/089440
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FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089801
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APPLICATION NUMBER: 60/089948
FILING DATE: 1998-06-19
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FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/090246
FILING DATE: 1998-06-22
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APPLICATION NUMBER: 60/090429
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090431
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APPLICATION NUMBER: 60/090435
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APPLICATION NUMBER: 60/089514
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APPLICATION NUMBER: 60/089598
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FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089532
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APPLICATION NUMBER: 60/088824
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APPLICATION NUMBER:
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| PRIOR PAPLICATION WURBER: 60/09657
| PRIOR PAPLICATION WURBER: 60/09656
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PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION UNMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR PLING DATE: 1998-06-17
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PRIOR PLING DATE: 1998-06-17
PRIOR PLING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR PLING DATE: 1998-06-18
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R FILING DATE: 1998-06-10
R PILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/088861
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R APPLICATION NUMBER: 60/08861
R FILING DATE: 1998-06-11
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APPLICATION NUMBER: 60/090349
FILING DATE: 1998-06-23
APPLICATION NUMBER: 60/090355
FILING DATE: 1998-06-23
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APPLICATION NUMBER: 60/090472
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090535
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FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089514
FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089532
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APPLICATION NUMBER: 60/089538
FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089947
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APPLICATION NUMBER: 60/089952
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APPLICATION NUMBER: 60/090246
FILING DATE: 1998-06-22
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FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090254
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APPLICATION NUMBER: 60/090431
FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
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                   LICATION NUMBER: 60/088738
ING DATE: 1998-06-10
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                                                                                   FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/08810
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FILING DATE: 1998-06-12
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FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/098824
FILING DATE: 1998-06-10
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FILING DATE: 1998-06-09
Grimaldi, J. Christopher
Gurney, Austin L.
                                                                                                                                     Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                                                                                             Paoni, Nicholas F.
                                                                     Napier, Mary A.
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APPLICANT:
APPLICANT:
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APPLICANT: Zhang, Zemin
TITLE DF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C8
                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/990,442
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
PRIOR PELICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065181
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: 60/06570
PRIOR APPLICATION NUMBER: 60/06570
PRIOR PILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/075945
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NR APPLICATION NUMBER: 60/087609

NR FILING DATE: 1998-06-02

NR APPLICATION NUMBER: 60/08759

NR FILING DATE: 1998-06-02

NR APPLICATION NUMBER: 60/087827

NR APPLICATION NUMBER: 60/087827

NR APPLICATION NUMBER: 60/087827

NR APPLICATION NUMBER: 60/087827

NR APPLICATION DATE: 1998-06-03
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R APPLICATION NUMBER: 60/086029

R FILING DATE: 1998-06-04

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R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/086033
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APPLICATION NUMBER: 60/084600
FILING DATE: 1998-05-07
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088028
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FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088212
FILING DATE: 1998-06-05
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APPLICATION NUMBER: 60/083322
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FILING DATE: 1998-06-05
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FILING DATE: 1998-06-05
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FILING DATE: 1998-06-09
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                                                                                                                  Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                                         Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ILING DATE: 1998-05-28
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR APPLICATION NUMBER: 60/090542
PRIOR PILING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-07
PRIOR PELING DATE: 1998-
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Patent No. US20020132252A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soddard, Audrey
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APPLICANT:
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PRIOR APPLICATION NUMBER: 66/108824
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PRIOR PILING DATE: 1988-06-12
PRIOR PILING DATE: 1988-06-16
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PRIOR PELICATION NUMBER: 60/089105
PRIOR PILING DATE: 1988-06-16
PRIOR PELICATION NUMBER: 60/089512
PRIOR PELICATION NUMBER: 60/089512
PRIOR PELICATION NUMBER: 60/089512
PRIOR PELICATION NUMBER: 60/089512
PRIOR PELICATION NUMBER: 60/089513
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## PRIOR FILING DATE: 1998-06-25
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| PRIOR PELICATION NUMBER: 60/090690
| PRIOR PELICATION NUMBER: 60/090690
| PRIOR PELICATION NUMBER: 60/090691
| PRIOR PELICATION NUMBER: 60/090695
| PRIOR FILING DATE: 1998-06-25
| PRIOR FILING DATE: 1998-06-25
| PRIOR PELICATION NUMBER: 60/090696
| PRIOR PELICATION NUMBER: 60/090696
| PRIOR PELICATION NUMBER: 60/090663
| PRIOR PELICATION NUMBER: 60/091606363
| PRIOR PELICATION

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US-09-991-163-197

Sequence 197, Application US/0991163

Patent No. US2002013253A1

GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Baker, Kevin P.
APPLICANT: Baker, Kevin P.
APPLICANT: Baco, Dan L.
APPLICANT: Ferrara Napoleone
APPLICANT: Ferrara Napoleone
APPLICANT: Geng, Sherman
APPLICANT: Geng, Sherman
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gengard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: May Grimaldi, J. Christopher
APPLICANT: Rijavin, Ivar J.
APPLICANT: Napies
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.

Zhang, Zemin

APPLICANT

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PRIOR FILING DATE: 1998-06-11
PRIOR PELING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089105
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PRIOR PLING DATE: 1998-06-19
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PRIOR PLING DATE: 1998-06-20
PRIOR APPLICATION NUMBER: 60/09035
PRIOR APPLICATION NUMBER: 60/09045
PRIOR PLING DATE: 1998-06-20
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R FILING DATE: 1998-06-24
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
                                                 CURRENT FILING DATE: 2001-11-14
PRICE REPERENCE: P2730PG.7
CURRENT FILING DATE: 2001-11-14
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PRICE FILING DATE: 1997-06-16
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PRICE FILING DATE: 1997-11-13
PRICE FILING DATE: 1997-11-13
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PRICE PRILOGATION NUMBER: 06/06910
PRICE PRILOGATION NUMBER: 06/06910
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FILING DATE: 1998-06-11
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PRIOR FILING DATE: 1997-11-12
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PRIOR PILING DATE: 1998-06-02
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PRIOR FILING DATE: 1998-06-04
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FILING DATE: 1998-06-11
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ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITLE OF INVENTION: Acids Encoding the Same
ITLE REFERENCE: P2730PIC25
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R FILING DATE: 1998-07-01
R APPLICATION NUMBER: 60/09154
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R APPLICATION NUMBER: 60/091638
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R FILING DATE: 1998-07-07
               R APPLICATION NUMBER: 60/090695
R FILING DATE: 1998-06-25
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R FILING DATE: 1998-06-26
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R APPLICATION NUMBER: 60/091360
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Patent No. US20020137075A1
GENERAL INFORMATION:
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PRIOR FILING DATE: 1997-06-16
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FILING DATE: 1998-07-09
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Gurney, Austin L.
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Stewart, Timothy
Tumas, Daniel
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Gerritsen, Mary E.
Goddard, Audrey
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Best Local Similarity 100.
Matches 5; Conservative
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Botstein, David
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PRIOR PLING DATE: 1999
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PLC22
CURRENT APPLICATION NUMBER: US/09/990,456
CURRENT PILING DATE: 2001-11-14
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100.0%; Score 30; DB 11; Length 346;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels (
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PRIOR FILING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091549
PRIOR PILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091519
PRIOR PELING DATE: 1998-07-02
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PRIOR APPLICATION NUMBER: 60/09163
PRIOR PELING DATE: 1998-07-07
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PRIOR FILING DATE: 1997-06-16
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PRIOR PELING DATE: 1997-11-12
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PRIOR PELING DATE: 1997-11-13
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Patent No. USS0020137890A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Stewart, Timothy
1998-06-26
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Gerber, Hanspeter
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Eaton, Dan L.
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PRIOR FILING DATE: 1998-06-10
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PRIOR FILING DATE: 1998-06-11
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FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087827
FILING DATE: 1998-06-03
APPLICATION NUMBER: 60/088021
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APPLICATION NUMBER: 60/088738
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PLICATION NUMBER: 60/089599
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APPLICATION NUMBER: 60/087609
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088033
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APPLICATION NUMBER: 60/088212
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088824
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088858
FILING DATE: 1998-06-11
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PPLICATION NUMBER: 60/089598
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PRIOR APPLICATION NUMBER: 60/089600
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FILING DATE: 1998-06-04
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FILING DATE: 1998-06-04
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FILING DATE: 1998-06-04
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FILING DATE: 1998-06-05
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FILING DATE: 1998-06-10
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FILING DATE: 1998-06-05
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APPLICATION NUMBER: 60/088655
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APPLICATION NUMBER: 60/088734
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C55
CURRENT APPLICATION NUMBER: US/09/989,721
PRIOR APPLICATION NUMBER: 60/049787
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PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FLING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
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R APPLICATION NUMBER: 60/062250
R FILING DATE: 1997-10-17
R FILING DATE: 1997-10-17
RR FILING DATE: 1997-11-12
RR APPLICATION NUMBER: 60/065186
RR APPLICATION NUMBER: 60/065311
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Patent No. US20020142961A1
GENERAL INFORMATION:
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APPLICATION NUMBER: 60/066770
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Grimaldi, J.Christopher
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Williams, P. Mickey
Wood, William I.
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APPLICATION NUMBER: 60/0
FILING DATE: 1998-04-28
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Stewart, Timothy
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Best Local Similarity 100.
Matches 5; Conservative
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PLICATION NUMBER: 60/090676
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APPLICATION NUMBER: 60/091360
ATE: 1998-06-17
ION NUMBER: 60/089653
ATE: 1998-06-17
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APPLICATION NUMBER: 60/089908
FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089947
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FILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/090246
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APPLICATION NUMBER: 60/090252
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APPLICATION NUMBER: 60/090349
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LING DATE: 1998-06-24
PLICATION NUMBER: 60/090431
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APPLICATION NUMBER: 60/090445
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APPLICATION NUMBER: 60/090678
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FILING DATE: 1998-06-25
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APPLICATION NUMBER: 60/090862
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APPLICATION NUMBER: 60/090863
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APPLICATION NUMBER: 60/089801
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APPLICATION NUMBER: 60/089907
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APPLICATION NUMBER: 60/090254
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APPLICATION NUMBER: 60/090355
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PPLICANT: Zhang, Zemin
ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITLE OF INVENTION: Acids Encoding the Same
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Pred. No. 2e+02;
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CURRENT APPLICATION NUMBER: US/09/992,598
CURRENT FILING DATE: 2001-11-14
CURRENT FILING DATE: 2001-11-14
PRIOR PELICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR PRIOR DATE: 1997-11-13
PRIOR PLING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/065710
PRIOR APPLICATION NUMBER: 60/065710
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PRIOR APPLICATION NUMBER: 60/065710
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PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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FILING DATE: 1998-04-28
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APPLICATION NUMBER: 60/087106
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APPLICATION NUMBER: 60/087607
FILING DATE: 1998-06-02
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PRIOR APPLICATION NUMBER: 60/087609
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Williams, P. Mickey
Wood, William I.
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Ferrara, Napoleone
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Stewart, Timothy
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Botstein, David
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Tumas, Daniel
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R APPLICATION NUMBER: 60,088029
R FILING DATE: 1998-06-04
R FILING DATE: 1998-06-04
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R APPLICATION NUMBER: 60,088126 R APPLICATION NUMBER: 60/088861
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R APPLICATION NUMBER: 60/088876
R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/089105
R FILING DATE: 1998-06-12
R APPLICATION NUMBER: 60/089440 APPLICATION NUMBER: 60/088742 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088810 APPLICATION NUMBER: 60/089532 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089538 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/088025 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088026 APPLICATION NUMBER: 60/088217 FILING DATE: 1980-06-05 APPLICATION NUMBER: 60/088655 FILING DATE: 1998-06-09 FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/08824
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/08826
FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/087759 FILING DATE: 1998-06-02 APPLICATION NUMBER: 60/087827 FILING DATE: 1998-06-03 APPLICATION NUMBER: 60/088021 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088028 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088212 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088734 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088738 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088858 FILING DATE: 1998-06-11 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/089512 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/089514 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/089598 FILING DATE: 1998-06-17 FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089600
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089653 APPLICATION NUMBER: 60/088202 APPLICATION NUMBER: 60/089599 60/089907 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/0 FILING DATE: 1998-06-18 FILING DATE: 1998-06-04 FILING DATE: 1998-06-05 FILING DATE: 1998-06-05 PRIOR 

PRIOR APPLICATION NUMBER: 60/08996
PRIOR PELLING DATE: 1998-06-19
PRIOR PILLING DATE: 1998-06-22
PRIOR PILLING DATE: 1998-06-23
PRIOR PILLING DATE: 1998-06-24
PRIOR PILLING DATE: 1998-06-25
PRIOR PILLING DATE: 1998-06-26
PRIOR PILLING DATE: 1998-07-01
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PRIOR PILLING DATE: 1998-07-01
PRIOR PILLING DATE: 1998-07-02
PRIOR PILLING DATE: 1998-07-07

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PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR FILING DATE: 1998-06-16
PRIOR PLILING DATE: 1998-06-16
PRIOR PLILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-06-17
PRIOR PLING DATE: 1998-06-17
PRIOR PLING DATE: 1998-06-17
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R APPLICATION NUMBER: 60/08655
R FILING DATE: 1998-06-09
R APPLICATION NUMBER: 60/088734
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088738
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R APPLICATION NUMBER: 60/088658
R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/08861
R APPLICATION NUMBER: 60/08861
R APPLICATION NUMBER: 60/088976
R APPLICATION NUMBER: 60/089105
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R FILING DATE: 1998-06-11
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PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
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PRIOR FILING DATE: 1998-06-18
PRIOR PELICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
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LICATION NUMBER: 60/089948
                                                  LICATION NUMBER: 60/088026
ING DATE: 1998-06-04
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FILING DATE: 1998-06-10
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088826
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APPLICATION NUMBER: 60/089947
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PRIOR APPLICATION NUMBER: 60/089952
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                                                      Gaps
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      100.0%; Score 30; DB 11; Length 346; 100.0%; Pred. No. 2e+02;
                                                  0; Indels
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CURRENT APPLICATION NUMBER: US/09/989,293A
CURRENT FILING DATE: 2001-11-20
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US-09-989-293A-197
US-09-989-293A-197
Sequence 197, Application US/09989293A
; Patent No. US20020177164A1
; GENERAL INFORMATION:
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TRILING DATE: 1997-06-16

TRILING DATE: 1997-01-17

TRILING DATE: 1997-10-17

TRILING DATE: 1997-11-12

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APPLICATION NUMBER: 60/075945
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APPLICATION NUMBER: 60/078910
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APPLICATION NUMBER: 60/083322
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APPLICATION UNMBER: 60/084600
FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/087106
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APPLICATION NUMBER: 60/088021
FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/087607
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Williams, P. Mickey
Wood, William I.
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Ferrara, Napoleone
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Goddard, Audrey
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Query Match
Best Local Similarity 100.
Matches 5; Conservative
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Botstein, David
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/989,735
CURRENT APPLICATION NUMBER: US/09/989,735
CURRENT FILING DATE: 1200.11.19
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-11.12
PRIOR FILING DATE: 1997-11.13
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PRIOR PLING DATE: 1997-11.13
PRIOR APPLICATION NUMBER: 60/065311
PRIOR PLING DATE: 1997-11.13
PRIOR APPLICATION NUMBER: 60/06770
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/08910
PRIOR PILING DATE: 1998-02-20
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PRIOR PILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/08910
PRIOR PILING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-03
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Stewart, Timothy
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Goddard, Audrey
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                                JS-09-989-735-197
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R APPLICATION NUMBER: 60/090694

R FILING DATE: 1998-06-25

R APPLICATION NUMBER: 60/090695

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R APPLICATION NUMBER: 60/090696

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                                                       R FILING DATE: 1998-06-22
R APPLICATION NUMBER: 60/090254
R FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090349
R FILING DATE: 1998-06-23
R APPLICATION NUMBER: 60/090355
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R APPLICATION NUMBER: 60/090445
R FILING DATE: 1998-06-24
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R APPLICATION NUMBER: 60/090535
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APPLICATION NUMBER: 60/090429
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090431
FILING DATE: 1998-06-24
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APPLICATION UNMBER: 60/090435
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090444
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APPLICATION NUMBER: 60/090540
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090542
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APPLICATION NUMBER: 60/090678
FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090690
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APPLICATION NUMBER: 60/091360
FILING DATE: 1998-07-01
APPLICATION NUMBER: 60/091478
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APPLICATION UNMBER: 60/091544
FILING DATE: 1998-07-01
APPLICATION NUMBER: 60/091519
FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090252
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090676
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FILING DATE: 1998-07-09
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Best Local Similarity 100.
Matches 5; Conservative
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REING APPLICATION NUMBER: 60/08030
REING APPLICATION NUMBER: 60/08033
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REING RELING DATE: 1938-66-04
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REING RELING DATE: 1938-66-10
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RESULT 17
US-09-990-444-197
; Sequence 197, Application US/09990444
; Publication No. US20020193300A1
; GENERAL INFORMATION:

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PRIOR FILING DATE: 1998-00-1,
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
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; PRIOR FILING DATE: 1998-06-18
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R FILING DATE: 1998-06-09
R APPLICATION NUMBER: 60/088734
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088738
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PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
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PRIOR APPLICATION NUMBER: 60/088742
annum FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/088826
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PRIOR APPLICATION NUMBER: 60/088861
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APPLICATION NUMBER: 60/089598
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APPLICATION NUMBER: 60/089947
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FILING DATE: 1998-06-19
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FILING DATE: 1998-06-22
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FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/090431
                                                       FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088212
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PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
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FILING DATE: 1998-06-12
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RIOR APPLICATION NUMBER: 60/089532
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IOR APPLICATION NUMBER: 60/089538
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FILING DATE: 1998-06-17
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998-06-05
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CURRENT FILING DATE: 2001-11-14
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APPLICATION NUMBER: 60/062250
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IOR FILING DATE: 1997-06-16
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APPLICATION NUMBER: 60/065186
FILING DATE: 1997-11-12
APPLICATION NUMBER: 60/065311
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APPLICATION NUMBER: 60/075945
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APPLICATION NUMBER: 60/078910
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APPLICATION NUMBER: 60/084600
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FILING DATE: 1998-05-28
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APPLICATION NUMBER: 60/087759
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APPLICATION NUMBER: 60/088025
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APPLICATION NUMBER: 60/066770
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APPLICATION NUMBER: 60/083322
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APPLICATION NUMBER: 60/087827
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APPLICATION NUMBER: 60/088021
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                                                                                                                                                                                                                                                                                                              Grimaldi, J. Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Roy, Margaret Ann
Stewart, Timothy A
Tumas, Daniel
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                                                                                                                   Perrara, Napoleone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Watanabe, Colin K
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                                                                                                                                                                                                                  Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Paoni, Nicholas F
                                                                                                                                                                                                                                                                                                                                               Gurney, Austin L
                                                                                                                                                                                                                                                Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                              Napier, Mary A.
                                                                                                                                                                                                                                                                                                                                                                                Kljavin,Ivar J
                                                           Desnoyers, Luc
                                                                                                                                                                                                                                                                                 Godowski, Paul
                                                                                                                                                    ong, Sherman
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APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730PIC53

CURRENT APPLICATION NUMBER: US/09/991,181

CURRENT FILING DATE: 2001-11-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2001-11-16
PRIOR PEDLICATION NUMBER: 60/049787
PRIOR PELLING DATE: 1997-06-16
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PRIOR PELLING DATE: 1997-10-17
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PRIOR PELLING DATE: 1997-11-13
PRIOR PELLING DATE: 1997-11-24
PRIOR PELLING DATE: 1999-02-25
PRIOR APPLICATION NUMBER: 60/076910
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PRIOR PAPLICATION NUMBER: 60/088212
PRIOR PAPLICATION NUMBER: 60/088212
                                                                                                                                                                                                                                                                         Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                                                                          Paoni, Nicholas F.
                                                                                                                                             Kljavin, Ivar J
                                                                                                                                                                            Napier, Mary A.
                                                Godowski, Paul
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Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels (
R APPLICATION NUMBER: 60/090444

R APPLICATION NUMBER: 60/090444

R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090535

R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090540

R FILING DATE: 1998-06-24

R PELLING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090540
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R APPLICATION NUMBER: 60/090557
R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090676
R FILING DATE: 1998-06-25
R APPLICATION NUMBER: 60/090678
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R APPLICATION VUMBER: 60/090690

R APPLICATION NUMBER: 60/090694

R APPLICATION NUMBER: 60/090694

R APPLICATION NUMBER: 60/090695

R APPLICATION NUMBER: 60/090695

R FILING DATE: 1998-06-25

R FILING DATE: 1998-06-25

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R APPLICATION NUMBER: 60/090895
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R APPLICATION NUMBER: 60/091478
R FILING DATE: 1998-07-02
R APPLICATION NUMBER: 60/091544
R FILING DATE: 1998-07-01
R APPLICATION NUMBER: 60/091519
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. Sequence 197. Application US/09991181
. Publication No. US2020197615A1
. GENERAL INFORMATION:
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APPLICATION UNDRER: 60/090863
FILING DATE: 1998-06-26
APPLICATION NUMBER: 60/091360
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APPLICATION NUMBER: 60/091626
ALING DATE: 1998-07-02
APPLICATION NUMBER: 60/091633
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FILING DATE: 1998-07-09
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Eaton, Dan L.
Ferrara, Napoleone
Fong, Sherman
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088738
FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/089598
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APPLICATION NUMBER: 60/090435
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                                                             60/088742
                                                                                                      APPLICATION NUMBER: 60/088810
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FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/08861
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                                                           APPLICATION NUMBER: 60/0
FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/0
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APPLICATION NUMBER: 60/
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PRIOR PLING DATE: 1998-06-25
PRIOR PLING DATE: 1998-06-25
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PRIOR PLING DATE: 1998-06-25
PRIOR FILING DATE: 1998-06-25
PRIOR PLING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR APPLICATION NUMBER: 60/090695
PRIOR APPLICATION NUMBER: 60/090696
PRIOR PLING DATE: 1998-06-25
PRIOR PLING DATE: 1998-06-25
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PRIOR FILING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
PRIOR PILING DATE: 1998-06-36
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
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PRIOR PELING DATE: 1998-07-02
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US-00-989-730-197
Sequence 197, Application US/09989730
Publication No. US20020197674A1
                                                                               APPLICATION NUMBER: 60/090540
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090542
FILING DATE: 1998-06-24
                                                                                                                                                                                          APPLICATION NUMBER: 60/090557
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PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
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                                                            LING DATE: 1998-06-24
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998-06-2
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Best Local Similarity 100.
Matches 5, Conservative
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Eaton, Dan L.
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Kljavin, Ivar J

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| APPLICANT: Thumbs Danie | APPLICANT: Thumbs Danie | APPLICANT: Thumbs Danie | APPLICANT: Thumbs Danie | APPLICANT: Witched | APPLICANT: Danie | APPLICA
                                                                                                                  Stewart, Timothy A.
Tumas, Daniel
                                                                                         Roy, Margaret Ann
                                                    Paoni, Nicholas F.
Napier, Mary A.
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PRIOR FILING DATE: 1998-06-10
PRIOR FILING DATE: 1998-06-10
PRIOR PELLING DATE: 1998-06-10
PRIOR PELLING DATE: 1998-06-10
PRIOR PELLING DATE: 1998-06-10
PRIOR PELLING DATE: 1998-06-11
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PRIOR PELLING DATE: 1998-06-16
PRIOR PELLING DATE: 1998-06-16
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PRIOR PELLING DATE: 1998-06-18
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PRIOR PELLING DATE: 1998-06-22
PRIOR PELLING DATE: 1998-06-23
PRIOR PELLING DATE: 1998-06-23
PRIOR PELLING DATE: 1998-06-24
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PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
    Williams, P. Mickey
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RELING DATE: 1998-06-24

RAPPLICATION NUMBER: 60/090557

RAPLICATION NUMBER: 60/090676

RETLING DATE: 1998-06-25

RAPLICATION NUMBER: 60/090676

RETLING DATE: 1998-06-25

RAPLICATION NUMBER: 60/090690

RETLING DATE: 1998-06-25

RAPLICATION NUMBER: 60/090690

RETLING DATE: 1998-06-25

RAPLICATION NUMBER: 60/090695

RETLING DATE: 1998-06-25

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RETLING DATE: 1998-06-25

RETLING DATE: 1998-06-26

RETLING DATE: 1998-07-01

RAPPLICATION NUMBER: 60/091478

RETLING DATE: 1998-07-01

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R FILING DATE: 1998-07-02
R APPLICATION NUMBER: 60/091626
R FILING DATE: 1998-07-02
R APPLICATION NUMBER: 60/091633
R FILING DATE: 1998-07-02
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Publication No. US20020198148A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/091982
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APPLICATION NUMBER: 60/092182
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Stewart, Timothy,
Tumas, Daniel
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Gerber, Hanspeter
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Best Local Similarity 100.
Matches 5; Conservative
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Botstein, David
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US-09-990-436-197
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PRIOR APPLICATION NUMBER: 60/08861
PRIOR FILING DATE: 1998-66-11
PRIOR PILING DATE: 1998-66-12
PRIOR PILING DATE: 1998-66-12
PRIOR PILING DATE: 1998-66-16
PRIOR PILING DATE: 1998-66-16
PRIOR PAPLICATION NUMBER: 60/08910
PRIOR PAPLICATION NUMBER: 60/08912
PRIOR PAPLICATION NUMBER: 60/08926
PRIOR PAPLICATION NUMBER: 60/08936
PRIOR PAPLICATION NUMBER: 60/08938
PRIOR PAPLICATION NUMBER: 60/08939
PRIOR APPLICATION NUMBER: 60/08939
PRIOR PAPLICATION NUMBER: 60/09343
PRIOR PAPLICATION NUMBER:
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1011
CURRENT APPLICATION NUMBER: US/09/993,687
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PRIOR APPLICATION UNMER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION UNMER: 60/090695
PRIOR APPLICATION NUMBER: 60/090695
PRIOR APPLICATION NUMBER: 60/090695
PRIOR PILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090863
PRIOR PILING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR PILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR PILING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-07
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Publication No. US20020198149A1
GENERAL INFORMATION:
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Gurney, Austin L.
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Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
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Goddard, Audrey
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Best Local Similarity 100.
Matches 5; Conservative
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ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITLE OF INVENTION: Acids Encoding the Same
TLE REFERENCE: P2730PLC64
URRENT APPLICATION NUMBER: US/09/989,734
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Gurney,Austin L.
Kljavin,Ivar J.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Ferrara, Napoleone
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Gerritsen, Mary E.
Goddard, Audrey
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Paoni,Nicholas F.
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APPLICATION NUMBER: 60/090694
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APPLICANT: Anany, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PlC38
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Pred. No. 2e+02;
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CURRENT FILING DATE: 2001-11.15

PRIOR APPLICATION NUMBER: 60/049787

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PRIOR APPLICATION NUMBER: 60/066770

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PRIOR APPLICATION NUMBER: 60/075945
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PRIOR FLING DATE: 1998-07-01
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PRIOR FILING DATE: 1998-07-02
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PRIOR APPLICATION NUMBER: 60/091633
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A
Tumas, Daniel
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1998-07-02
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Gerber, Hanspeter
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Napier, Mary A.
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Eaton, Dan L.
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APPLICATION UNMBER: 60/088824
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APPLICATION NUMBER: 60/088876
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APPLICATION NUMBER: 60/089105
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APPLICATION NUMBER: 60/087609
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APPLICATION NUMBER: 60/088167
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APPLICATION NUMBER: 60/08861
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APPLICATION NUMBER: 60/087607
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FILING DATE: 1998-06-02
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PRIOR APPLICATION NUMBER: 00/0904/2
PRIOR PLING DATE: 1998-06-24
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PRIOR PILING DATE: 1998-06-27
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PRIOR APPLICATION NUMBER: 60/090690
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R PILING DATE: 1998-06-22
R APPLICATION NUMBER: 60/090252
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R FILING DATE: 1998-06-18
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APPLICATION NUMBER: 60/089801
FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089907
FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/090431 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090435 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090862 APPLICATION NUMBER: 60/089952 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/090429 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090444 ILING DATE: 1998-07-02 FILING DATE: 1998-07-01 1998-06-1 PRIOR PRIOR PRIOR PRIOR PRIOR

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PRIOR APPLICATION NUMBER: 60/088876
PRIOR PLILIG DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088824
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APPLICATION WINBER: 60/088876
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APPLICATION NUMBER: 60/089105
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APPLICATION NUMBER: 60/089653
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089801
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APPLICATION NUMBER: 60/087759
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APPLICATION NUMBER: 60/087827
FILING DATE: 1998-06-03
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APPLICATION NUMBER: 60/088028
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APPLICATION NUMBER: 60/088030
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APPLICATION NUMBER: 60/088033
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FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/088202
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APPLICATION NUMBER: 60/088738
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APPLICATION NUMBER: 60/088742
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APPLICATION NUMBER: 60/088858
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FILING DATE: 1998-06-16
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APPLICATION NUMBER: 60/089532
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APPLICATION NUMBER: 60/088026
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APPLICATION NUMBER: 60/088167
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APPLICATION NUMBER: 60/08861
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FILING DATE: 1998-06-04
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CURRENT APPLICATION NUMBER: US/09/993,667

CURRENT FILING DATE: 2001-11-14

PRIOR PELICY DATE: 1997-06-16

PRIOR FILING DATE: 1997-06-16

PRIOR FILING DATE: 1997-10-17

PRIOR PELICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR FILING DATE: 1997-11-12

PRIOR FILING DATE: 1997-11-24

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PRIOR FILING DATE: 1998-03-20

PRIOR FILING DATE: 1998-04-28

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100.0%; Score 30; DB 12; Length 346;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0
                   R APPLICATION NUMBER: 60/091633
R FILING DATE: 1998-07-02
R APPLICATION NUMBER: 60/091978
R FILING DATE: 1998-07-07
R APPLICATION NUMBER: 60/091982
R FILING DATE: 1998-07-07
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APPLICATION NUMBER: 60/08/106
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Gurney, Austin L.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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  FILING DATE: 1998-07-02
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Goddard, Audrey
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Gerber, Hanspeter
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APPLICATION NUMBER: 60/089907
FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/08908
APPLICATION NUMBER: 60/089947
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APPLICATION NUMBER: 60/089948
FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/089952
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APPLICATION NUMBER: 60/090355
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APPLICATION NUMBER: 60/090444
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APPLICATION NUMBER: 60/090445
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APPLICATION UNMBER: 60/090678
FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090690
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FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091626
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APPLICATION NUMBER: 60/090254
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APPLICATION NUMBER: 60/090429
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APPLICATION NUMBER: 60/090431
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APPLICATION NUMBER: 60/090540
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APPLICATION NUMBER: 60/090694
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APPLICATION NUMBER: 60/091478
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: P2730101C44
CURRENT APPLICATION NUMBER: US/09/997,428
CURRENT FILING DATE: 2001-11-15
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                                                                   Score 30; DB 12; Length 346;
Pred. No. 2e+02;
; Mismatches 0; Indels (
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PRIOR APPLICATION NUMBER: 60/049787
PRIOR PILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-11-12
PRIOR PILING DATE: 1997-11-12
PRIOR PILING DATE: 1997-11-12
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Publication No. US20030027162A1
DEBRAL INCORMATION:
APPLICANT: Ashkenazi,Avi J.
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FILING DATE: 1998-05-28
APPLICATION NUMBER: 60/087607
FILING DATE: 1998-06-02
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APPLICATION WINBER: 60/087759
FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/087827
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PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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FILING DATE: 1998-03-20
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Gurney, Austin L.
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Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                                                   Query Match
Best Local Similarity 100.0%;
Matches 5; Conservative 0;
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Paoni, Nicholas F.
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US-09-997-428-197
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R APPLICATION NUMBER: 60/089532

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089538

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089598

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089599

R FILING DATE: 1998-06-17

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R APPLICATION NUMBER: 60/089600

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089613

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R APPLICATION NUMBER: 60/089613

R FILING DATE: 1998-06-18

R FILING DATE: 1998-06-18
R APPLICATION NUMBER: 60/088021
RR APPLICATION NUMBER: 60/088021
RR APPLICATION NUMBER: 60/088025
RR FILING DATE: 1998-06-04
RR APPLICATION NUMBER: 60/088025
RR FILING DATE: 1998-06-04
RR APPLICATION NUMBER: 60/088028
RR FILING DATE: 1998-06-04
RR PILING DATE: 1998-06-04
RR PELICATION NUMBER: 60/088033
RR PILING DATE: 1998-06-04
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FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088212
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APPLICATION NUMBER: 60/088655
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APPLICATION NUMBER: 60/088742
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088810
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APPLICATION NUMBER: 60/088824
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088826
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FILING DATE: 1998-06-12
APPLICATION NUMBER: 60/089440
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APPLICATION NUMBER: 60/089908
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APPLICATION NUMBER: 60/089947
FILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/088167
FILING DATE: 1998-06-05
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APPLICATION NUMBER: 60/088734
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APPLICATION NUMBER: 60/088738
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FILING DATE: 1998-06-11
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APPLICATION UNMBER: 60/089512
FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089514
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PRIOR FILING DATE: 1998-06-19

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PRIOR PLILACATION UNMERS: 60/0925

PRIOR PAPLICATION UNMERS: 60/0925

PRIOR PLILACATION UNMERS: 60/0943

PRIOR PLILACATION UNMERS: 60/0943

PRIOR PLILACATION UNMERS: 60/0943

PRIOR PLILACATION UNMERS: 60/0944

PRIOR PLILACATION UNMERS: 60/09445

PRIOR PLILACATION UNMERS: 60/09445

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PRIOR PLILACATION UNMERS: 60/09659

PRIOR PLILACATION UNMERS: 60/09659

PRIOR PLILACATION UNMERS: 60/09659

PRIOR PLILACATION UNMERS: 60/09669

PRIOR PLILACATION UNMERS: 60/09167

PRIOR APPLICATION UNMERS: 60/09167

PRIOR PLILACATION UNMERS: 6

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Query Match 100.0%; Score 30; DB 12; Length 346; Best Local Similarity 100.0%; Pred. No. 2e+02; Matches 5; Conservative 0; Mismatches 0; Indels

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERBNCE: P2130PL042
CURRENT APPLICATION NUMBER: US/09/997,666
URRENT FILING DATE: 2001-11-15
                                                                                                                ; Sequence 197, Application US/09997666; Publication No. US20030027163A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NT FILING DATE: 2001-11-15
APPLICATION NUMBER: 60/049787
ELING DATE: 1997-06-16
APPLICATION NUMBER: 60/062250
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APPLICATION NUMBER: 60/065186
FILING DATE: 1997-11-12
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APPLICATION NUMBER: 60/065311
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FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/087106
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APPLICATION NUMBER: 60/087759
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APPLICATION NUMBER: 60/087827
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FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/088021
                                                                                                                                                                                                                                                                                                                                                   Grimaldi, J. Christopher
Gurney, Austin L.
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Stewart, Timothy A.
Tumas, Daniel
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Watanabe, Colin K.
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Ferrara, Napoleone
Fong, Sherman
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Paoni, Nicholas F.
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                                                                                                                                                                APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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APPLICATION NUMBER:
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                        160 SCYNA 164
SCYNA 5
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US-09-997-666-197
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FILING DATE: 1998-06-12
APPLICATION UNMBER: 60/089440
FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089512
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APPLICATION NUMBER: 60/089538
FILING DATE: 1998-06-17
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PRIOR APPLICATION NUMBER: 60/090246
PRIOR PLILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
                   LICATION NUMBER: 60/088029
ING DATE: 1998-06-04
                                      FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088030
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088033
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APPLICATION NUMBER: 60/088326
FILING DATE: 1998-06-04
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FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088202
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APPLICATION NUMBER: 60/088212
FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088217
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APPLICATION NUMBER: 60/088738
FILING DATE: 1998-06-10
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FILING DATE: 1998-06-11
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APPLICATION NUMBER: 60/089532
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FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089600
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APPLICATION NUMBER: 60/089907
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FILING DATE: 1998-06-18
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FILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/088810
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0-90-8661
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic FILE REPRENCE: P2730PLC3
CURRENT PAPLICATION: Acids Encoding the Same CURRENT PAPLICATION NUMBER: US/09/990,438
CURRENT FILING DATE: 2010-11-14
PRIOR FILING DATE: 1997-10-15
PRIOR PALICATION NUMBER: 60/06226
PRIOR PAPLICATION NUMBER: 60/06310
PRIOR PILING DATE: 1997-11-12
PRIOR PILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-14
PRIOR PILING DATE: 1997-11-12
PRIOR PILING DATE: 1997-11-24
PRIOR PILING DATE: 1997-11-24
PRIOR PILING DATE: 1997-11-24
PRIOR PILING DATE: 1999-0-25
PRIOR PILING DATE: 1999-0-6-25
PRIOR PILING DATE: 1999-0-6-25
PRIOR PILING DATE: 1999-0-6-25
PRIOR PILING DATE: 1999-0-6-20
PRIOR APPLICATION NUMBER: 60/08900
PRIOR PILING DATE: 1999-0-6-20
PRIOR PILING DATE: 1999-0-6-3
      Sequence 197, Application US/09990438 Publication No. US20030027754A1 GENERAL INFORMATION:
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Roy, Margaret Ann
Stewart, Timothy A.
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TITLE OF INVENTION: Secreted
TITLE OF INVENTION: Acids En
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Gerritsen, Mary E.
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Kljavin, Ivar J.
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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R FILING DATE: 1998-06-22

R APPLICATION NUMBER: 60/090254

R FILING DATE: 1998-06-22

R APPLICATION NUMBER: 60/090349

R FILING DATE: 1998-06-23

R APPLICATION NUMBER: 60/090355

R APPLICATION NUMBER: 60/090429

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R APPLICATION NUMBER: 60/090429
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R APPLICATION NUMBER: 60/090540

R APPLICATION NUMBER: 60/090542

R FILING DATE: 1998-06-24

R FILING DATE: 1998-06-24

R FILING DATE: 1998-06-24

R FILING DATE: 1998-06-26

R FILING DATE: 1998-06-26

R FILING DATE: 1998-06-25

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R APPLICATION NUMBER: 60/090678

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R APPLICATION NUMBER: 60/090678
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R APPLICATION NUMBER: 60/090694
R FILING DATE: 1998-06-25
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R APPLICATION NUMBER: 60/090696
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R APPLICATION NUMBER: 60/091544
R FILING DATE: 1998-07-01
R APPLICATION NUMBER: 60/091519
R FILING DATE: 1998-07-02
R APPLICATION NUMBER: 60/091626
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APPLICATION NUMBER: 60/090445
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090472
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APPLICATION NUMBER: 60/090862
FILING DATE: 1998-06-26
APPLICATION NUMBER: 60/090863
FILING DATE: 1998-06-26
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APPLICATION UNMBER: 60/090435
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090444
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APPLICATION NUMBER: 60/090535
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FILING DATE: 1998-07-01
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FILING DATE: 1998-07-09
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FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088030 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088033

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R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088742
R APPLICATION NUMBER: 60/08810
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R APPLICATION NUMBER: 60/08824
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R APPLICATION NUMBER: 60/08858
R FILING DATE: 1998-06-10
R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/08858
                      R FILING DATE: 1998-06-04
R APPLICATION UNMERS: 60/088167
R FILING DATE: 1998-06-05
R APPLICATION NUMBER: 60/088202
R FILING DATE: 1998-06-05
R APPLICATION NUMBER: 60/088212
R FILING DATE: 1998-06-05
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FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088655
FILING DATE: 1998-06-09
APPLICATION NUMBER: 60/088734
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APPLICATION NUMBER: 60/089440
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FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089653
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089801
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APPLICATION NUMBER: 60/089907
FLILING DATE: 1988-06-18
APPLICATION NUMBER: 60/089908
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FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/090246
FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090252
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APPLICATION NUMBER: 60/090349
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APPLICATION NUMBER: 60/088738
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APPLICATION NUMBER: 60/088876
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APPLICATION NUMBER: 60/089105
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APPLICATION UNDBER: 60/089532
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089538
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APPLICATION NUMBER: 60/089598
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APPLICATION NUMBER: 60/089599
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APPLICATION NUMBER: 60/090254
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APPLICATION NUMBER: 60/0
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APPLICATION NUMBER: 60/
FILING DATE: 1998-06-23
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| PRIOR FILING ADME: 1399-06.24
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| PRIOR PILING ADME: 1399-07.0
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PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR PILING DATE: 1998-06-23
PRIOR PILING DATE: 1998-06-23
PRIOR PLING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR APPLICATION NUMBER: 67/09049
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PRIOR PILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-18
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PRIOR PILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
                                                      PRIOR FILING DATE: 1998-06-05

RIOR APPLICATION NUMBER: 60/088655

RRIOR FILING DATE: 1998-06-05

PRIOR PILING DATE: 1998-06-10

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PRIOR FILING DATE: 1998-06-10

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PRIOR APPLICATION NUMBER: 60/088742

PRIOR APPLICATION NUMBER: 60/08810

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PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR PELLING DATE: 1998-06-17
PRIOR PEPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR PILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/08959
PRIOR PLILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/08963
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/08963
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APPLICATION NUMBER: 60/090444
      0-90-866
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HITTE OF INVENTION: Acids Enceding the Same
TITLE OF INVENTION: Acids Enceding the Same
CURRENT ENTER PRESENCE: P2730PT. Acids Enceding the Same
CURRENT PAPLICATION UNDRER: US/04/990.562
CURRENT APPLICATION UNDRER: 05/04/990
CURRENT FILMS DATE: 1997-06.16
FRIOR FILING DATE: 1997-06.16
FRIOR PLING DATE: 1997-06.16
FRIOR PLING DATE: 1997-10-17
FRIOR PLING DATE: 1997-11-12
FRIOR PLING DATE: 1997-11-12
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FRIOR PLING DATE: 1998-12-5
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FRIOR FILING DATE: 1998-12-5
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APPLICATION NUMBER: 60/088167
FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088202
                                                                                                                                                                Godowski, Paul J.
Grimaldi, J. Christopher
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Williams, P. Mickey
Wood, William I.
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Tumas, Daniel
Ferrara, Napoleone
Fong, Sherman
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                                                                                               Gerritsen, Mary E.
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Paoni, Nicholas F.
                                                                    Gerber, Hanspeter
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                                                                                                                                     Goddard, Audrey
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: P2730P1C2
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CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/06250
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-01-17
PRIOR PELICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/06511
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/06670
PRIOR APPLICATION NUMBER: 60/06794
PRIOR PILING DATE: 1997-11-24
PRIOR PILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR PILING DATE: 1998-02-25
PRIOR PILING DATE: 1998-03-20
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PRIOR PLING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR APPLICATION NUMBER: 60/087759
PRIOR PILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-03
PRIOR PILING DATE: 1998-06-04
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PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR PILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR PLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
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PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
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APPLICATION NUMBER: 60/088655
FILING DATE: 1998-06-09
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PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
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PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
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Grimaldi, J. Christopher
                                                                                                                                                                            Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
                                                                                                                                                            Timothy A
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PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1998-06-02
                                                                                                                                     Roy, Margaret Ann
                                                                                                                Paoni, Nicholas F.
                       Gurney, Austin L.
Kljavin, Ivar J.
                                                                   Napier, Mary A.
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R APPLICATION NUMBER: 60/090557

R FILING DATE: 1998-06-24

R FILING DATE: 1998-06-24

R FILING DATE: 1998-06-25

R APPLICATION NUMBER: 60/090678

R APPLICATION NUMBER: 60/090690

R RILING DATE: 1998-06-25

R APPLICATION NUMBER: 60/090690

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R APPLICATION NUMBER: 60/090690
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Publication No. US20030032023A1
GENERAL INFORMATION:
                                     FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090472
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090535
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APPLICATION UNMBER: 60/090540
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090542
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APPLICATION NUMBER: 60/090862
FILING DATE: 1998-06-26
APPLICATION NUMBER: 60/090863
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APPLICATION NUMBER: 60/091478
FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091544
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APPLICATION UNMBER: 60/091519
FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091626
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APPLICATION NUMBER: 60/091978
FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/091982
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APPLICATION NUMBER: 60/090695
FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090696
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APPLICATION NUMBER: 60/091633
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FILING DATE: 1998-07-09
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APPLICATION NUMBER: 60/091360
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Fong, Sherman
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Goddard, Audrey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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Botstein, David
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R FILING DATE: 1998-06-19
R APPLICATION NUMBER: 60/089952
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R PILING DATE: 1998-06-22
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R APPLICATION NUMBER: 60/090252
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R APPLICATION NUMBER: 60/088810
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APPLICATION WUNBER: 60/090431
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090435
  FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088742
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APPLICATION UNDRER: 60/08858
FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/08861
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APPLICATION UNMBER: 60/089105
FILING DATE: 1998-06-12
APPLICATION NUMBER: 60/089440
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APPLICATION NUMBER: 60/089538
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APPLICATION NUMBER: 60/089907
FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089908
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APPLICATION NUMBER: 60/089948
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APPLICATION UNMBER: 60/090254
FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090349
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APPLICATION NUMBER: 60/090355
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APPLICATION NUMBER: 60/090429
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APPLICATION NUMBER: 60/090444
FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/089514
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APPLICATION NUMBER: 60/089600
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APPLICATION NUMBER: 60/089653
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1998-06-10
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APPLICATION NUMBER:
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APPLICATION NUMBER:
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                                      PRIOR FILING DATE: 1998-06-24

RIOR APPLICATION NUMBER: 60/090557

REALTHING DATE: 1998-06-24

REALTHING DATE: 1998-06-25

PRIOR FILING DATE: 1998-06-25

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PRIOR APPLICATION NUMBER: 60/090690

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PRIOR APPLICATION NUMBER: 60/090863
PRIOR PILING DATE: 1998-06-26
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PRIOR PILING DATE: 1998-07-01
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PRIOR APPLICATION NUMBER: 60/091549
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o. US20030040473A1
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APPLICATION NUMBER: 60/092182
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PRIOR APPLICATION NUMBER: 60/C
PRIOR FILING DATE: 1998-07-09
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998-06-2
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Gerber, Hanspeter
Gerritsen, Mary E
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Botstein, David
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Eaton, Dan L.
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US-09-989-726-197
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Grimaldi, J. Christopher

Goddard, Audrey

Godowski, Paul

Gurney, Austin L

Kljavin, Ivar J

Napier, Mary A.

Paoni, Nicholas F. Roy, Margaret Ann

APPLICANT APPLICANT

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FALUR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION TOWNER: 60/088861
PRIOR APPLICATION TOWNER: 60/088861
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APPLICATION NUMBER: 60/090435
FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/090254
FILING DATE: 1998-06-22
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APPLICATION NUMBER: 60/090355
FILING DATE: 1998-06-23
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090431
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APPLICATION NUMBER: 60/090535
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090542
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PLICATION NUMBER: 60/090557
LING DATE: 1998-06-24
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FILING DATE: 1998-06-12
APPLICATION NUMBER: 60/089440
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APPLICATION NUMBER: 60/089512
FILING DATE: 1998-06-16
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APPLICATION NUMBER: 60/089538
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FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089599
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APPLICATION NUMBER: 60/089600
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FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089947
FILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/090246
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APPLICATION NUMBER: 60/090252
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FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/088876
FILING DATE: 1998-06-11
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APPLICATION NUMBER: 60/089907
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                                                APPLICANT: watenabe, Colin K.
APPLICANT: watenabe, Colin K.
APPLICANT: Walliams, P. Mickey
APPLICANT: Walliams, P. Mickey
APPLICANT: Walliams, P. Mickey
APPLICANT: Walliams, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PLG6
CURRENT APPLICATION NUMBER: US/09/989,726
CURRENT APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR PELLOATION NUMBER: 60/062250
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APPLICATION NUMBER: 60/087609
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APPLICATION NUMBER: 60/088029
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APPLICATION NUMBER: 60/088212
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APPLICATION NUMBER: 60/065186
FILING DATE: 1997-11-12
APPLICATION NUMBER: 60/065311
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APPLICATION NUMBER: 60/066770
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APPLICATION NUMBER: 60/075945
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APPLICATION NUMBER: 60/078910
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APPLICATION NUMBER: 60/088026
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APPLICATION NUMBER: 60/088202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ION NUMBER: 60/087607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/088028
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Stewart, Timothy A.
Tumas, Daniel
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TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: P2730P1C28
CURRENT APPLICATION NUMBER: US/09/998,156
CURRENT FILING DATE: 2001-11-15
                                                                                                 CURRENT FILING DATE: 1907-06-10-11-15

PRIOR APPLICATION NUMBER: 60/049787

PRIOR PLING DATE: 1997-06-16

PRIOR PLING DATE: 1997-06-16

PRIOR PELING DATE: 1997-10-17

PRIOR FILING DATE: 1997-11-12

PRIOR PELING DATE: 1997-11-12

PRIOR PELING DATE: 1997-11-12

PRIOR PELING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR PELING DATE: 1997-11-24

PRIOR PELING DATE: 1998-10-25

PRIOR PELING DATE: 1998-00-25

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PRIOR PELING DATE: 1998-00-26

PRIOR PELING DATE: 1998-05-28

PRIOR PELING DATE: 1998-05-07

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PRIOR PELING DATE: 1998-06-02

PRIOR PELING DATE: 1998-06-02
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APPLICATION NUMBER: 60/088028
FILING DATE: 1998-06-04
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FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088212
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FILING DATE: 1998-06-05
PILICATION NUMBER: 60/088655
FILING DATE: 1998-06-09
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FILING DATE: 1998-06-04
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FILING DATE: 1998-06-04
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FILING DATE: 1998-06-04
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FILING DATE: 1998-06-04
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FILING DATE: 1998-06-04
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088738
FILING DATE: 1998-06-10
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FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/088021
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FILING DATE: 1998-06-05
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FILING DATE: 1998-06-10
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R APPLICATION NUMBER: 60/090694
R FILING DATE: 1998-06-25
R APPLICATION NUMBER: 60/090695
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R APPLICATION NUMBER: 60/090696
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Publication No. US20030044806A1
GENERAL INFORMATION:
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APPLICATION NUMBER: 60/090863
FILING DATE: 1998-06-26
APPLICATION NUMBER: 60/091360
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FILING DATE: 1998-07-02
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FILING DATE: 1998-07-01
APPLICATION NUMBER: 60/091519
FILING DATE: 1998-07-02
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APPLICATION NUMBER: 60/090862
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APPLICATION NUMBER: 60/092182
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Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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PRIOR APPLICATION NUMBER: 60/0
PRIOR FILING DATE: 1998-07-09
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Stewart, Timothy
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Gerber, Hanspeter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Paoni, Nicholas F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 5; Conservative
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Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160 SCYNA 164
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US-09-998-156-197
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R FLLING DATE: 1998-06-16
R APPLICATION NUMBER: 60/089532
R APPLICATION NUMBER: 60/089538
R APPLICATION NUMBER: 60/08959
R FILING DATE: 1998-06-17
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R APPLICATION NUMBER: 60/089600
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089653
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089801
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R APPLICATION NUMBER: 60/090246
R FILING DATE: 1998-06-22
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R APPLICATION NUMBER: 60/090254
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R APPLICATION NUMBER: 60/090535
R FILING DATE: 1998-06-24
A PPLICATION NUMBER: 60/090540
R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090542
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R APPLICATION NUMBER: 60/089440
R FILING DATE: 1998-06-16
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R APPLICATION NUMBER: 60/089514
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APPLICATION NUMBER: 60/089947
FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/089948
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APPLICATION NUMBER: 60/090429
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090431
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APPLICATION NUMBER: 60/090445
                                               FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/089105
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FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089908
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APPLICATION NUMBER: 60/089952
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APPLICATION NUMBER: 60/090349
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APPLICATION NUMBER: 60/090355
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APPLICATION NUMBER: 60/090435
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APPLICATION NUMBER: 60/090444
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APPLICATION NUMBER: 60/090472
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APPLICATION NUMBER: 60/090557
FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/090694
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ö APPLICANT: Vatanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PlC49
CURRENT FILING DATE: 2001-11-16
PRIOR PILING DATE: 2001-11-16
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/062250 Gaps ; 0 100.0%; Score 30; DB 12; Length 346; 100.0%; Pred. No. 2e+02; ive 0; Mismatches 0; Indels ( PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/09062
PRIOR APPLICATION NUMBER: 60/09063
PRIOR FILING DATE: 1998-06-26
PRIOR FILING DATE: 1998-07-01
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PRIOR APPLICATION NUMBER: 60/091549
PRIOR PELING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR PELING DATE: 1998-07-02
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PRIOR PELING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR PELING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/09163
PRIOR PELING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07 US-09-990-437-197; Application US/09990437; Sequence 197, Application US/0990437; Publication No. US20030045463A1; GENERAL INFORMATION: Grimaldi,J.Christopher Gurney,Austin L. Kljavin,Ivar J. Roy, Margaret Ann Stewart, Timothy A Ferrara, Napoleone Gerritsen, Mary E. Goddard, Audrey Paoni, Nicholas F. Gerber, Hanspeter APPLICANT: Ashkenazi, Avi J. APPLICANT: Baker, Kevin P. APPLICANT: Botstein, David Query Match 100. Best Local Similarity 100. Matches 5; Conservative Napier, Mary A. Pan, James Desnoyers, Luc Godowski, Paul Daniel Fong, Sherman Eaton, Dan L. Stewart, Tumas, Da 160 SCYNA 164 . 1 SCYNA 5 ਨੇ

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PRIOR PILING DATE: 1998-06-16
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PRIOR PILING DATE: 1999-06-18
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PRIOR FILING DATE: 1998-06-05
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APPLICATION NUMBER: 60/088858
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APPLICATION NUMBER: 60/08861
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CURRENT APPLICATION NUMBER: US/09/991,157
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-17
PRIOR FILING DATE: 1997-06-10-17
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PR APPLICATION NUMBER: 60/091519

PR FILING DATE: 1998-07-02

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Publication No. US20030049638A1
GENERAL INFORMATION:
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APPLICATION NUMBER: 60/065186
FILING DATE: 1997-11-12
APPLICATION NUMBER: 60/065311
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PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
FILING DATE: 1998-06-26
APPLICATION NUMBER: 60/091360
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APPLICATION NUMBER: 60/091478
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APPLICATION NUMBER: 60/091544
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Williams, P. Mickey
Wood, William I.
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Fong, Sherman
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Paoni, Nicholas F.
Roy, Margaret Ann
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Matches 5; Conservative
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Botstein, David
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RELIGIOR DATE: 1998-06-22

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RAPPLICATION NUMBER: 60/090439

RETLING DATE: 1998-06-24

RAPPLICATION NUMBER: 60/090431

RETLING DATE: 1998-06-24

RETLING DATE: 1998-06-25

                                                            R AFFLICATION NUMBER: 60/089599
R APPLICATION NUMBER: 60/089599
R APPLICATION NUMBER: 60/089600
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089631
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089601
R APPLICATION NUMBER: 60/089901
R APPLICATION NUMBER: 60/089901
R APPLICATION NUMBER: 60/089901
R FILING DATE: 1998-06-18
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R APPLICATION NUMBER: 60/090696
R FILING DATE: 1998-06-25
R APPLICATION NUMBER: 60/090862
R FILING DATE: 1998-06-26
R FILING DATE: 1998-06-26
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R FILING DATE: 1998-06-26
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APPLICATION UNMBER: 60/089948
FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/089952
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APPLICATION UNMBER: 60/090246
FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090252
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APPLICATION NUMBER: 60/091544
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PRIOR PRIOR
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TITLE OF INVENTION: Sereted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Sereted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same TITLE OF INVENTION: Acids Encoding the Same CURRENT APPLICATION NUMBER: US/09/997,514

CURRENT APPLICATION NUMBER: US/09/997,514

CURRENT FILING DATE: 1997-06-16

PRIOR PELING DATE: 1997-06-16

PRIOR PILING DATE: 1997-11-12

PRIOR PELING DATE: 1997-11-12

PRIOR PILING DATE: 1997-11-13

PRIOR PILING DATE: 1997-11-24

PRIOR PILING DATE: 1998-02-25

PRIOR PILING DATE: 1998-03-25

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PRIOR PILING DATE: 1998-03-25
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100.0%; Score 30; DB 12; Length 346;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels (
                   PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR APPLICATION NUMBER: 60/091978
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
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US-09-997-514-197
Sequence 197, Application US/09997514
Publication No. US20030049681A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICATION NUMBER: 60/091519
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PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-3
PRIOR APPLICATION NUMBER: 60/084600
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Grimaldi, J. Christopher
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A
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Ferrara, Napoleone
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Gerritsen, Mary E.
Goddard, Audrey
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Napier, Mary A.
Pan, James
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PRIOR PILLING DATE: 1938-05-07
PRIOR PILLING DATE: 1938-06-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR PILLING DATE: 1938-06-02
PRIOR PILLING DATE: 1938-06-03
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PRIOR APPLICATION NUMBER: 60/08026
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PRIOR APPLICATION NUMBER: 60/088528
PRIOR PILLING DATE: 1938-06-17
PRIOR APPLICATION NUMBER: 60/088528
PRIOR PILLING DATE: 1938-06-17
PRIOR APPLICATION

PRIOR APPLICATION NUMBER: 60/08961
PRIOR FILING DATE: 1998-06-18
PRIOR FLINKO BATE: 1998-06-18
PRIOR PLINKO BATE: 1998-06-19
PRIOR PLINKO BATE: 1998-06-19
PRIOR PLINKO BATE: 1998-06-19
PRIOR PLINKO BATE: 1998-06-12
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PRIOR PLINKO BATE: 1998-06-22
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PRIOR PLINKO BATE: 1998-06-24
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PRIOR PLINKO BATE: 1998-06-25
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PRIOR APPLICATION NUMBER: 60/090658
PRIOR PLINKO BATE: 1998-06-25
PRIOR PLINKO BATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090658
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PRIOR APPLICATION NUMBER: 60/090666
PRIOR PLINKO BATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090666
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FILING DATE: 1998-06-04
APPLICATION UNDHER: 60/088025
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088026
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APPLICATION NUMBER: 60/088029
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088030
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APPLICATION NUMBER: 60/088033
APPLICATION UNBER: 60/088326
APPLICATION NUMBER: 60/088326
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APPLICATION NUMBER: 60/089440
FILING DATE: 1998-06-16
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APPLICATION NUMBER: 60/088028
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APPLICATION NUMBER: 60/088167
FILING DATE: 1998-06-05
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FILING DATE: 1998-06-05
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APPLICATION NUMBER: 60/088655
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APPLICATION NUMBER: 60/088810
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FILING DATE: 1998-06-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/089105
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FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089598
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FILING DATE: 1998-06-18
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APPLICATION NUMBER: 60/089908
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APPLICATION NUMBER: 60/08824
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ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITLE OF INVENTION: Acids Encoding the Same
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                                                                                                                                                                                               100.0%; Score 30; DB 12; Length 346; 100.0%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                              0; Mismatches
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Publication No. US20030049682A1
GENERAL INFORMATION:
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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APPLICATION NUMBER: 60/087609
FILING DATE: 1998-06-02
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Williams, P. Mickey
Wood, William I.
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Best Local Similarity 100.
Matches 5; Conservative
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Botstein, David
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US-09-997-573-197
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Best Local Similarity 100.0%; P?
Matches 5; Conservative 0;
                                                                                 Ferrara, Napoleone
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                                                                                               Gerritsen, Mary E
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                                                          APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
                                                                                                                          Napier, Mary A.
                                                                         Desnoyers, Luc
Eaton, Dan L.
                                                                                                    Goddard, Audrey
                                                                                                        Godowski, Paul
                                                                                       Fong, Sherman
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                     160 SCYNA 164
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PRIOR FILING DATE: 1
PRIOR APPLICATION NU
              1 SCYNA 5
                                    RESULT 36
US-09-991-172-197
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100.0%; Score 30; DB 12; Length 346;

Query Match

ö APPLICANT: Zhang, Zemin TITILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITILE OF INVENTION: Acids Encoding the Same FILE REPERENCE: P2730P1C50 Gaps ö Indels Pred. No. 2e+02; Mismatches 0; FILE KEREKENEE: P4/3-DILCO
CURRENT PEPLICATION NUMBER: US/09/991,172
CURRENT PELLING DATE: 2001-11-16
PRIOR PAPLICATION NUMBER: 06/049787
PRIOR PELLING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-12
PRIOR PELLING DATE: 1997-11-24
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PRIOR PELLING DATE: 1998-01-24
PRIOR PELLING DATE: 1998-01-25
PRIOR PELLING DATE: 1998-03-20
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PRIOR APPLICATION NUMBER: 60/078910
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PRIOR APPLICATION NUMBER: 60/078910
PRIOR PELLING DATE: 1998-03-20
PRIOR PELLING DATE: 1998-03-20
PRIOR PELLING DATE: 1998-03-20
PRIOR PELLING DATE: 1998-04-08
PRIOR PELLING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600
PRIOR PELLING DATE: 1998-05-07
PRIOR PELLING DATE: 1998-05-07 Sequence 197, Application US/09991172 Publication No. US20030050457A1 GENERAL INFORMATION: PRIOR FILING DATE: 1998-05-28 PRIOR APPLICATION NUMBER: 60/087607 PRIOR FILING DATE: 1998-06-02 APPLICATION NUMBER: 60/087609 FILING DATE: 1998-06-02 APPLICATION NUMBER: 60/087759 FILING DATE: 1998-06-02 APPLICATION NUMBER: 60/087827 FILING DATE: 1998-06-03 APPLICATION NUMBER: 60/088021 PRIOR FILING DATE: 1998-06-04 PRIOR APPLICATION NUMBER: 60/088025 Grimaldi,J.Christopher Gurney,Austin L. Kljavin,Ivar J. Roy, Margaret Ann Stewart, Timothy A. Tumas, Daniel Watanabe, Colin K. Williams, P. Mickey

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R APPLICATION NUMBER: 60/088026
RR APPLICATION NUMBER: 60/088026
RR FILING DATE: 1998-06-04
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RR FILING DATE: 1998-06-04
RR APPLICATION NUMBER: 60/088031
RR APPLICATION NUMBER: 60/088031
RR APPLICATION NUMBER: 60/088036
RR FILING DATE: 1998-06-04
RR FILING DATE: 1998-06-05
RR APPLICATION NUMBER: 60/088022
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R FILING DATE: 1998-06-05
R PILING DATE: 1998-06-05
R FILING DATE: 1998-06-09
R APPLICATION NUMBER: 60/086734
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/08738
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088738
R FILING DATE: 1998-06-10
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FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/088876
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APPLICATION NUMBER: 60/089105
FILING DATE: 1998-06-12
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FILING DATE: 1998-06-16
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APPLICATION NUMBER: 60/089514
FILING DATE: 1998-06-16
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FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089538
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APPLICATION NUMBER: 60/089598
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089599
FILING DATE: 1998-06-17
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FILING DATE: 1998-06-17
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FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089947
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FILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/088826
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FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/088861
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PRIOR PILING DATE: 1998-06-22
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PRIOR APPLICATION NUMBER: 60/090359
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PRIOR PILING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-24
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PRIOR PILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/09186
PRIOR PILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-02
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PRIOR PILING DATE: 1998-07-03
PRIOR PILING DATE: 1998-07-03
PRIOR PILING DATE: 
998-06-22
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Gaps

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Length 346; Indels

100.0%; Score 30; DB 12; 100.0%; Pred. No. 2e+02; Mismatches

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Query Match 100. Best Local Similarity 100. Matches 5; Conservative

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PRIOR PILLING DATE: 1998-06-04
PRIOR FILLING DATE: 1998-06-04
PRIOR FILLING DATE: 1998-06-04
PRIOR FILLING DATE: 1998-06-05
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PRIOR PELLING DATE: 1998-06-05
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PRIOR FILLING DATE: 1998-06-05
PRIOR FILLING DATE: 1998-06-05
PRIOR PELLOATION NUMBER: 60/080217
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PRIOR APPLICATION NUMBER: 60/08073
PRIOR APPLICATION NUMBER: 60/08073
PRIOR PILLING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/08073
PRIOR PILLING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/08070
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PRIOR FILING DATE: 1998-06-17
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APPLICATION UNDHER: 60/089948
FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/089952
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FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089907
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APPLICATION NUMBER: 60/089947
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FILING DATE: 1998-06-22
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APPLICATION NUMBER: 60/090254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730P1016 CURRENT APPLICATION NUMBER: US/09/990,726 CURRENT FILING DATE: 2001-11-14 PRIOR APPLICATION NUMBER: 60/049787 PRIOR FILING DATE: 1997-06-16
                           Sequence 197, Application US/09990726
Publication No. US20030054359A1
GENERAL INFORMATION:
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APPLICATION NUMBER: 60/087759
FILING DATE: 1998-06-02
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FILING DATE: 1997-10-17
APPLICATION NUMBER: 60/065186
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APPLICATION NUMBER: 60/066770
FILING DATE: 1997-11-24
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APPLICATION NUMBER: 60/078910
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FILING DATE: 1998-04-28
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APPLICATION NUMBER: 60/087106
FILING DATE: 1998-05-28
APPLICATION NUMBER: 60/087607
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APPLICATION NUMBER: 60/088021
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APPLICATION NUMBER: 60/088025
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APPLICATION NUMBER: 60/065311
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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       JS-09-990-726-197
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APPLICANT: Zhang, Zemin
IITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
IITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/997,559
CURRENT FILING DATE: 2001-11-15
PRIOR PEDLICATION NUMBER: 0/049787
PRIOR PEDLICATION NUMBER: 60/062250
PRIOR PEDLICATION NUMBER: 60/062250
PRIOR PELLING DATE: 1997-06-16
PRIOR PELLING DATE: 1997-10-17
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PRIOR PELLING DATE: 1998-06-02
PRIOR PELLING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/088326
FILING DATE: 1998-06-04
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PRIOR APPLICATION NUMBER: 60/088167
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
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R FILING DATE: 1998-06-23
R FILING DATE: 1998-06-24
R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090431
R APPLICATION NUMBER: 60/090431
R APPLICATION NUMBER: 60/090435
R APPLICATION NUMBER: 60/090435
R APPLICATION NUMBER: 60/090445
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R APPLICATION NUMBER: 60/090678

R FILING DATE: 1998-06-25

R FILING DATE: 1998-06-25

R APPLICATION NUMBER: 60/090690

R FILING DATE: 1998-06-25

R APPLICATION NUMBER: 60/090694

R FILING DATE: 1998-06-25

R FILING DATE: 1998-06-25

R FILING DATE: 1998-06-25

R FILING DATE: 1998-06-25

R APPLICATION NUMBER: 60/090695
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R FILING DATE: 1998-07-02
R FILING DATE: 1998-07-01
R FILING DATE: 1998-07-01
R APPLICATION NUMBER: 60/091519
R FILING DATE: 1998-07-02
R FILING DATE: 1998-07-02
R FILING DATE: 1998-07-02
R FILING DATE: 1998-07-02
R APPLICATION NUMBER: 60/091626
R FILING DATE: 1998-07-02
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R APPLICATION NUMBER: 60/090472
R APPLICATION NUMBER: 60/090472
R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090535
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US-097-559-197
Sequence 197, Application US/09997559
Publication No. US20030054403A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
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APPLICATION NUMBER: 60/090540
FILING DATE: 1998-06-24
FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/092182
FILING DATE: 1998-07-09
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090676
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APPLICATION UNMBER: 60/090862
FILING DATE: 1998-06-26
APPLICATION NUMBER: 60/090863
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APPLICATION NUMBER: 60/091360
FILING DATE: 1998-07-01
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APPLICATION NUMBER: 60/091982
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R FILING DATE: 1998-06-05
R APPLICATION NUMBER: 60/088217
R FILING DATE: 1998-06-05
A PAPLICATION NUMBER: 60/088655
R FILING DATE: 1998-06-09
R APPLICATION NUMBER: 60/088734
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APPLICATION NUMBER: 60/088742
                                                                                                                                                                                                                     FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088810
                                                                                                                                                                                                                                                              FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/08824
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APPLICATION NUMBER: 60/088858
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FILING DATE: 1998-06-11
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FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090254
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Query Match 100.0%; Score 30; DB 12; Length 346; Best Local Similarity 100.0%; Pred. No. 2e+02; Matches 5; Conservative 0; Mismatches 0; Indels
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PRIOR PELING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
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PRIOR APPLICATION NUMBER: 60/090695
PRIOR PELING DATE: 1998-06-25
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PRIOR PELING DATE: 1998-06-25
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PRIOR APPLICATION NUMBER: 60/091519
PRIOR PLING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR PLING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-07
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R R PILING DATE: 1998-07-01
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R FILING DATE: 1998-07-01
R APPLICATION NUMBER: 60/091548
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R FILING DATE: 1998-07-01
R FILING DATE: 1998-07-02
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PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
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R APPLICATION NUMBER: 60/090557

R FILING DATE: 1998-06-24

A APPLICATION NUMBER: 60/090676

R FILING DATE: 1998-06-25

R APPLICATION NUMBER: 60/090678

R FILING DATE: 1998-06-25
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Publication No. US20030054404A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
LICATION NUMBER: 60/090444
ING DATE: 1998-06-24
                                                             APPLICATION NUMBER: 60/090445
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1998-07-07
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Eaton, Dan L.
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US-09-997-601-197
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PRIOR APPLICATION NUMBER: 60/089948
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PRIOR FILING DATE: 1998-06-23
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PRIOR PLING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR PLING DATE: 1998-06-24
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R APPLICATION NUMBER: 60/088742
R FILING DATE: 1998-06-10
A PPLICATION NUMBER: 60/088810
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088824
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FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089512
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PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088858
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APPLICATION NUMBER: 60/089105
FILING DATE: 1998-06-12
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FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089532
FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089907
FILING DATE: 1998-06-18
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PRIOR APPLICATION NUMBER: 60/090444
                                      LICATION NUMBER: 60/088734
                                                                                                                                                                                                                                                                                                              FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/088876
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APPLICATION NUMBER: 60/089598
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REPERENCE: P2730PIC36 CURRENT APPLICATION NUMBER: US/09/997,601 CURRENT FILING DATE: 2001-11-15
                                                                                                                                                                                                                                                                                                                                                                                                                                       R FILING DATE: 1997-10-17

R APPLICATION NUMBER: 60/065186

R FILING DATE: 1997-11-12

R FILING DATE: 1997-11-12

R FILING DATE: 1997-11-13

R FILING DATE: 1997-11-24

R FILING DATE: 1997-11-24

R PLING DATE: 1997-11-24
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R APPLICATION NUMBER: 60/087827
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R FILING DATE: 1998-06-03
R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088025
R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088026
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R FILING DATE: 1998-06-04
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IOR FILING DATE: 1997-06-16
IOR APPLICATION NUMBER: 60/062250
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FILING DATE: 1998-06-04
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APPLICATION UNDBER: 60/078910
FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/083322
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APPLICATION NUMBER: 60/08/106
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APPLICATION NUMBER: 60/087607
FILING DATE: 1998-06-02
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FILING DATE: 1998-06-02
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APPLICATION NUMBER: 60/088029
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APPLICATION NUMBER: 60/088030
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FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088217
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APPLICATION NUMBER: 60/084600
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                                                   Grimaldi, J. Christopher
                                                                                                                                                                                                                                   Williams, P. Mickey
Wood, William I.
                                                                                                                        Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A
Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1998-06-04
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Watanabe, Colin K
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Gerritsen, Mary E.
                                                                          Gurney, Austin L.
                                  Godowski, Paul J
                                                                                          Kljavin, Ivar J
                                                                                                         Napier, Mary A.
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FILING DATE: 1998-06
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC12
CURRENT APPLICATION NUMBER: US/09/990,443
                                                                                                                                                                                                      FILING DATE: 1998-06-04
APPLICATION WINBER: 60/088326
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088167
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APPLICATION NUMBER: 60/088217
FILING DATE: 1998-06-05
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APPLICATION NUMBER: 60/088202
                                                  Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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                                                                                                                    R APPLICATION NUMBER: 60/09676

R APPLICATION NUMBER: 60/09676

R FILING DATE: 1998-06-24

R FILING DATE: 1998-06-25

R FILING DATE: 1998-06-25

R FILING DATE: 1998-06-25

R APPLICATION NUMBER: 60/09690

R FILING DATE: 1998-06-25

R APPLICATION NUMBER: 60/09694

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R APPLICATION NUMBER: 60/090696

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R APPLICATION NUMBER: 60/090862

R APPLICATION NUMBER: 60/090863

R FILING DATE: 1998-06-26

R APPLICATION NUMBER: 60/090863

R FILING DATE: 1998-06-26

R APPLICATION NUMBER: 60/090863

R FILING DATE: 1998-06-26

R APPLICATION NUMBER: 60/091360

R FILING DATE: 1998-06-26

R APPLICATION NUMBER: 60/091360
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Publication No. US20030054987A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 1998-07-02
APPLICATION UNMBER: 60/091544
FILING DATE: 1998-07-01
APPLICATION NUMBER: 60/091519
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APPLICATION UNMBER: 60/091633
FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091978
                                                      FILING DATE: 1998-06-24
APPLICATION UNMBER: 60/090542
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090557
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APPLICATION NUMBER: 60/091626
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FILING DATE: 1998-07-09
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Eaton, Dan L.
Ferrara, Napoleone
                                                    1998-06-24
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Gerber, Hanspeter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Baker, Kevin P.
Botstein, David
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PRIOR APPLICATION NUMBER: 60/08826
PRIOR APPLICATION NUMBER: 60/08826
PRIOR APPLICATION NUMBER: 60/08826
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PRIOR PLING DATE: 1989-66-12
PRIOR PLING DATE: 1989-66-12
PRIOR PLING DATE: 1989-66-16
PRIOR APPLICATION NUMBER: 60/08559
PRIOR PLING DATE: 1989-66-17
PRIOR PL
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Query Match

Query Match

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels

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Search completed: July 18, 2003, 15:35:53 Job time : 14.9 secs

160 SCYNA 164

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July 18, 2003, 15:02:20 ; Search time 6.82 Seconds (without alignments) 66.897 Million cell updates/sec Run on:

US-10-007-790-7 61

1 SGAYYRYGVVY 11 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 segs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		Q12630 kluyveromyc				O95406 homo sapien	035372 mus musculu	P49858 drosophila			P58961 drosophila		P03773 bacteriopha		Q95005 caenorhabdi	Q9yfm2 aeropyrum p		P31260 homo sapien		P78710 neurospora	P76585 escherichia	P32568 saccharomyc				P28074 h proteasom		Q9pbjl xylella fas	Q97pm9 streptococc	_	Q9uxa8 sulfolobus	Q9vyz2 drosophila	P40372 schizosacch
SUMMARIES	. di	META BACSU			STT3 HUMAN	STT3 MOUSE	CNIH_HUMAN	CNIH_MOUSE	CNI DROME	CNI_DROVI	G10A DROME	G47B DROME	TKT1_YEAST	Y64_LAMBD	YEWS YEAST	PSA7_CAEEL	RL3 AERPE						SNQ2_YEAST		GON1_CAVPO	NP1_RHOPR	PSB5_HUMAN	PSB5 MOUSE	KDKA_XYLFA			RL3 SULSO	m	RL3A_SCHPO
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de	Query	60.7	ö		60.7	60.7	59.0	59.0	59.0		59.0	59.0	59.0	57.4	57.4	57.4	57.4	57.4	57.4	57.4	57.4	57.4	57.4	55.7	55.7	55.7	55.7	55.7	55.7	55.7	55.7	55.7	55.7	55.7
	Score	37	37	37	37	37	36	36	36	36	36	36	36	35	35	32	35	35	35	35	35	35	35	34	34	34	34	34	34		34		34	34
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	.5 saccharomyc )6 klebsiella							
P36584 O94039	P3331 P0720	P0781	00652	Q9y3b	596Ed	P4548	08381	P3406
RL3B_SCHPO TKT1_CANAL	TKT2 YEAST PULA KLEPN	PULA KLEAE RNMS ASPSA	VTU3 DROME	CSL4_HUMAN	DSBC ERWCH	Y990 CAMJE	AMPM TREPA	PSB5_CHICK
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## ALIGNMENTS

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3 E	16-UCI-2001	7 7	Last sequ	sequence update)	paar	nadre)		
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ä ë	cranssuccinylase, (HIS).	Tase) (HIS)						
Z (	META OK METB							
S	Bacillus subtilis	c1118.			:			
ပ	Bacteria; Firmicutes;	rmicutes; B	Baciliales;	s; Bac	1119	Bacillaceae;	Bacilius.	
ŏ	NCBI TaxID=1423;	423;						
RN	[1]							
RP	SEOUENCE FROM N.A	M N.A.						
2	STEATN=168 /	/ Marburg:						
Ä	MEDI.TNE-96349105 . DibMed-8760912 .	9105 · DuhMa	d-876091	٠,				
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RT	the serA and	kdg loci c	Toned 1r	a yea	st a	rtitic	clal chromosome.";	
RL	Microbiology	142:2005-2	016(1996					
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RA	Bairoch A.;							
Æ	Unpublished	observation	s (DEC-2	. (000				
ပ္ပ	-!- CATALYTIC ACTIVITY: Succinyl-CoA + L-homoserine	C ACTIVITY:	Succiny	1-CoA	+ L-1	homose	erine = CoA + O-	
S	succinvl	succinvl-L-homoserine.	ne.					
Ü	-! - PATHWAY:	PATHWAY: Methionine biosynthesis: HTS	biosvnt	hesis:	HTS		ant: first step.	
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DR	EMBL: L77246	. AAA96625.	1: ALT E	RAME.				
E E	EMBL: 299115	Z99115; CAB14109.1; ALT FRAME.	1: ALT	RAME.				
DR	-	G11534; met	· A					
DR	TIGREAMS: TI	GR01001: me	t.A: 1.					
Ž	Methionine biosynthesis: Transferase: Acvitransferase	iosvnthesis	Transf	erase	ACV	ltrans	sferase:	
X	Complete pro	proteome.						
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ös		' . ¥	35451 MW;	1BE392	C62D	30321	1BE392C62D30321F CRC64;	
8	Query Match			Score 37;	Δ.	DB 1;	Length 302;	
ď	Rest Local Similarity			Pred No. 16:	16			

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Gaps .; 0 Indels 2; Best Local Similarity 66.7%; Pred. No. 16; Matches 6; Conservative 1; Mismatches

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1 SGAYYRYGV 9

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                                                                                            Metzger M., Hollenberg C.;
"Isolation and characterization of the Pichia stipitis transketolase
gene and expression in a xylose-utilising Saccharomyces cerevisiae
                                                                                                                                                                                                        . Biotechnol. 42:319-325(1994)
                                                                      MEDLINE=95151296; PubMed=7765773;
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Best Local Similarity 77.8
Matches 7; Conservative
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HSSP; P23254; ITRK
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                                                SEQUENCE FROM N.A.
    NCBI_TaxID=4924;
                                                                                                                                                                                          Appl. Microbiol
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                                                                                                                                                                       ransformant.";
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STT3_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CES 2359/152;
MEDLINE=91153463; PubMed=9000376;
Jacoby J.J., Heinisch J.J.;
Jacoby J.J., Heinisch J.J.;
Analysis of a transketolase gene from Kluyveromyces lactis reveals that the yeast enzymes are more related to transketolases of prokaryotic origins than to those of higher eukaryotes.";
Curr. Genet. 31:15-21(1997).
-!- CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyceraldehyde 3-phosphate = D-ribose 5-phosphate + D-xylulose 5-phosphate.
-!- COPACTOR: THIAMINE PYROPHARE.
-!- SUBUNIT: HOWODIMER (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE TRANSKETOLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
NCBI _TaxID=28985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.7%; Score 37; DB 1; Length 679; 77.8%; Pred. No. 36; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BC5F3CF61A78CD4A CRC64;
                                                                                                                                                                                        15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
39-MAY-2000 (Rel. 39, Last annotation update)
Transketolase (EC 2.2.1.1) (TK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-CT-1996 (Rel. 34, Last annotation update)
Transketolase (EC 2.2.1.1) (TK).
                                                                                                                                              679 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  695 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Thiamine pyrophosphate.
679 AA; 73703 MW; BC5F3
                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000360; Transketolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00456; transketolase; 1.
Pfam; PF02779; transket pyr; 1.
Pfam; PF02780; transketolase C; 1.
                                                                                                                                                                                                                                                                                                            Kluyveromyces lactis (Yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U65983; AAB05935.1; -.
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les 7; Conservative
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407 SGRYIRYGV 415
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P34736;
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Matches
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TKT_PICST
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Merregaert J.;
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MEDLINE=96435424; PubMed=8838310;
Hong G., Deleersnjider W., Kozak C.A., van Marck E., Țylzanowski P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Oligosaccharyl transferase STT3 subunit homolog (B5) (Integral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB 1; Length 695;
Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lransferase; Thiamine pyrophosphate.
sEQUENCE 695 AA; 75159 MW; 1FBC1C7B6E0B5DB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  705 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                               Pfam; PF00456; transketolase; 1.
Pfam; PF02779; transket_pyr; 1.
Pfam; PF02780; transket_lase c; 1.
TIGREAMS; TIGR00232; tktlase_bact; 1.
PROSITE; PS00801; TRANSKETOLASE 1; 1.
PROSITE; PS00802; TRANSKETOLASE 2; 1.
ISSP; P23254; 1TRK.
nterPro; IPR000360; Transketolase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Merregaert J.;
"Molecular cloning of a highly conserved mouse and human integral membrane protein (Itml) and genetic mapping to mouse chromosome 9."; Genomics 31:295-30(1996).
-1- FUNCTION: INVOLVED IN PROTEIN GLYCOSYLATION. EITHER REQUIRED FOR THE ASSEMBLY OF THE OLICOSACCHARYL TRANSFERASE (OTASE) COMPLEX OR REQUIRED IN SUBSTOCHIOMETRIX AMOUNTS FOR OTASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-BALB/c; TISSUE-Mandibular condyle;
MEDLINE-96435424; PubMed-8838310;
Hong G., Deleersnjider W., Kozak C.A., van Marck E., Tylzanowski P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 34, Last sequence in update)
01-OCT-1996 (Rel. 34, Last series annotation update)
01igosaccharyl transferase STT3 subunit homolog (BS) (Integral
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                      DBF50C217EA40AE4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BY SIMILARITY).
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO THE STT3 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37; DB 1;
Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          705 AA
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1; Mismatches
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                                                                                                                                                      MIM; 601134; -.
InterPro; IPR003674; OTase_STT3.
Pfam; PF02516; STT3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                      80471 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                   60.7%;
75.0%;
                                                                                                                            EMBL; L38961; AAB05994.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                             HGNC:6172; ITM1.
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644 YYRFGQVY 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 YYRYGVVY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               membrane protein 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                301
360
384
406
454
573
705 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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                                                                                                                                                                                                     Fransmembrane
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P46978;
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TRANSMEM
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                     (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99227056; PubMed=10209299;
MEDLINE=99227056; PubMed=10209299;
Utku N., Bulwin G.-C., Beinke S., Heinemann T., Beato F., Randall J., Schnieders B., Sandhoff K., Volk H.-D., Milford E., Gullans S.R.;
"The human homolog of Drosophila cornichon protein is differentially expressed in alloactivated T-cells.";
Biochim. Biophys. Acta 1449:203-210(1999).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- TISSUB SPECIFICTY: HIGHLY EXPRESSED IN HEART, LIVER, SKELETAL MUSCLE, PANCREAS, ADRENAL MEDULLA AND CORTEX, THYROID, TESTIS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 37; DB 1; Length 705; Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plisov S.Y., Ivanov S.V., Lerman M., Perantoni A.O., Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
Usage by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CD1D796D0479F321 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
modified and this statement is not removed.
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                       entities requires a license agreement (Son send an email to license@isb-sib.ch).
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                                                                                                                                           InterPro; IPR003674; OTase_STT3. Pfam; PF02516; STT3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Res. 10:1546-1560(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80597 MW;
                                                                                              EMBL; L34260; AAB47775.1; -. MGD; MGI:105124; Itml.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cornichon homolog (TGAM77).
CNIH OR CNIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                          644 YYRFGQVY 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 YYRYGVVY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         705 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. TISSUE=Carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                  Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Blood
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095406;
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TRANSMEM
TRANSMEM
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CNIH HUMAN
ID 130-MAY.
DT 30-MAY.
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MGD; MGI:1277202; Cnih.
InterPro; IPR003377; Cornichon.
Pfam; PF03131; Cornichon; I.
PROSITE; PS01340; CORNICHON; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81:967-978 (1995).
                                                                                                                                                                                                                     132 YYLYGMIY 139
                                                                                                                                                                                           4 YYRYGVVY 11
                                                                  11
57
123
144 AA;
                                                                                                                                                                                                                                                                                                                                                            Cornichon protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=7227;
                                                      Transmembrane.
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                                                                                                             SEQUENCE
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Matches
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CNI_DROME
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                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEVELOPMENTAL STAGE: ABUNDANT IN FULL GROWN OOCYTE AND THE OVULATED UNFERTILIZED EGG, SHOWS A SLIGHT DECREASE 12 HOURS AFTER FERTILIZATION. TRANSCRIPTS FROM THE ACTIVATED EMBRYONIC GENOME ARE PRESENT IN THE EIGHT-CELL EMBRYO. SIMILARITY: BELONGS TO THE CORNICHON FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99147138; PubMed=10022955;
Hwang S.-Y., Oh B., Zhang Z., Miller W., Solter D., Knowles B.B.;
Hwang S.-Y., Oh B., Zhang Z., Miller W., Solter D., Knowles B.B.;
Hwan ecornichon gene family.";
Dev. Genes Evol. 209:120-125(1999).
-!- SUBCELLIUAR LOCATION: Integral membrane protein (Potential).
-!- SUBCELLIUAR LOCATION: OF G.WEER-OLD MOUSE. EXPRESSED IN ADULT
                                                                                                                                                                                                                                                                                                                                                                        Gaps
SPLEEN, APPENDIX, PERIPHERAL BLOOD LYMPHOCYTES AND BONE MARROW. LOWER EXPRESSION FOUND IN BRAIN, PLACENTA, LUNG, KIDNEY, OVARY, SMALL INTESTINE, STOMACH, LYMPH NODE, THYMUS AND FETAL LIVER. SIMILARITY: BELONGS TO THE CORNICHON FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                           Score 36; DB 1; Length 144; Pred. No. 12; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                   59BD114D24C455CD CRC64;
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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PROSITE, PS01340; CORNICHON, 1.
Transmembrane.
                                                                                                                                                                                                                    InterPro; IPR003377; Cornichon.
Pfam; PF03311; Cornichon; 1.
                                                                                                                                                                                          EMBL; AF070654; AAD20960.1; -. EMBL; AF031379; AAD32301.1; -.
                                                                                                                                                                               EMBL; AF104398; AAC98388.1; -.
                                                                                                                                                                                                                                                                                                                   144 AA; 16699 MW;
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132 YYLYGMIY 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cornichon homolog
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035372;
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Adams M.D., Celniker S.E., Holf R.A, Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A decorge R.A., Lewis S.E., Holf B.W., Hoskins R.A., Galle R.F.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wootrman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Abril J.F., Agbayani A., An H.-J., Andrews-Feannkoch C., Baldwin D.,
Ballew R.M., Banu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Banos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Buuck J., Erokstein P., Brottier P., Abantis K.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Punkov B.C., Dunn P.,
A Durbin K.J., Evangelista C.C., Ferriera S., Fleischmann W.,
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Hexapoda,
Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera,
Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Ovary;
MEDLINE=95300228; PubMed=7540118;
Roth S., Neuman-Silberberg F.S., Barcelo G., Schuepbach T.;
"Cornichon and the EGF receptor signaling process are necessary for both anterior-posterior and dorsal-ventral pattern formation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Forex. S., Rubin G.M.,
Celniker S., Rubin G.M.,
"An exploration of the sequence of a 2.9-Mb region of the genome of
Proscophila melanogaster: the Adh region.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Berkeley;
MEDLINE=99403001; PubMed=10471707;
Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T.,
Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,
Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.
Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw
                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                 DB 1; Length 144;
                                                                                                                                                                                                                                                           Indels
                                                                 143 POTENTIAL.
16713 MW; DF66786D24C455CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CXI DROME STANDARD; PRT; 144 AA. P49858; Q9V423; 01-OCT-1996 (Rel. 34, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                         Score 36; DE
Pred. No. 12;
                                  POTENTIAL
POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                 59.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster: the
Genetics 153:179-219(1999).
                                                                                                                                                                                                                    Local Similarity 62.5
nes 5; Conservative
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Drosophila...,
Cell 81:967-978(1995)
-- FORNILO BASSOCIATED WITH GURKEN, PRODUCES A SIGNAL RECEIVED BY
TORPEDO RESULTING IN A SIGNALING PATHWAY THAT FIRST ESTABLISHES
POSTERIOR FOLLICLE CELL FATES AND NORMAL LOCALIZATION OF THE
ANTERIOR AND POSTERIOR DETERMINANTS, LATER THEY ACT IN A SIGNALING
EVENT INDUCING DORSAL FOLLICLE CELL FATES AND REGULATING THE
DORSAL-VENTRAL PATTERN OF EGG AND EMBRYO (BY SIMILARITY).
-- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-- SIMILARITY BELONGS TO THE CORNICHON FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-2019606; PubMed=10731132; Adams M. Gocayne J.D., Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beaaley E.M., Beeson K.Y., Bernos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Broketein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
                                                                                                                    Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Hexapoda,
Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera,
Muscomorpha, Ephydroidea, Drosophilidae, Drosophila,
                                                                                                                                                                                                                                                                                                                          Roth S., Neuman-Silberberg F.S., Barcelo G., Schuepbach T., "Cornichon and the EGF receptor signaling process are necessary for both anterior-posterior and dorsal-ventral pattern formation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36; DB 1; Length 144;
Pred. No. 12;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOF4E65560409164 CRC64;
                  30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       408 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Developmental protein; Transmembrane.
TRANSMEM 11 31 POTENTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                MEDLINE=95300228; PubMed=7540118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUN-2002 (Rel. 41, Last annot Putative gustatory receptor 10a.
                                                                                               (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003377; Cornichon.
Pfam; PF03311; Cornichon; 1.
PROSITE; PS01340; CORNICHON; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16927 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.0%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 AA;
                                                                                            Drosophila virilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                               Cornichon protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Muscomorpha; Eph
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Berkeley;
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G10A_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harry D., Heiman T.J., Hernandez J.S., Harris M.,
Harris N.L., Havary D., Heiman T.J., Hernandez J.S., Harris M.,
Hostin D., Houston K.A., Howland T.J., Heimandez J.S., Houston K.A.,
RA Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraff C., Kravitz S., Mulp D., Lia Z.,
Lisako P., Lei J., McIntcsh T.C., McLeod M.P., McPherson D.,
Lu X., Mattei B. M., McIntcsh T.C., McLeod M.P., McPherson D.,
RA Mulson B., McIntcsh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Stupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Stupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Mang Z.-Y. Wassarman D.A., Weinsteck G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang G., Zhao Q., Zheng K.H., Zhong F.N., Zhong W., Zhong G., Zhao Q., Zheng K.H., Zhong F.N., Zhong W., Zhou S., Zha X., Myers B.W., Rubin G.M., Venter J.C.;
Science 287:2185-2195 (2000)
C.-- FUNCTION: ASSOCIATED WITH GURKEN, PRODUCES A SIGNAL RECEIVED BY TORREDO RESULTING IN A SIGNALING PATHRAY THE TREF ESTABLISHES
C. FUNCTION: ASSOCIATED WITH GURKEN, PRODUCES A SIGNAL ROT IN A SIGNALING
C. FURL DORSAL-VENTRAL PATTERS AND NORMAL LOCALIZATION OF THE
CELL OCCYTE CLUIAR LOCATION: INEGERA DESENTING THE STRESSED IN THE NURSE
C.-- SUBCELLUIAR LOCATION: INEGERE SURING STAGE I IN STAGE I - E EGG
CHAMBERS, EXPRESSION CEASE DURING STAGE IO, IT IS REEXPRESSED IN THE NURSE
C. CELL OCCYTE CLUSTER: IN BRALY STAGE IO, IT IS REEXPRESSED IN THE BURNOT BE DISTABLED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE CORNICHON FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 34, Created)
(Rel. 34, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 12;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PR003377; Cornichon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF03311; Cornichon; 1.
PROSITE; PS01340; CORNICHON; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE003415; AAF45003.1; -. EMBL; AE003650; AAF53521.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 143 P<sup>2</sup>
144 AA; 16931 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U28069; AAA86527.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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TRANSMEM
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IN STAGES
CELLS.
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P52159;
01-OCT-1996 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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RESULT 9
CNI\_DROVI
ID \_ CNI\_D
AC P5215
DT 01-0C
DT 01-0C

Matches

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Gaps

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Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

Dodoson K., Doup L.E., Downes M., Dugan-Rochas S., Dunkov B.C., Dunn P.,

A Durbin K.J. Evangelista C.C., Ferract S., Fleischmann W.,

RA Godek A., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris N.L.,

Harris N.L., Harvey D., Heiman T.J., Weil M.-H., Ibegwam C.,

A Jalai M., Kalush F., Karpen G.H., Ke Z., Kannison J.A., Ketchum K.A.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Wei M.-H., Ibegwam C.,

Lu X., Mattei B., McIntosh T.C., McLeod M.P., McDherson D.,

RA Markei B., McIntosh T.C., McLeod W.P., McDherson D.,

RA Malson D.R., Mison K., Nixon K., Nusskern D.R., Pacled J.M.,

Rajson D.K., Nelson K.A., Nixon K., Nusskern D.R., Pacled J.M.,

Rajson D.K., Nelson K.A., Nixon K., Nusskern D.R., Pacled J.M.,

Raine B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Shen H.,

Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,

Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

Zheng X.H., Zhong F.N., Zaveri J.S., Zhan M., Zhou X., Zhu X., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,

Ra Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,

Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dunipace L., Meister S., McNealy C., Amrein H.; "Spatially restricted expression of candidate taste receptors in the Drosophila gustatory system."; Curr. Biol. 11:822-835(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Probable role in the gustatory response.
SUBCELLULAR LOCATION: Integral membrane protein (Potential).
SIMILARITY: BELONGS TO FAMILY DR-TR OF G-PROTEIN COUPLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 (POTENTIAL).

**TYOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL)

N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE003486; -; NOT ANNOTATED_CDS.
Flybase; FBgn0045502; Grl0a.
Fypothetical protein; Receptor; G-protein coupled receptor;
Transmembrane; Glycoprotein; Multigene family.
DOMAIN
1 20 EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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63FEBB27DDE856AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 (FOIENTIAL).
EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21407712; PubMed=11516643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONCEPTUAL TRANSLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1444
1165
270
270
291
3325
402
402
408
1192
205
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326
382
403
192
408 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Robertson H.;
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TRANSMEM
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SEQUENCE
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48391 MW;

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RC STRAIN-Berkeley;

RX MEDLINE=2019606; PubMed=10731132;

RR Adams M.D. Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

Adams M.D. Celniker S.E., Richards S., Ashburner M., Henderson S.N.,

RA Adams M.D. Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Adams M.D. Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Abril J.F. Agbayaria A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballaw R.M., Bauu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beson K.Y., Baun D.A., Buller C., Davenport L.B., Dolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Botchier P.,

RA Borkova D., Botchan M.R., Davise S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Botchier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Botchier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Botchier P.,

RA Borkova D., Botchan A.E., Garg N.S., Gelbarr W.M., Glasser K.,

RA Borson K.J. Evangelista C.C., Ferraz C., Ferriara S., Pleistchmann W.,

RA Borson K.J. Evangelista C.C., Ferraz C., Ferriara S., Pleistchmann W.,

RA Hostin D., Houston K.A., Heiman T.J., Hernandez J.R., Harris M.

Allali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.

Alalali M., Kalush F., Karpen G.H., Wa Z., Kanp D., Lai Z.,

Lasko P., Lei Y., Leviteky A.A., Li J., Li Z., Liang Y., Lin X.,

Alacon R.M., Moy M., Murphy B., Murphy L., Murzhy D.M., Nelson D.L.,

RA Hostin D., Houston K.A., Nixon K., Nusskern D., Puri, V., Resen M.G.,

RA Bazzolo M., Pittman G.S., Pan S., Pollact J., Ward S., Ban H.,

Sylekas R., Medony R., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Bazzolo M., Pittman G.S., Pan S., Pollact E., Wang A.H., Wang C.-Y., Wassarman D.A., Weilsenbach J.,

RA Bener K., Zhong F.N., Robing W., Zhong W., Zhu S., Zhu X., Smith H.O.,

Ra Bener K., Zhong F.N., Robing W., Zhong R., S
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished observations (NOV-2001).

-i FUNCTION: Probable role in the gustatory response.

-i SUBCELLULAR LOCATION: Integral membrane protein (Potential).

-i SIMILARITY: BELONGS TO FAMILY DR-TR OF G-PROTEIN COUPLED
                                                                          ö
Score 36; DB 1; Length 408;
Pred. No. 33;
                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Myers E.W., Rubin G.M., Venter J.C., sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                         408 AA
                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Putative gustatory receptor 47b.
   59.0%;
75.0%;
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                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONCEPTUAL TRANSLATION.
                                                                                                                                                                                               :|||| ||
18 FYRYGHVY 25
                                                                                                                                                  4 YYRYGVVY 11
       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Muscomorpha; Eph
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Robertson H.;
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G47B_DROME
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SEQUENCE OF
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sundstroem M., Lindqvist Y., Schneider G., Hellman U., Ronne H., "Yeast TKLI gene encodes a transketclase that is required for efficient glycolysis and biosynthesis of aromatic amino acids.", J. Biol. Chem. 268:24346-24352(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1991 (Rel. 20, Created)
01-FBB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Transketolase 1 (EC 2.1.1) (TK 1).
TKL1 OR YRRO74C OR YP9499.29C.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes;
                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=92144611; PubMed=1737042;
Fletcher T.S., Kwee I.L., Nakada T., Largman C., Martin B.M.;
Blacher T.S., Fub yeast transketolase gene.";
Biochemistry 31:1892-1896(1992).
                                                                                       EMBL, AE003486; -; NOT ANNOTATED_CDS.
Flydase; FBgn0041241; Gr47b.
Flydothetical protein; Receptor; G-protein coupled receptor;
Transmembrane; Glycoprotein; Multigene family.
DOMAIN
1 20 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                             Score 36; DB 1; Length 408;
Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                           63FEBB27DDE856AD CRC64;
                                                                                                                                                           2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                   6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                        '1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                             3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                    679 AA.
                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                4 (POTENTIAL)
                                                                                                                                                                                                                                                        7 (POTENTIAL)
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MEDLINE-94043273; PubMed-8226984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-S288c / AB972;
MEDLINE-97313271; PubMed-9169875;
                                                                                                                                                                                                                                                                                            48391 MW;
                                                                                                                                                                                                                                                                                                              59.0%;
                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 75.v
                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                         :|||| ||
FYRYGHVY 25
                                                                                                                                                                                                                                                                                                                                                  4 YYRYGVVY 11
                                                                                                                                                                                                                                                                403
192
205
408 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4932;
                                                                                                                                                                                                                                              326
                                                                                                                                                                                                                                                                                                                                                                                                                  YEAST
                                                                                                                                DOMAIN
TRANSMEM
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TRANSMEM
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TRANSMEM
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TRANSMEM
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CARBOHYD
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                                                                                                                                                                                              FRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                  TKT1 YEA
P23254;
                                                                                                                                                 DOMAIN
                                                                                                                                                                                      DOMAIN
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TKT1_YEAST
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Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansorge W., Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V., Botstein D., Bowman S., Burckner M., Carpenter J., Cherry J.M., Churcher C.M., Coster F., Davis K., Davis R.W., Dietrich F.S., Delius H., DiRaolo T., Dubois E., Duesterhoeft A., Duncan M., Flocth M., Fortin N., Friesen J.D., Fritz C., Goffeau A., Hall J., Hebling U., Heumann K., Hibbert H., Hillier L., Amicke-Smith S., Hyman R., Johnston M., Kalman S., Kleine K., Amarathe R., Messenguy F., Mewes H.-W., Mirtipati S., Moestl D., Amarathe R., Messenguy F., Mewes H.-W., Mirtipati S., Moestl D., Amarathe R., Moll T.W., Purnelle D., Schafer M., Scharfe M., Scherens B., Schramm S., Schraeder M., Scharfe M., Acherens B., Schramm S., Schraeder M., Scharfe M., Walsh S., Wannubutt R., Wang Y., Wedler F., Vissers S., Voss H., Walsh S.W., Zollner A., Vo D.H., Hani J.; Meller H., Winnett E., Marken, 2011ner A., Vo D.H., Hani J.; Marken, 2011ner A., Vo D.H., Hani J.; Minnett E., Minnett E., Minnett E., Minnett E., Minner, S., Marken, 2011ner A., Wo D.H., Hani J.; Minnett E., Minne
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Lindqvist Y., Schneider G., Ermler U., Sundstroem M.;
"Three-dimensional structure of transketolase, a thiamine diphosphate
dependent enzyme, at 2.5-A resolution.";
EMBO J. 11:2373-2379(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94231561; PubMed=8176731;
Nikkola M., Lindqvist Y., Schneider G.;
"Refined structure of transketolase from Saccharomyces cerevisiae at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "His103 in yeast transketolase is required for substrate recognition and catalysis.";
Eur. J. Biochem. 233:750-755(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MUTAGENESIS OF HIS-102.
MEDLINE=96085137; PubMed=8521838;
wixner C., Meshalnika L., Nilsson U., Baeckstroem S., Lindqvist Y.,
Schneider G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUTAGENESIS OF HIS, AND X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS). MEDLINE=98062276; PubMed=939829; Wikner C., Nilsson U., Meshalkina L., Udekwu C., Lindqvist Y., Schneider G.; aldentification of catalytically important residues in yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92253546; PubMed=1812485;
Nixon P.F., Duggleby R.G.;
"The N-terminal amino acid sequence of yeast transketolase.";
Protein Seq. Data Anal, 4:325-326(1991)...
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or send an email to license@isb-sib.ch)
                                                               EMBL; J02459; AAA96596.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alpha 4).
PAS-4 OR C36B1.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1995
01-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YEAST
                                                                                                                                                                       SEQUENCE
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P40082;
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PSA7_CAEEL
ID PSA7_C
DT 06-0CT
DT 16-0CT
DT 16-0CT
DT 15-JUN
DE PIOLEA
GN PAS-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YEWS_YEAST
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S X R R C C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROBABLE.
HA-AA,FV, 1. LOSS OF ACTIVITY.
MA. -> RS (IN REF. 1).
WSQMRMNPTNPDWINNDRFVLSNGHAVALLYSM -> GESN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RQNLPQLEGSS -> PDKTCHNWKVAL (IN REF. 1).
SGKAPEVFKFFGFTPEGVAERAQKTIAFYKGDKLISPLKKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -> PVRHQKSSSSSVSPQKVLLKELKRPLHSIRVTS
                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00456; transketolase; 1.
Pfam; PF00456; transketolase; 1.
Pfam; PF02779; transketolase C: 1.
TIGRFAMs; TIGROA3; tktlase bact; 1.
PROSITE; PS00801; TRANSKETOLASE 1; 1.
PROSITE; PS00802; TRANSKETOLASE 2; 1.
Transferase; Thiamine pyrophosphate; Magnesium; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteriophage lambda.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
Lambda-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQA -> RQR (IN REF. 1).
LIKMTTTIGYGSLHA -> FDQNDHNHWLRFLRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36; DB 1; Length 679;
Pred. No. 54;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AHEPNQPKTGSTEIDLSCLTVTRSLCCIY
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L -> LVLPIL (IN REF. 1).
D -> S (IN REF. 1).
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MEDLINE=83189071; PubMed=6221115;
Sanger F., Coulson A.R., Hong G.F., Hill D.F., Peter Sanger F., Coulson A.R., Hong G.F., Hill D.F., Peter "Nucleoride sequence of bacteriophage lambda DNA.";
J. Mol. Biol. 162:729-773(1982).
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21-JUL-1986 (Rel. 01, Last sequence update)
01-NOV-1988 (Rel. 09, Last annotation update)
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SGD, S0006278; TKL1.
InterPro; IPR000360; Transketolase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
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679
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                                                                                               PDB; 1TRK; 30-APR-94.
PDB; 1TKA; 30-NOV-94.
PDB; 1TKA; 30-NOV-94.
PDB; 1TKC; 30-NOV-94.
PDB; 1NGS; 12-FEB-97.
PDB; 1AYO; 13-MAX-98.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3D-structure.
INIT_MET
ACT_SITE 1
                                                               $21067;
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Y64 LAMBD
IND TAMBD
DT 21-JU

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=S288C / AB972;
Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M. Chung E., Duncan M., Guzman E., Hartzell G., Hunicke-Smith S., Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D., Hyman R., Rayser A., Namath A., Norgren R., Oefner P., Oh C., Petel F.X., Roberts D., Schramm S., Shogren T., Smith V., Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.; Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSAT CREEL STANDARD; FK1; 400 ..... 095005; 1400, Created) 140-CT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annocation update) Proteasome subunit alpha type 7 (EC 3.4.25.1) (Proteasome subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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01-FEB-1995 (Rel. 31, Last annotation update)
Hypothetical 15.4 kDa protein in GLC7-GDI1 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35; DB 1; Length 130;
Pred. No. 16;
2; Mismatches 2; Indels
                                                                                                                 Score 35; DB 1; Length 64;
Pred. No. 7.9;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
SEQUENCE 130 AA; 15421 MW; 795C1E2348F47234 CRC64;
                                                           CFBA2CBCAD4E3C0F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 AA
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                                                                                                                 Similarity 66.7%; 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U18916; AAC03233.1; -. SGD; S0000937; YER135C.
                                                           7083 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Conservative
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                                                                                                                                                                                                                                                                                                    5 GAYYRFRLV 13
                               l protein.
64 AA; 70
PIR; A04398; Q1BP2L.
Hypothetical proteir
                                                                                                                    Query Match
Best Local Similarity
Matches 6; Conserv
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us-10-007-790-7.rsp

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Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                   344 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhodobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RHOCA
                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P42447;
                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 17
RECA_RHOCA
ID RECA_R
    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                     Lennard N.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE PROTEASONE IS A MULTICATALYTIC PROTEINASE COMPLEX WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PERTIDES WITH ARG, PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT NEUTRAL OR SLIGHTLY BASIC PH. THE PROTEASOME HAS AN ATP-DEPENDENT PROTEOLYTIC
                                                                                                                                                                                                                         proteolytic pathway.
SUBINIT: THE PROTEASOME IS COMPOSED OF AT LEAST 15 NON IDENTICAL
SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
               Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99310339; PubMed=10382966;
Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
Jin-no K., Takahashi M., Sekine M., Baba S.I., Ankai A., Kosugi H.,
Hosoyama A., Fukui S., Magai Y., Nishijima K., Nakazawa H.,
Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity). SIMILARITY: BELONGS TO PEPTIDASE FAMILY TIA.
                                                                                                                                                                       ACTIVITY.
CATALYTIC ACTIVITY: Cleavage at peptide bonds with very broad
                                                                                                                                                                                                             PATHWAY: Involved in an ATP/ubiquitin-dependent non-lysosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.4%; Score 35; DB 1; Length 253;
85.7%; Pred. No. 31;
1ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00227; proteasome; 1.
PROSITE; PS00388; PROTEASOME A; 1.
Proteasome; Hydrolase; Protease.
SEQUENCE 253 AA; 28239 MW; 345078EDBE908EDC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000 (Rel. 39, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) 50S ribosomal protein L3P. RPL3P OR APE0227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEROPS, T01.974; -. WormPep, C36B1.4; CE05371.

InterPro; IPR000426; Proteasome A.

InterPro; IPR001353; Protsme_protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
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NCBI_TaxID=56636;
                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z80215; CAB02269.1; -. HSSP; P40303; 1RYP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 85.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
 Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 SGAYYEY 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SGAYYRY 7
                                                               SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aeropyrum pernix
                                                                                                                                                                                                  specificity.
                                        NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                   SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RL3 AERPE
Q9YFM2;
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RESULT 16
RIJ ARRPE
AC Q9YFM
DT 30-MA
DT 16-OC
BE 50S r
GN REPL3P
CO DESUL
CO DESUL
CO DESUL
RN (1)
RP SEQUE
RC STRAI
RX KAWAR
RA HJD-D
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Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
"Complete genome sequence of an aerobic hyper-thermophilic
crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
-i- SIMILARITY: BELONGS TO THE L3P FAMILY OF RIBOSOWAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
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Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                355 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00297; Ribosomal L3; 1.
ProDom; PD001374; Ribosomal L3; 1.
PROSITE; PS00474; RIBOSOMAL L3; 1.
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MEDLINE=95331467; PubMed=7607398;
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Pfam; PF00154; recA; 1.
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283 AGGFLRYGVV 292
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PIR; S14930; S14930.
PIR; S26402; S26402.
PIR; A34425; A34425.
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CONFLICT
SEQUENCE
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PRINTS; PR00142; KECA.
PRODOM; PD000229; RECA.1.
PROSITE; PS00321; RECA.1; 1.
PROSITE; PS50162; RECA.2; 1.
PROSITE; PS50163; RECA.2; 1.
PROSITE; PS50163; RECA.2; 1.
DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
38 ATP (BY SIMILARITY).
30027 MW; 64E408A33A2DE77E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94145486; Pubmed=7906121;
Castronovo V., Kusaka M., Chariot A., Gielen J., Sobel M.;
Castronovo V., Kusaka M., Chariot A., Gielen J., Sobel M.;
Homeobox genes: potential candidates for the transcriptional control
of the transformed and invasive phenotype.";
Biochem. Pharmacol. 47:137-143(1994).
-! FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR AXIS.
BINDS TO THE DNA SEQUENCE 5'-AA[AT]TTTATTAC-3'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE=91288229; PubMed=1676505;
Lowney P., Corral J.C., Detmer K., Lebeau M.M., Deaven L.,
Lawrence H.J., Largman C.;
"A human Hox 1 homeobox gene exhibits myeloid-specific expression of
allernative transcripts in human hematopoietic cells.";
Nucleic Acids Res. 19:3443-3449 (1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shen W.-F., Largman C., Lowney P., Corral J.C., Detmer K., Hauser C.A., Simonitch T.A., Hack F.M., Lawrence H.J.; "Lineage-restricted expression of homeobox-containing genes in human hematopoletic cell lines.";
                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=90098876; PubMed=2574852;
Acampora D., D'Esposito M., Faiella A., Pannese M., Migliaccio Moralli F., Stornaiuolo A., Nigro V., Simeone A., Boncinelli E. "The human HOX gene family ":
Nucleic Acids Res. 17:10385-10402(1989).
                                                                                                                                                             ö
                                                                                                                              57.4%; Score 35; DB 1; Length 355; 75.0%; Pred. No. 43; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bradshaw H., Hinds K., Keppler D.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mi X., Winters J.L., Stevens D.B., Fleischman R.A.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 86:8536-8540(1989).
                                                                                                                                                                                                                                                                                 HXAA HUMAN STANDARD; PRT; 393 AA. P81260; 015949; 043605; 043100; 01010L.1993 (Rel. 26, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Homeobox protein Hox-AlO (Hox-11) (Hox-1.8) (PL): HOXALO OR HOXIH.
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MEDLINE=90046832; PubMed=2573064;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 319-384 FROM N.A.
                                                                                                                                             Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                 SGAWYSYG 306
                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                      1 SGAYYRYG 8
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-:- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1/PL1 (SHOWN HERE) AND 2/PL2;
ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- SIMILARITY: BELONGS TO THE ABD-B HOMEOBOX FAMILY.
-!- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A NUMBER OF FRAMESHIFTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 OLY-GEN 2 POLY-GEN 2 POLY-GEN 2 POLY-GEN 2 POLY-GEN 2 POLY-PRO. 215 POLY-PRO. 215 POLY-PRO. 378 POLY-PRO. 378 POLY-PRO. 378 POLY-PRO. 378 MONECOBOX. 299 MISSING (IN ISOFORM 2). 6 MSCSES -> MFCTRNVSQKGLSAPFAKLSHNNVMLGE (IN REF. 1). 6 G -> R (IN REF. 1). 6 G -> R (IN REF. 1).
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PRINTS; PR00024; HOMEOBOX.

ProDom; PD000010; Homeobox; 1.

SMART; SM00189; HOX; 1.

PROSITE; PS00027; HOMEOBOX 1; 1.

PROSITE; PS50071; HOMEOBOX 2; 1.

Homeobox; DNA-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.4%; Score 35; DB 1; Length 393; 60.0%; Pred. No. 48;
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L -> F (IN REF. 4).
R -> P (IN REF. 4).
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19.1011-1993 (Rel. 26, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
HOMEODOX protein HOX-A10 (HOX-1.8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 48;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AC004080; -; NOT ANNOTATED CDS.
EMBL; M30599; AAA36006.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X58430; CAB86198.1; ALT_FRAME
EMBL; AF040714; AAB96917.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                393 AA; 40536 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S69029; AAD14031.1;
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Genew; HGNC:5100; HOXA10.
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                                                                                                                                                                                                                                                                                         SEQUENCE OF 346-370 FROM N.A.

STRAIN=C57BL/6; TISSUE-Spleen;

MEDLINE=92073357; bubMed=1720547;

MEDLINE=92073357; bubMed=1720547;

AM WITCH M.T., Leckman J.F., Ruddle F.H.;

The foction of homeobox genes in development and evolution.";

The foct Natl Acad. Sci. US.A. 88:10711-10715(1991).

SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH SPRICTION: SEQUENCE. SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF A DEVELOUAR LOCATION: Nuclear.

-I- SUBCELLULAR LOCATION: Nuclear.

-I- ALTERNATIVE PRODUCTS: 2 ISOPORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCTS: 2 ISOPORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCTS TO THE MESENCHYME ALONG THE PROXIMAL-DISTAL AXIS.

-I- TISSUE SPECIFICITY: EXPRESSED IN THE DEVELOPING LIMB BUD WHERE IT ISSUE, BOTH FORMS FOUND IN KIDNEY BUT ONLY ISOFORM I IS EXPRESSED TO SHE MUSCLE.

-I- SUBCELOMMATAL STAGE: EMBRYONIC EXPRESSION INCREASES FROM DAY 9 TO DAY 12 AND THEN DECLINES TO DAY 15.

-I- STMILARITY: BELONGS TO THE ABD-B HOMEOBOX FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation—the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                 STRAIN=CD-1; TISSUE=Kidney;
MEDLINE=95;66244; PubMed=7862151;
MEDLINE=95;66244; PubMed=7862151;
Benson G.V., Nguyen T.-H.E., Mass R.L.;
"The expression pattern of the murine Hoxa-10 gene and the sequence recognition of its homeodomain reveal specific properties of Abdominal B-like genes.";
Mol. Cell. Biol. 15:1591-1601(1995).
              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00024; HOMEOBOX.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
Homeobox; DNA-binding; Developmental protein; Nuclear protein; Transcription regulation; Alternative splicing.
                                                                                                                                                                                               SEQUENCE OF 325-384 FROM N.A.
MEDLINE=92073356; PubMed=1683707;
Sigh G., Kaur S., Stock J.L., Jenkins N.A., Gilbert D.J.,
Copeland N.G., Potter S.S.;
"Identification of 10 murine homeobox genes.";
Proc. Natl. Acad. Sci. U.S.A. 88:10706-10710(1991).
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GLN/PRO-RICH.
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POLY-GLY.
HOMEOBOX.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:96171; Hoxa10.
InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
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PIR, F38809, F38809.
PIR, F37290; F37290.
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90
144
222
274
384
musculus (Mouse)
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TRANSFAC; T01715; -
                                                                    SEQUENCE FROM N.A.
                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetics 146:531-540(1997).

-!- FUNCTION: COULD BE A PECTINOLYTIC ENZYME THAT HYDROLYSES THE ALPHA-L-RHAMNOPYRANOSYL.

GLYCOSLIDIC LINKAGE BY BETA-ELIMINATION, THEREBY GENERATING OLIGOSACCHARIDES TERMINATING AT THE NON-REDUCING END WITH A HEX-4-ENOPYRANOSYLLORDIC ACID RESIDUE.

-!- DEVELOPMENTAL STAGE: EXPRESSED PREPERENTIALLY DURING THE SEXUAL CYCLE AND ESSENTIAL FOR NORWAL SEXUAL DEVELOPMENT.

-!- SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 4.
                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative rhamnogalacturonaes precursor (EC 4.2.2..)
(Rhamnogalacturonan lyase) (RGase) (Ascus development protein 1) (Asd-
                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MarbinE-3731281, PubMed=9178004;
Nelson M.A., Merino S.T., Merzenberg R.L.;
"A putative rhamnogalacturonase required for sexual development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL,
PUTATIVE RHAMNOGALACTURONASE:
N-LINKED (GLCNAC. . ) (POTENTIAL)
N-LINKED (GLCNAC. . . ) (POTENTIAL)
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Pungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariales, Sordariaceae, Neurospora.
NCBI_TaxID=5141;
                                                                                        DB 1; Length 399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57.4%; Score 35; DB 1; Length 540; 70.0%; Pred. No. 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
MISSING (IN ISOFORM 2).

DSL -> MCQ (IN ISOFORM 2).

7529624FC6057042 CRC64;
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                                                                                                                                                                                                                                                                                                                                       540 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1124 AA
                                                                                        Score 35; DB
Pred. No. 48;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 65;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                            41415 MW;
                                                                                                                                                                                                                                                                                                                                                                                 15-DEC-1998 (Rel. 37, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58011 MW;
                                                                                        57.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lyase; Glycoprotein; Signal.
SIGNAL 1 23
                                                                 Query Match
Best Local Similarity 60...
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U70861; AAB39649.1;
                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
  305
308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            488 GAYRGYGEVY 497
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368
                                                                                                                                                                                                       37 GGYYAHGGVY 46
                                                                                                                                                                              2 GAYYRYGVVY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GAYYRYGVVY 11
  1
306
399 AA;
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540 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neurospora crassa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neurospora crassa.
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ID YPHG_ECOLI
AC P76585;
                                                                                                                                                                                                                                                                                                                                   ASD1 NEUCR
P78710;
VARSPLIC
VARSPLIC
SEQUENCE
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                                                                                                                                                                                                                                                                                         RESULT 20
ASD1_NEUCR
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Query Match 57.4
Best Local Similarity 63.6
Matches 7; Conservative
                                                        Yeast 12:1085-1090(1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 548 SGAFSRGGVLY 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SGAYYRYGVVY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1501 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                889
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CONFLICT
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                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                         STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          t
C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93173094; PubMed=8437567;
Servos J., Haase E., Brendel M.;
Gene SNQ2 of Saccharomyces cerevisiae, which confers resistance 4-nitroquinoline-Noxide and other chemicals, encodes a 169 kDa protein homologous to ATP-dependent permeases.";
Mol. Gen. Genet. 236:214-218(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales, Saccharomycetaceae; Saccharomyces.
                                                                     Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=S288c / AB972;
Murphy L., Richards C., Gentles S., Harris D., Barrell B.G.,
                                                                                                                                                                                                                                                                                                                                                                                                               Score 35; DB 1; Length 1124;
Pred. No. 1.3e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                         EA3F919BC8F491F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1993 (Rel. 27, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1501 AA
                                                                                                                                                                                                                                                                                                                                                                              protein; Complete proteome.
                                                                                                                                                                                                                                                                                                                                EMBL; AE000341; AAC75602.1; -.
 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                57.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNQ2 protein.
SNQ2 OR YDR011W OR YD8119.16
15-JUL-1998 (Rel. 36, Cree
15-JUL-1998 (Rel. 36, Last
16-OCT-2001 (Rel. 40, Last
Hypothetical protein yphG
                                                                                                                                                                                                                                                                                                                                           EcoGene; EG13468; yphG.
InterPro; IPR001440; TPR.
                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 7/...
7/...
7/. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00515; TPR; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGAVYPYGV 76
                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein SEQUENCE 1124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCAYYRYGV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                            Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4932;
                                                                                             NCBI_TaxID=562;
                                               (PHG OR B2549
                                                                                   Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNQ2 YEAST
ID SNQ2 YEAST
AC P32568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 22
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                                                                                                                                                                                                   CHARACTERIZATION, AND SEQUENCE OF 1243-1247.

MEDLINE=95355421; Pubbded=7629127;

MEDLINE=95355421; Pubbded=7629127;

MOYER ROWLEY W.S., Balzi E., Goffeau A.;

Identification and characterization of SNQ2, a new multidrug ATP binding casester transporter of the yeast plasma membrane.";

L. J. Biol. Chem. 270:18150-18157(1995).

RESISTANCE TO THE MUTAGENS 4-NITROQUINGLINE-N-OXIDE (4-NQO) AND TRAZIQUONE, AS WELL AS TO THE CHEMICALS SULPHOMETHURON METHYL PHEMBARE. COPIES: EXHIBITS

NUCLEOSIDE TRIPHOSPHATASE ACTIVITY.

C. I. SUBCELLULAR LOCATION: Integral membrane protein.

C. I. SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. PDR5 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
MEDLINE=97051598; PubMed=8896275;
Eide L.G., Sander C., Prydz H.;
"Sequencing and analysis of a 35.4 kb region on the right arm of
chromosome IV from Saccharomyces cerevisiae reveal 23 open reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
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168766 MW; 96BE3D30CCFB76AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interrio,
Interrio,
Interrio,
Interrio,
Pfam, PF00005, ABC_tran; 2.
Probom, PD000006; ABC_transportr; 2.
SMART, SM00382; AAA, Il
TIGRRAMS, TIGR00386; 3a01205; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
Interrior of Transmembrane; Glycoprotein; Transport.
PAGE ATTANSPORTER; 1.
Interrior of Transmembrane; Glycoprotein; Transport.
Potential.
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Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
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EMBL; Z48008; CAA88071.1; --
EMBL; X59566; CAA65203.1; --
EMBL; Z74307; CAA98831.1; --
PIR; S30918; S30918.
SGD; S0002418; SNQ2.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003585; PDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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ID FER7 METJA
AC Q58132;
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                                                                                                                                                                                                                                                                                                                                        Endocrinology 138:4123-4130(1997).
-!- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS; IT STIMULATES
THE SECRETION OF BOTH LUTEINIZING AND FOLLICLE-STIMULATING
                                                                                                                                                                                                                                  MEDLINE=97462693; PubMed=9322926;
Jimenez-Linan M., Rubin B.S., King J.C.;
Examination of guinea mail and promone-releasing hormone gene
reveals a unique decapeptide and existence of two transcripts in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00473; GNRH; 1.
Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
Placenta; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY).
AMIDATION (G-34 PROVIDE AMIDE GROUP) (BY
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Hexapoda,
Insecta, Pterygota, Neoptera, Paraneoptera, Hemiptera, Euhemiptera,
Heteroptera, Panheteroptera, Cimicomorpha, Reduviidae, Triatominae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GNRH-ASSOCIATED PEPTIDE I.
APPEARS TO BE ESSENTIAL FOR BIOLOGICAL
                              (Luteinizing hormone releasing hormone I) (Gonadotropin releasing hormone I) (GnH I) (Luliberin I); GnRH-associated peptide I). GNRHI OR GNRH OR LHRH.
                                                                                      Cavia porcellus (Guinea pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Caviidae, Cavia.
        Progonadoliberin I precursor (Contains: Gonadoliberin I (LHRH I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTIVITY (BY SIMILARITY).
PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB 1; Length 92; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACF74613F456D663 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL,
PROGONADOLIBERIN I.
GONADOLIBERIN I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     $
                                                                                                                                                                                                                                                                                                                                                                                                                                                  -! - SIMILARITY: BELONGS TO THE GNRH FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                  STRAIN=Hartley white; TISSUE=Hypothalamus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002012; GnRH.
InterPro; IPR004079; GonadoliberinI.
                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nitrophorin 1 precursor (NP1). Rhodnius prolixus (Triatomid bug).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR01541; GONADOLIBRNI.
PROSITE; PS00473; GNRH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF033346; AAB87688.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10279 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00446; GnRH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SGAYYRYGV
                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92 AA;
                                                                                                                                                      NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NP1 RHOPR
Q26239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhodnius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEPTIDE
PEPTIDE
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                                                                                                                                                                                                                                                                                                                         brain."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NP1_RHOPR
        g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                               MEDLINE=96337999; PubMed=868087;
Bult C.J., White O. Olsen G.J., Zhou L., Fleischmann R.D.,
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Karlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D.,
Geograph D., Tomb J.-F., Adams M.D., Glodek A.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoglagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.M., Hanna M.C.,
Cotton M.D., Roberts K.M., Smith H.O., Woese C.R., Venter J.C.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
Jannaschii.",
Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: FERREDOXINS ARE IRON-SULFUR PROTEINS THAT TRANSFER ELECTRONS PROBABLY IN THE CO-DEHYDROGENASE COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- COFACTOR: BINDS TWO 4FE-4S CLUSTERS (BY SIMILARITY)
-!- SIMILARITY: BELONGS TO THE BACTERIAL TYPE FERREDOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
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PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.
Hypothetical protein; Electron transport; Iron-sulfur; 4Fe-4S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 34; DB 1; Length 77;
Pred. No. 14;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BY
(BY
(BY
(BY
(BY
                                                                                                                              Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IRON-SULFUR 1 (4FE-4S) (B
IRON-SULFUR 1 (4FE-4S) (B
IRON-SULFUR 1 (4FE-4S) (B
IRON-SULFUR 2 (4FE-4S) (B
  01-NOV-1997 (Rel. 35, Created)
101-NOV-1997 (Rel. 35, Last sequence update)
101-NOV-2002 (Rel. 41, Last annotation update)
Putative ferredoxin MJ0722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 37, Created)
(Rel. 37, Last sequence update)
(Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001450; 4Fe4S_ferredoxin.
Pfam; PF00037; fer4; 2.
                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U67519; AAB98718.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.7%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8847 MW;
                                                                                                        Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SGAYYRYGVVY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 NGKYYAYDVEY 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1DUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome.
METAL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
01-NOV-1997 (Rel
01-NOV-1997 (Rel
15-JUN-2002 (Rel
                                                                                                                                                                   NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998 (
15-DEC-1998 (
30-MAY-2000 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGR; MJ0722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GON1 CAVPO
054713;
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Gaps

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Query Match

Matches

GON1\_CAVPO

RESULT 24

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METAL METAL METAL

METAL

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InterPro, IPR000243; Proteasome B.
(Proteasome subunit MB1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECUENCE OF 5-30.
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                                                                                        NCBI_TaxiD=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rissum=Skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      600306
                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions and its and the statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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P28074; 016242;
01-AUG-1992 (Rel. 23, Created)
01-AUG-1995 (Rel. 32, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
15-UNN-2002 (Rel. 41, Last annotation update)
15-UNN-2001 (Rel. 41, Last annotation update)
16-UNN-2002 (Rel. 41, Last annotation update)
17-UNN-2002 (Rel. 41, Last annotation update)
18-UNN-2002 (Rel. 41, Last annotati
                                                                                                                                                                                                                                                                                                                                                                                                       Ding X.D., Weichsel A., Andersen J.F., Shokhireva T.K., Balfour C., Pierik A., Averill B.A., Montfort W.R., Walker F.A.; Submitted (JUN-1998) to the Bod data bank.

-!- FUNCTION: HENR-BASED PROTEIN THAT DELIVER NITRIC OXIDE GAS (NO) TO THE VICTIM WHILE FEEDING, RESULTING IN VASOBILATION AND INHIBITION OF PLATELET AGGREGATION. ALSO BIND TIGHTLY TO HISTAMINE, WHICH IS RELEASED BY THE HOST TO INDUCE WOUND HEALING.
                                                                                          Champagne D.E., Nussenzveig R.H., Ribeiro J.M.C.;
"Purification, partial characterization, and cloning of nitric oxide-carrying heme proteins (nitrophorins) from salivary glands of the blood-sucking insect Rhodnius prolixus.";
J. Biol. Chem. 270:8691-8695(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                        Weichsel A., Andersen J.F., Champagne D.E., Walker F.A.,
Montfort W.R.;
"Crystal structures of a nitric oxide transport protein from a blood-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 34; DB 1; Length 207;
Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY: EXPRESSED BY THE SALIVARY GLANDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IRON (HEME PROXIMAL LIGAND).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4AB9EE803FDA0EB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NITROPHORIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                        AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002351; Nitrophorin.
Pfam; PF02087; Nitrophorin; 1.
Heme; Vasodilator; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement ((or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
                                                                                                                                                                                                                   K-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                    Nat. Struct. Biol. 5:304-309(1998)
                                                                              PubMed=7721773;
                                                                                                                                                                                                                                     TISSUE=Salivary gland;
MEDLINE=98206297; PubMed=9546222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22763 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, L39654; AAA74407.1; -. PDB; 1NP1; 27-MAY-98. PDB; 2NP1; 27-MAY-98. PDB; 3NP1; 12-AUG-98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.7%;
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SGNYYTFTVMY 134
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                                        SEQUENCE FROM N.A., AN
TISSUE=Salivary gland;
MEDLINE=95238361; Pubm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDB; 4NP1; 11-NOV-98
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      NCBI_TaxID=13249;
                                                                                                                                                                                                                                                                                                                                  sucking insect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ,
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 26
PSBS_HUMAN
1D PSBS_4
DT 01-AUG
DT 01-NOV
DT 15-JUN
DE PFOLESI
DE COMPLE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: The proteasome is composed of at least 15 non identical subunits which form a highly ordered ring-shaped structure. This subunit can be displaced by the equivalent immune-specific subunit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIJINE=55120465; PubMed=7820546; Belich M.P., Glynne R.J.; Senger G., Sheer D., Trowsdale J.; Periceasome components with reciprocal expression to that of the MHC-encoded LMP proteins."; Curr. Biol. 4:769-776(1994).
                                                                                                                                                                        Akiyama K.-Y., Yokota K.-Y., Kagawa S., Shimbara N., Tamura T., Akioka H., Nothwang H.G., Noda C., Tanaka.K., Ichihara A.; "cDNA cloning and interferon gamma down-regulation of proteasomal subunits X and Y.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- PATHWAY: Involved in an ATP/ubiquitin-dependent non-lysosomal
                           Craniata, Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Relationships among the subunits of the high molecular weight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=90167111; PubMed=2306472;
Lee L.W., Moomaw C.R., Orth K., McGuire M.J., DeMartino G.N.,
Slaughter C.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Abdulla S., Beck S., Behlich M., Jackson A., Nakamura T.,
Trowsdale J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Cytoplasmic and nuclear. SIMILARITY: BELONGS TO PEPTIDASE FAMILY T1B.
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EMBL; D29011; BAA06097.1; -.
EMBL; V05586; CAA64838.1; ALT_INIT.
                                                                                                                                                                     MEDLINE=94345396; PubMed=8066462;
                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BC004146; AAH04146.1;
                                                                                                                                                                                                                                                                                                                   Science 265:1231-1234(1994).
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HSSP; P30656; 1RYP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (APR-1996)
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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modified and this statement is not removed.
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Best Local Similarity
Matches 6; Conserv
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Xylella fastidiosa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSES_MOUSE STANDARD, PRT; 209 AA.
055234; Q9R1P2;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 41, Last annotation update)
17-JUN-2002 (Rel. 41, Last annotation update)
18-JUN-2002 (Rel. 41, Last annotati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Elenich L.A., Nandi D., Kent E.A., McCluskey T.S., Cruz M., Iyer M.N., Woodward E.C., Conn C.W., Ochoa A.L., Ginsburg D.B., Monaco J.J.;
"The complete primary structure of mouse 20S proteasomes.";
Immunogenetics 49:835-842(1999)
-!- FUNCTION: THE PROTEASOME IS A MULTICATALYIC PROTEINASE COMPLEX WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH ARG, PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT NEUTRAL OR SLIGHTLY BASIC PH. THE PROTEASOME HAS AN ATP-DEPENDENT PROTEOLYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: The proteasome is composed of at least 15 non identical subunits which form a highly ordered ring-shaped structure. This subunit can be displaced by the equivalent immune-specific subunit
                                                                                                                                                                                                                                                                                             Gaps
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MEDLINE=28044207; PubMed=9382924;
Kohda K., Matsuda Y., Ishibashi T., Tanaka K., Kasahara M.;
"Structural analysis and chromosomal localization of the mouse Psmb5
gene coding for the constitutively expressed beta-type proteasome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: Cleavage at peptide bonds with very broad
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                                                                                                                          PROTEASOME SUBUNIT BETA TYPE
                                                                                                                                             I -> F (IN REF. 5).
A -> G (IN REF. 3).
T -> S (IN REF. 3).
; 480BBC96FC478DB4 CRC64;
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          Pfam; PF00227; proteasome; I.PRINTS; PR00141; PROTEASOME.
PRINTS; PR00141; PROTEASOME.
PROSITE; PS00854; PROTEASOME B; I.
Proteasome; Hydrolase; Protease; Zymogen.
InterPro; IPR001353; Protsme_protease.
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MEDLINE=99367391; PubMed=10436176;
                                                                                                                     208
30 I
54 A
103 T
22897 MW;
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Matches 6; Conservative
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103
208 AA;
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
3-deoxy-D-manno-octulosonic acid kinase (EC 2.7.1.-) (KDO kinase)
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PROSITE; PS00854; PROTEASONE B; 1.
Proteasome; Hydrolase; Protease; Zymogen.
PROPEP BY SIMILARITY.
S 209 PROTEASONE SUBUNIT BETA TYPE
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                                                                                  or send an email to license@isb-sib.ch)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:1194513; Psmb5.
InterPro; IPR000243; Proteasome B.
InterPro; IPR001353; Protsme_protease.
Pfam; PF00227; proteasome; 1.
                                             entities requires a license agreement
                                                                                                                                                                EMBL; AB003306; BAA24917.1; ALT_INIT.

EMBL; AB003304; BAA24916.1; ALT_INIT.

EMBL; AF060091; AAD50536.1; ALT_INIT.

HSSP; P30656; 1RYP.

MEROPS; T01.012; -.
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MEDLINE=20365717; Pubmed=10910347;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
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EMBL; AE007452; AAK75662.1;
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P27129;
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                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the between the Swiss Institute of Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                    -! - FUNCTION: ATP-dependent phosphorylation of 3-deoxy-D-manno-octulosonic acid at the 4-OH position (By similarity).
-! - PATHWAY: Lipopolysaccharide core biosynthesis.
-! - SUBCELLULAR LOCATION: Membrane-bound (By similarity).
-! - SIMILARITY: BELONGS TO THE KDKA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                EMBL, AE004029; AAF84952.1; -
Lipopolysaccharide biosynthesis; Transferase; Kinase; Membrane;
ATP-binding; Complete proteome.
ACT SITE 185 185 POTENTIAL.
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-!- CATALYTIC ACTIVITY: Succinyl-CoA + L-homoserine = CoA + O-succinyl-L-homoserine.

-!- PATHWAY: Methionine Dosynthesis; HTS variant; first step.

-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

-!- SIMILARITY: BELONGS TO THE HTS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34; DB 1; Length 259;
Pred, No. 48;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Homoserine O-succinyltransferase (EC 2.3.1.46) (Homoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pneumoniae.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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54.5%;
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les 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 AACYVRYGVQY 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transsuccinylase) (HTS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        META OR SP1576.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pneumoniae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local 9
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META_STRPN
AC 097PM95)
DT 15-JUN-
DT 15-JUN-
DE HOMOSED
GN META OI
OC STREPTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94316500; PubMed=8041620; Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.; Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.; "Analysis of the Escherichia coli genome. V. DNA sequence of the region from 76.0 to 81.5 minutes."; Mucleic Acids Res. 22:2256(1994).
-! - CATALYTIC ACTIVITY: UDP-glucose + lipopolysaccharide = UDP + D-
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RYKHLLVQHHYISGIIAGVCYLCRKYYRK -> DINIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EcoGene; EG11353; rfaJ.
Interpro: IPR002495; GT_8.
Pfam; PP01501; Glyco transf 8; 1.
Lipopolysaccharide blosynthesis; Glycosyltransferase; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pradel E., Parker C.T., Schnaltman C.A., "Structures of the rfaB, rfaI, rfaJ, and rfaS genes of Escherichia coli K-12 and their roles in assembly of the lipopolysaccharide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Proteobacteria, gamma subdivision; Enterobacteriaceae,
                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                           DB 1; Length 314;
58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1992 (Rel. 23, Created)
01-OCT-1994 (Rel. 30, Last sequence update).
15-JUN-2002 (Rel. 41, Last annotation update)
Lippopolysaccharide 1,2-glucosyltransferase (EC 2.4.1.58).
RFAJ OR WAAJ OR B3626.
                                                                                                                                                                                                                                                      2; Indels
                                                                                                            142 POTENTIAL..
36926 MW; 9CA22016E26A4F24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IN REF. 1).
338 AA; 39040 MW; 819428EA13F1959A CRC64;
                                                 Methionine biosynthesis; Transferase; Acyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glucosyl-lipopolysaccharide.
-!- PATHWAY: Lipopolysaccharide core biosynthesis.
-!- SIMILARITY: TO S.TYPHIMURIUM RFAJ AND TO RFAI.
                                                                                                                                                                                              Score 34; DB 1
Pred. No. 58;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            338 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=K12; MEDLINE=92325066; PubMed=1624461; Schnaitma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteriol. 174:4736-4745(1992)
TIGRFAMB; TIGR01001; metA; 1.
                                                                                                                                                                                              55.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M80599; AAA24087.1; -. EMBL; U00039; AAB18603.1; -.
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                                                                                                                                                                 Query Match
Best Local Similarity 66...
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  338
                                                                                                                                                                                                                                                                                                                                                                     147 AGLYLRYGV 155
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                                                                                                                                      314 AA;
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                                                                                                                                                                                                                                                                                                             1 SGAYYRYGV
                                                                                  Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli
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295 AGGFVRYGIV 304
                                                                                                                                   09V\overline{X}\overline{Z}_2;
                                                                                                   G10B_DROME
                                                                               RESULT 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    She Qi. Singh R. K., Confaloneri F., Zivanovic Y., Allard G.,
Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
De Moors A., Erauso G., Fletcher C., Gordon P.M. K.,
Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
Garrett R.A., Ragan M.A., Sonsen C.W., Van der Oost J.;
"The complete genome of the crenarchaeon Sulfolobus solfataricus P2.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Charlebois R.L., Singh R.K., Chan-Weiher C.C.-Y., Allard G., Chow C., Confalonieri F., Curtis B., Duguet M., Erauso G., Faguy D., Gaasterland T., Garrett R.A., Gordon P., Jeffries A.C., Kozera C., Kushwaha N., Lafleur E., Medina N., Peng X., Penny S.L., She Q., St Jean A., van der Oost J., Young F., Zivanovic Y., Doolittle W.F., Ragan M.A., Sensen C.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Gene content and organization of a 281-kbp contig from the genome of the extremely thermophilic archaeon, Sulfolobus solfataricus P2.";
                                                                                                                                                                                                                                                                                                                                                                                   Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
SIMILARITY: BELONGS TO THE L3P FAMILY OF RIBOSOMAL PROTEINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.7%; Score 34; DB 1; Length 351; 50.0%; Pred. No. 64; 1:ve 3; Mismatches 2; Indels
                       DB 1; Length 338;
                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06D86BA37FA38008 CRC64;
                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Last sequence update)
15-UTO-2002 (Rel. 41, Last annotation update)
Solosomal protein Lipp.
RPLipp OR RPLia OR SSO0719 OR C10_011.
                   Score 34; DB 1
Pred. No. 62;
1; Mismatches
                                                                                                                                                                                                                                   351 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ribosomal protein; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=ATCC 35092 / DSM 1617 / P2;
MEDLINE=21332296; PubMed=11427726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=ATCC 35092 / DSM 1617 / P2;
MEDLINE=20165948; Pubmed=10701121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE006697; AAK41018.1; -. InterPro; IPR000597; Ribosomal L3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00297; Ribosomal L3; 1.
ProDom; PD001374; Ribosomal L3; 1.
PROSITE; PS00474; RIBOSOMAL L3; 1.
                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39670 MW;
               55.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Y18930; CAB57584.1; -.
                                                       Conservative
                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                   Sulfolobus solfataricus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome 43:116-136(2000).
                                                                                                                                   176 GOYFNSGVVY 185
                                                                                               GAYYRYGVVY 11
Query Match
Best Local Similarity
--hea 6; Conserv?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the extremely
                                                                                                                                                                                                                               RL3 SULSO
Q9UXA8;
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RA Adams M.D.; Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D.; Celniker S.E., Holt R.A., Evans C.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA Guton G.G., Wortnan J.R., Yandell M.D., Zhang O., Chen L.X., Braton G.G., Wortnan J.R., Yandell M.D., Zhang O., Chen L.X., RA Batan M. H.-J., Andrews-Pfannkoch C., Baldwin D., RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., RA Beeson K.Y., Basud A., Baxendala J., Baytaktarollu L., Beasley E.M., RA Beeson K.Y., Banos P.V., Berman B.P., Bhandari D., Bolchakov S., Borkova D., Borchan M.R., Bouck J., Broketein P., Brottier P., Ra Burkys D., Bullke C., Davengoll L., Boasley E.M., RA Berty J.M., Cawley S., Dallke C., Davengort L.B., Davies P., Acharty J.M., Cawley S., Dallke C., Davengort L.B., Davies P., Barky D., Br. Delcher A., Daveng Z., May A.D., Davies P., Dodgon K., Doup L.E., Downes M., Dugan-Rocha S., Pleistchmann W., RA Berlow B., Gabriellan A.E., Gabriell J.H., Gu Z., Galbart W.M., Glasser K., A Hostin D., Houston K.J., Evalesky A.B., Liu K., Mattei B., McIntosh T.C., McLeod M.P., McGorg F., Gorrell J.H., Gu Z., Glan P., Harris M., Andrei B., McIntosh T.C., McLeod M.P., McRock M., Moy M., Wurphy B., Murphy L., Muzny D.M., Nelson D.L., Andrei B., McIntosh T.C., McLeod M.P., Mort S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Andrei B., McIntosh T.C., McLeod M.P., Puri V., Rese M. A., Shork M., Wassaker R.D.C., Scheeler F., Shen H., Shork S., Shen S., Pollard J., Wang X., Mang X., Wassariano D.R., Was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: Probable role in the gustatory response.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO FAMILY DR-TR OF G-PROTEIN COUPLED
RECEPTORS.
                                                                 Last sequence update)
Last annotation update)
373 AA
                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20196006; PubMed=10731132;
                                                                                                                 Putative gustatory receptor 10b.
GR10B OR CG12622.
                                         EMBL; AE003486; AAF48041.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 287:2185-2195(2000)
STANDARD;
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                              Muscomorpha; Ephy
NCBI_TaxID=7227;
DROME
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Gaps

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Best Local Similarity 50.0 Matches 5; Conservative

1 SGAYYRYGVV 10

8

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SEQUENCE FROM N.A.
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P36584;
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Matches
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 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21648401; PubMed=11859360;
WebLine=21648401; PubMed=11859360;
Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Squrosd V., Gwilliam R., Hayles J., Baker S., Basham D., Bowman S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Genles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Hornsby T., Howarth S., Horlber E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., A. Money P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Olver K., O'Neil S., Barrson D., Quali M.A., Rabbinowitsch E., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor K., Taylor K., Taylor K., Taylor K., Malsh S., Walsh S.V., Warren T., Whitehead S., Weltjens I., Vanstreels E., Rieger M., Schaefer M., Meller Auer S., Abeltjens I., Vanstreels E., Rieger M., Schaefer M., Meller Auer S., Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94237476; PubMed=8181745;
Liebich I., Kohler G., Witt I., Gross T., Kaufer N.F.;
"Two genes encoding ribosomal protein L3 of Schizosaccharomyces pombe
and their proximal promoter regions.";
Gene 142:119-122(1994).
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                               ö
                   Pfam, PF02949; 7tm 6; 1.
Hypothetical protein; Receptor; G-protein coupled receptor;
                                                                                                                                                                                                                                                        Score 34; DB 1; Length 373
                                                                                                                                                                                                                                                                               2; Indels
                                         Glycoprotein; Multigene family.

SETRACELLULAR (POTENTIAL).
                                                                                                                                                                                  6 (FOTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                             57CF481BF6139B14 CRC64;
                                                                                     2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                           3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                      N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
62 ribosomal protein L3-A.
                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                   Pred. No
                                                                                                                                                                                                                                    44030 MW;
                                                                                                                                                                                                                                                         55.7%;
FlyBase; FBgn0030297; Gr10b.
InterPro; IPR004117; 7tm_6.
                                                                                                                                                                                                                                                                   62.5%;
                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                29
103
1132
1132
1170
1191
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3350
3371
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                                                                                                                                                                                                                                                                                                                       YYRYAMTY 66
                                                                                                                                                                                                                       192
373 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schizosaccharomyces
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 5; Conserv
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                                            ransmembrane;
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P40372;
                                                      DOMAIN
TRANSMEM
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TRANSMEM
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DOMAIN
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DOMAIN
TRANSMEM
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SEQUENCE
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RL3A_SCHPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Coffeau A., Cadieu E., Dreano S., Gloux S.; Lelaure V., Mortler S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.; The genome sequence of Schizosaccharomyces pombe.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liebich I., Kohler G., Witt I., Gross T., Kaufer N.F.;
"Two genes encoding ribosomal protein L3 of Schizosaccharomyces pombe and their proximal promoter regions.";
Gene 142:119-122(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Wood V., GAilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgourcos V., GAilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Brocks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Genliss M., Gobbe A., Hamin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- MISCELLANEOUS: THERE ARE TWO GENES FOR L3 IN S.POMBE.
-!- SIMILARITY: BELONGS TO THE L3P FAMILY OF RIBOSOMAL PROTEINS.
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Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 34; DB 1;
Pred. No. 71;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
62 ribosomal protein L3-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000597; Ribosomal_L3.
Pfam; PF00297; Ribosomal_L3; 1.
PROSITE; PS00474; RIBOSOMAL_L3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94237476; PubMed=8181745;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U00798; AAA19655.1; -. EMBL; Z98849; CAB11503.1; -.
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Best Local Similarity
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RESULT 36
TKT2_YEAST
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James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Money P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Alver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitech E., Skutherford K., Rutter S., Sanders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Arylor K., Taylor K., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritzc C., Holzer E., Mosetl D., Hilbert H., Berzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Ber P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerrutti L., Lowe T., Moccombie W.R., Paulsen I., Potashkin J., Marke J., Marke J., Markel J., Markel J., Lowellow T., Woods Combie W.R., Paulsen I., Potashkin J., Lowellow J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P., The Genome sequence of Schizosaccharomyces pombe.";

Intra H. Stillarin S. There Are TWO Genes FOR LISIN S.POMBE.

Intra H. SIMILARITY: BELONGS TO THE LISP FAMILY OF RIBOSOMAL PROTEINS.
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Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
-!- CATALNTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyceraldehyde 3-phosphate = D-ribose 5-phosphate + D-xylulose 5-phosphate.
-!- COFACTOR: THIAMINE PYROPHOSPHATE. REQUIRES MAGNESIUM IONS FOR CATALYTIC ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
17-0CT-2001 (Rel. 40, Last annotation update)
18-0CT-2001 (Rel. 40, Last annotation update)
18-0CT-2001 (TR 1)
18-0CT-2001 (Yeast)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; LFRUNCOSOMAL L3; 1.
PERM: PF00297; Ribosomal L3; 1.
Ribosomal protein; Multigene family.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AL590902; CAC37425.1; -. PIR; S25592; S25592.
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GGFVRYGVV 316
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nes 6; Conserv
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Mannhaupt G., Stucka R., Ehnle S., Vetter I., Feldmann H.;
"Analysis of a 70 kb region on the right arm of yeast chromosome II.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schaaff-Gerstenschlager I., Mannhaupt G., Vetter I., Zimmermann F.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyceraldehyde 3-phosphate = D-ribose 5-phosphate + D-xylulose 5-phosphate. -!- COFACTOR: THIAMINE PYROPHOSPHATE. REQUIRES MAGNESIUM IONS FOR CATALYTIC ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "TKL2, a second transketolase gene of Saccharomyces cerevisiae.
Cloning, sequence and deletion analysis of the gene.";
Eur. J. Biochem. 217:487-492(1993).
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                                                                                                                                                                                                                                                        Score 34; DB 1; Lengtn o...
Pred. No. 1.2e+02;
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-I-SUBMINIT: HOMODIMER (BY SIMILARITY).
-I-SIMILARITY: BELONGS TO THE TRANSKETOLASE FAMILY.
-!- SUBUNIT: HOMODIMER (By similarity).
-!- SIMILARITY: BELONGS TO THE TRANSKETOLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Transketolase 2 (EC 2.2.1.1) (TK 2).
TKL2 OR YBR117C OR YBR0912.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                        EMBL, AL033501; CAA21989.1; -.
HSSP; P23254; 1TRK.
InterPro; IPR000360; Transketolase.
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75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Feldmann H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TKT2 YEAST
P33315;
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15-JUN-2002 (Rel. 41, Last annoctation update)
Pullulanase precursor (EC 3.2.1.41) (Alpha-dextrin endo-1,6-alpha-
glucosidase) (Pullulan 6-glucanohydrolase).
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MEDLINE=87194626; PubMed=3155373;
Katsuragi N., Takizawa N., Murooka Y.;
"Entire nucleotide sequence of the pullulanase gene of Klebsiella
-!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Klebsiella aerogenes.
Bacteria; Proteobacteria; gamma subdivision, Enterobacteriaceae;
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J. Bacteriol. 169:2301-2306(1987).
-!- CATALYTIC ACTIVITY: Hydrolysis of (1->6)-alpha-D-glucosidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33.5; DB 1; Length 1090; Pred. No. 2.4e+02; 2; Mismatches 1; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 -> MATA (IN REF. 2).
240AE7DFB3FF1BD6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase; Glycosidase; Membrane; Lipoprotein; Signal
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N-ACYL DIGLYCERIDE.

BY SIMILARITY.

BY SIMILARITY.

R -> C (IN REF. 2).

V -> F (IN REF. 2).

V -> F (IN REF. 2).

V -> S (IN REF. 2).

G -> S (IN REF. 2).

N -> S (IN REF. 2).

T -> N (IN REF. 2).

D -> DGNP (IN REF. 2).

T -> N GNAP (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
                                                                                                                                                                                                                                EMBL, X52181; CAA36431.1; -.
EMBL, M12503; AAA55087.2; -.
EMBL, M29037; AAA61976.1; -.
PIR, A25025; A25025.
PIR, A32880; A32880.
PIR, S11823; S11823; S11823; INTERPRO; IPRO04661; Alpha_amylase.
InterPro; IPRO0461; Alpha_amylase.
InterPro; IPRO05323; PUD.
                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00128; alpha-amylase; 1.
Pfam; PF02922; isoamylase N; 1.
Pfam; PF03714; PUD; 1.
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1090 AA;
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P07811;
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PULA_KLEAE
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      and for commercial
                      entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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D'Enfert C., Pugaley A.P.;
D'Enfert C., Pugaley A.P.;
Mitabsiella pneumoniae puls gene encodes an outer membrane
lipoprotein required for pullulanase secretion.";
J. Bacteriol. 171:3573-3679(1989).
-!- CATALYTIC ACTIVITY: Hydrolysis of (1-x6)-alpha-D-glucosidic
linkages in pullulan and in amylopectin and glycogen, and the
alpha- and beta-limit dextrins of amylopectin and glycogen.
-!- SUBGUIT: HOWOTRIMER.
-!- SUBGUIT: HOWOTRIMER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1988 (Rel. 07, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Pullulanase precursor (EC 3.2.1.41) (Alpha-dextrin endo-1,6-alpha-
glucosidase) (Pullulan 6-glucanohydrolase).
                                                                                                                                                                                                                                                                                                                                                                                       Transferase, Thiamine pyrophosphate; Magnesium; Multigene family.
SEQUENCE 681 AA; 75029 MW; 84D7477916D136D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Klebsiella pneumoniae.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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J. Bacteriol. 164:639-645(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 34; DB 1; Length 681;
Pred. No. 1.2e+02;
1; Mismatches 2; Indels
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    Usage
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      modified and this statement is not removed.
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InterPro; IRR00366; Transketolase.
Pfam, PF00456; transketolase; 1.
Pfam; PF02779; transket pyr; 1.
Pfam; PF02779; transketolase C; 1.
TIGRRAMS; TIGR00232; trklase_bact; 1.
PROSITE; PS00801; TRANSKETOLASE 1; 1.
PROSITE; PS00802; TRANSKETOLASE 2; 1.
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MEDLINE=90205629; PubMed=2181242;
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MEDLINE=86033621, PubMed=3902792;
Chapon C., Raibaud O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.7%;
                                                                                    EMBL, X73532, CAA51937.1; -. EMBL, X78993, CAA55619.1; -. EMBL, Z35985, CAA85074.1; -.
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Best Local Similarity 66.7.7,
6; Conservative
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PIR; S34170; S34170.
HSSP; P23254; 1TRK.
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NCBI_TaxID=573;
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MEDLINE=94123988; PubMed=8293994;
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MEDLINE=85257433; PubMed=3926479;
   complex at 2.5-A resolution.";
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Best Local Similarity
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VTU3_DROME
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Watanabe H., Ohgi K., Irie M.;
Primary structure of a minor ribonuclease from Aspergillus saitoi.";
J. Biochem. 91:1495-1509(1982).
                                                       SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Guanyl-specific ribonuclease Ms (EC 3.1.27.3) (RNase Ms).
Apperglllus saitoi (Aspergillus phoenicis).
Eukaryota: Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Titchocomaceae, mitosporic Trichocomaceae; Aspergillus.
NCBL TAXID=5063;
linkages in pullulan and in amylopectin and glycogen, and the alpha- and beta-limit dextrins of amylopectin and glycogen.
                                                                                            SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
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Nonaka T., Mitsui Y., Irie M., Nakamura K.T.;
"Three-dimensional structure of ribonuclease Ms*3'-guanylic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
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BY SIMILARITY.
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W: FE7D9167CDACFD79 CRC64;
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Watanabe H., Ohgi K., Irie M.;
Unpublished results, cited by:
Unpublished results, Irie M.;
FEBS Lett. 283:207-209(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 AA.
                                                                                                                                                                                                                                                                                                                      PIR; A26879; A26879.
InterPro; IPR000441; Alpha_amylase.
InterPro; IPR004193; Isoamylase_N.
InterPro; IPR005123; PUD.
Pfam; PF00128; alpha-amylase; 1.
Pfam; PF00222; isoamylase_N; 1.
Pfam; PF0314; PUD; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
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                                                                                                                KNOWN AS THE ALPHA-AMYLASE FAMILY
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371 GAFYRYAMTVY 381
                                   SUBUNIT: HOMOTRIMER
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"Comparative analysis of the sequence and structure of two Drosophila melanogaster genes encoding vitelline membrane proteins."; Gene 136:121-127(1993)
                                                    ending in
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Eukaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Hexapoda,
Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera,
Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 105;
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01-057-1996 (Rel. 34, Last sequence update)
115-JUL-1999 (Rel. 38, Last annotation update)
WM34CA OR WM34C1.
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                                                                                                                                  STRAIN=Oregon-R;
MEDLINE=89665296; PubMed=3143615;
Scherer L.J., Harris D.H., Petri W.H.;
"Drosophila vitelline membrane genes contain a 114 base pair region
                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: A 38 AMINO ACIDS REGION (VM DOMAIN) IS CONSERVED IN DROSOPHILA VITELLINE MEMBRANE PROTEINS.
                                  "Isolation and chromosomal location of putative vitelline membrane genes in Drosophila melanogaster."; EMBO J. 4:147-153(1985).
Mindrinos M.N., Scherer L.J., Garcini F.J., Kwan H., Jacobs K.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VITELLINE MEMBRANE PROTEIN VM34CA.
Wh DOMAIN
A -> R (IN REF. 2).
7 2F06298E52005BFC CRC64;
                                                                                                                                                                                                                                                              -i- TISSUE SPECIFICITY: FOLLICLE CELLS.
-i- DEVELOPMENTAL STAGE: EXPRESSED DURING VITELLINE MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 33; DB 1; Length 119;
Pred. No. 33;
2; Mismatches 3; Indels
                                                                                                                                                                                                          of highly conserved coding sequence.";
Dev. Biol. 130:786-788(1988).
-!- FUNCTION: MAJOR EARLY EGGSHELL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal; Structural protein; Eggshell SIGNAL 1 19
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119 AA; 11934 MW;
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Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                SEQUENCE OF 69-106 FROM N.A.
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Search completed: July 18, 2003, 15:07:17 Job time : 8.82 secs :||| :| || 102 AGAYSQYAPVY 112 g

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O23165 arabidopsis Q91eb4 nicotiana p Q94k88 arabidopsis

Q9PUS4 Q9SE35 Q06328 Q23165 Q9LEB4 Q94K88

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**QBWUB4 Q8TE35** 2913J5 **095YI8** 

014520 homo sapien 026815 methanobact 08wub4 homo sapien 0813j5 clostridium 09513j5 clostridium 09513j8 plasmodium 088611 oryza sativ 09wvg5 mus musculu 09wvg5 homo sapien 096hx2 homo sapien 096x2 homo sapien 08wvu2 homo sapien

Q8S6N1 Q9WVQ5 Q9Y318

Q8SV24. Q8REE0

Q96HK2 Q96GX9 Q8WVU2

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044148 Q9ZKJ8

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Length 306 Indels

Score 46; DB 16; Pred. No. 2.8;

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SEQUENCE FROM N.A.
STRAIN=ATCS 824 / DSM 792 / VKM B-1787;
MEDLINE=21359325; PubMed=11466286;
Noblling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Noblling J., Breton G., Ombois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Koonin E.V., Snith D.R.;
"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";
J. Bacteriol. 183:4823-4838 (2001).
EMBL; AR007697; AAK79850.1;
                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
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01-OCT-2001 (TrEMBLrel. 18, Last seq
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87.5%;
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O91fm9 chilo iride

O90rgd drosophila

O9vzm1 thermotoga

O9vxm3 thermotoga

O9v474 schizosacch

O96281 plasmodium
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O82039 petunia hyb
O82422 hordeum vul
O77309 plasmodium
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Med. Microbiol. Immunol. 175:43-53(1986).
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63.6%;
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Query Match
Best Local Similarity 63.6
Matches 7; Conservative
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213 TGSYYSYTVVY 223
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A Galagan J.B., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
A FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
A Linton L., Maylor J., Stange-Thomann N., DeArellano K., Johnson R.,
Linton L., McKernan F., Talamas J., Tirrell A., Ye W.,
A Linton L., McKernan F., Talamas J., Tirrell A., Guss A.M.,
Hedderich R., Ingarm-Smith C., Kuettner H.C., Krzycki J.A.,
A Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
A Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
A Metcalf W.W., Birren B.,
The genome of Methanosarcina acetivorans reveals extensive metabolic
and physiological diversity.",
EMBL, AE011103; AAM07265.1; -.
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Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,
Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
Siguare P., Thebault P., Whalen M., Wincker P., Levy M.,
Weissenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
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                                                                                                                                                    Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
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SEQUENCE 942 AA; 105833 MW; 6A5801A0566B47FB CRC64;
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InterPro; IPR000567; SBP bac_1.
Pfam; PF01547; SBP bactefial 1; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 580 AA; 64531 MW; 18CE800E37CAD51F CRC64;
                                                 01-JUN-2002 (TrEMBLrel. 20, Last Sequence update) Hypothetical signal peptide protein RSc3051. RSC3051. RASJOST. RASJOST.
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MEDLINE=21929760; PubMed=11932238;
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NCBI_TaxID=2214;
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Matches 7; Conservative
    PRELIMINARY;
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MEDILINE-93118-244; PubMed=1475907;
Sonntag K.C., Darai G.;
"Characterization of the third origin of DNA replication of the genome
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Fischer M., Schnitzler P., Delius H., Darai G.;
"Identification and characterization of the repetitive DNA element in
the genome of insect iridescent virus type 6.";
Virology 167:485-496(1988).
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Lorbacher de Ruiz H., Gelderblom H., Hofmann W., Darai G.;
"Insect iridescent virus type 6 induced toxic degenerative hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Identification and mapping of origins of DNA replication within the DNA sequences of the genome of insect iridescent virus type 6.1; Virus Genes 6:19-32(1992).
                                                                              Gaps
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Handermann M., Schnitzler P., Rosen-Wolff A., Raab K., Sonntag K.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDINE=87321126; PubMed=2820141; Schiz H., Scholz J., Schizzler P., Soltau J.B., Fischer M., Reisner H., Scholz J., Delius H., Darai G.; Molecular cloning and physical mapping of the genome of insect iridescent virus type 6: further evidence for circular permutation the viral genome "; Virology 160:66-74(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Delius H., Darai G., Fluegel R.M.;
"DNA analysis.of insect iridescent virus 6: evidence for circular
permutation and terminal redundancy.";
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Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus.
VCBI_TaxID=10488;
       Length 942
                                                                          Indels
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Score 41; DB 17;
Pred. No. 78;
2; Mismatches 2;
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                                                                              "Identification of genes encoding zinc finger proteins, non-histone chromosomal HMG protein homologue, and a putative GTP phosphohydrolase in the genome of Chilo iridescent virus."; Nucleic Acids Res. 22:158-158-166(1994).
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"Analysis of the First Complete DNA Sequence of an Invertebrate
Iridovirus: Coding Strategy of the Genome of Chilo Iridescent Virus.";
Virology 286:182-196(2001)
                                                                                                                                                                                                                    SEQUENCE FROM N.A. PubMed=8073636; MEDIAMS=353641; PubMed=8073636; Sonnteal G.; Schnitzler P., Koonin E.V., Darai G.; Schnitzler P., Koonin E.V., Darai G.; Chilo iridescent virus encodes a putative helicase belonging to a distinct family within the 'DEAD/H' superfamily: implications for the evolution of large DNA viruses."; virus Genes 8:151-158(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94292906; PubMed=8021587; Schnitzler P., Sonntag K.C., Muller M., Janssen W., Bugert J.J., Koonin E.V., Darai G., Insect irridescent virus type 6 encodes a polypeptide related to the Jargest subunit of eukaryotic RNA polymerase II."; Gen. Virol. 75:1557-1567(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98141693; PubMed=9482589;
Bahr U., Tidona C.A., Darai G.;
"The DNA sequence of Chilo iridescent virus between the genome coordinates 0.101 and 0.391; similarities in coding strategy between binect and vertebrate iridoviruses.";
Virus Genes 15:235-245(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-99125223; PubMed-9926400;
Muller K., Tidona C.A., Bahr U., Darai G.;
"Identification of a thymidylate synthase gene within the genome of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99383793; PubMed=10456793; Muller K., Tidona C.A., Darah G.; Medler K., Tidona C.A., Darah G.; "Identification of a gene cluster within the genome of Chilo iridescent virus encoding enzymes involved in viral DNA replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      capacity of
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINES=92313160; PubMed=7698884;
MEDLINES=92313160; PubMed=7698884;
Sonntag K.C., Schnitzler P., Janssen W., Darai G.;
"Identification of the primary structure and the coding capacity the genome of insect iridescent virus type 6 between the genome coordinates 0.310 and 0.347 (7990 bp).";
                          Schnitzler P., Hug M., Handermann M., Janssen W., Koonin E.V., Delius H., Darai C.;
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Jakob N.J., Mueller K., Bahr U., Darai G.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF303741; ARK2156.1; -.
SEQUENCE 1343 AA; 156514 MW; 8267646EA7CDADOD CRC64;
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MEDLINE=21342589; PubMed=11448171;
  MEDLINE=94167241; PubMed=8121799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chilo iridescent virus.";
Virus Genes 17:243-258(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and processing.";
Virus Genes 18:243-264(1999).
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Best Local Similarity 75.0°,
6; Conservative
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A Adams M.D., Celniker S.E., Holf R.A, Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A Adams M.D., Celniker S.E., Holf R.A, Fvans C.A., Gocayne J.D.,
A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.E., Alazej R.G., Champe M., Pfeiffer B.D.,
A Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Abril J.F., Agbayani A., An H.-J., Andrews-Pfennkoch C., Baldwin D.,
Ballew R.M., Basu A., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Botchier P.,
Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
A Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
A cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davis P.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Pleischmann W.,
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

Van Buskirk C., Hawkins N.C., Schupbach T.;

Van Buskirk C., Hawkins N.C., Schupbach T.;

"Encore is a member of a novel class of proteins and affects multiple processes in Drosophila oogenesis.";

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF243382; AAF68440.1; -.
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Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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InterPro; IPR001374; R3H.
Pfam; PF001424; R3H; 1.
SMART; SW001939; R3H; 1.
SEQUENCE 1548 AA; 164364 MW; F2423CE7E7D5DOCF CRC64;
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                                                                     Last sequence update)
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1548 AA
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                                                                                                                                                                   Drosophila melanogaster (Fruit fly)
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Drosophila melanogaster (Fruit fly)
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                                     01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2002 (TrEMBLrel. 21, Cytoplasmic protein encore. ENC OR CG10847.
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54.5%;
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PRELIMINARY;
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Best Local Similarity
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                                  GAYYRYGVVY
                                                                               12 GYYYRLGAVY
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SEQUENCE 452 AP
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Matches
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O64882
                                                                                                                                                      RESULT 8
                                                                                                                                                                               28UW45
                                                                                                                                                                                                                              Glodek A., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., A Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Hehman T.J., Hernandez J.R., Houck J., Howland C.J., Howland C.J., Howland C.J., Howland C.J., Howland C.J., Main M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Laston E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lang Y., Lin X., Laston P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liak C., Mattei B., McIntosh T.C., McLeod M.P., Mohrerson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Markin W., Murphy E., Muzny D.M., Nelson D.L., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Rese M.G., Reinfard G.S., Pan S., Pollard J., Puri V., Rese M.G., Shon H., Sunders R.D.C., Scheeler F., Shen H., Spier E., Stadling A.C., Stapleton M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T., Spier E., Standers C., Wu D., Yang S., Yao Q.A., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Welliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yao K.H., Myers E.W., Rubin G.M., Venter J.C.; Shu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
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Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
Horbonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
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Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
MG-protoporphyrin IX monomethyl ester oxidative cyclase-related
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Pred. No. 76;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=MSB8 / DSM 3109;
MEDLINE=99287316; Pubmed=10360571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE001800; AAD36604.1; -.
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InterPro, IPR001374; R3H.
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1754 SGVYFKYGQTY 1764
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les 6; Conserv
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Best Local Similarity
Matches 7; Conserv
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SEQUENCE 441 AA
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10 09X1M3

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Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophytas Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Surosids II; Brassicales; Brassicaces; Arabidopsis.
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MEDLINE=20031487; bubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ayele K., Beckstrom-Sternberg S.M., Benjamin B., Blakesley R.W., Bouffard G.G., Brinkley C., Brooks S., Dietrich N.L., Granite S., Guan X., Gupta J., Ho S.-L., Idol J.R., Karlins E., Lee-Lin S.-Q., Legaspi R., Lim M., Maduro Q.L., Maduro V.B., Masiello C., Mastrian S.D., McCloskey J.C., McDowell J., Pearson R., Prasad A., Shevchenko Y., Snyder B., Stantripop S., Thomas J.W., Thomas P.J., Tiongson B.E., Touchman J.W., Tsurgeon C., Vogt J.L., Walker M.A., Wetherby K.D., Zhang L.-H., Green E.D.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                 Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          452 AA; 50824 MW; 7CF7BC6E601955EF CRC64;
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative beta-glucosidase (At2g44480/P411.29).
                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.9%; Score 39; DB 13;
66.7%; Pred. No. 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE, PS00132, CARBOXYPEPT_ZN_1, UNKNOWN 1.
PROSITE, PS00133, CARBOXYPEPT_ZN_2, UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
452
                                                                      Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpro; IPR003146; Propep M14.
InterPro; IPR000834; Zn carbOpept.
Bfam, PF02244; Propep M14; 1.
Pfam; PF00246; Zn carbOpept: 1.
PRINTS; PR00765; ČRBOXYPTASEA.
                                                                                                                                                                         Pancreatic carboxypeptidase Al
                                                              01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-JUN-2002 (TrEMBLrel. 21,
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
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715
790
961
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       687 71
762 79
933 96
1389 AA;
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                                                                                                                                                                                                                                                                           540 AYYRYGI 546
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       REPEAT
REPEAT
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                096281;
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Matches
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          SHH
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Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; "Salzberg S.L., Fraser C.M., Venter J.C.; the plant Arabidopsis thaliana."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Shinn P., Chen H., Cheuk R., Kim C.J., Lim J., Meyers M.C., Banh J.,
Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lynnin, J., Harris D.E., Murphey L.D., Rajandream M.A., Barrell B.G., Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.

-!-SIMILARITY: CONTAINS 6 TPR DOMAINS.

EMBL, AL035075; CAA22636.1; --
InterPro; IPR001440; TPR.

Pfam; PR00515; TPR; 9.

PMART; SM00028; TPR; 9.

Hypothetical protein; Transmembrane; TPR domain; Repeat.

TRANSMEM 861 881

PPR 1.

REPEAT 578 606 TPR 2.

REPEAT 653 681 TPR 3.
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Hypothetical 157.9 kDa protein C1919.05 in chromosome III.
SPCC1919.05.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ecker J.R.;
"Arabidopsis cDNA clones.",
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AC004521; AAC16094.1; -.
EMBL; PX074629; AAL69445.1; -.
HSSP; PXC075, 1CBG.
InterPro; IPR001360; GH_1.
                                                                                                                                                                                                                                                                                Lin X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PERINTS: PRO0131; GIVCO NYGEO1; 1.
PRINTS: PRO0131; GLHYDRLASE1.
PROSTITE; PRO01653; GH 1, 1.
PROSTITE; PRO01653; GH 1, 1.
SEQUENCE 517 AA; 59120 MW; 1A9E4DD65EE1A760 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schizosaccharomycetales; Schizosaccharomycetacea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1999 (TrEMBLrel. 10,
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                                                                                                                                                                         Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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GYKYRYGLVY 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GAYYRYGVVY 11
                                                                                                                                                                                                                                                    STRAIN-CV. COLUMBIA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
tes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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00 94477
AC 09447
DT 01-MA
DT 01-MA
DT 01-JU
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DE HYPOT
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II; Brassicales, Brassicaceae, Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Koonin E.V., Shallom S., Mason T., Yu K., Fujii C., Pederson J., Shonin E.V., Shallom S., Mason T., Yu K., Fujii C., Pederson J., Shonin K., Jing J., Aston C., Lai Z., Schwartz D.C., Pertea M., Salzberg S., Zhou L., Sutton G.G. Clayton R., White O., Smith H.O., Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L., "Chromosome 2 sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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MEDLINE=96392406; PubMed=8799194;
Jacobsen S.E., Binkowski K.A., Olszewski N.E.;
WSPINDLY, a terratricopeptide repeat protein involved in gibberellin signal transduction in Arabidopsis.";
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                          Score 39; DB 3; Length 1389;
Pred. No. 2.7e+02;
1; Mismatches 0; Indels
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15 TPR 4.
90 TPR 5.
51 TPR 6.
157874 MW; PC5C9A785034APE0 CRC64;
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740 AA; 88263 MW; 983C34B795942CC8 CRC64;
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Last annotation update)
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Last annotation update)
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50.0%; Pred. No. 2.1e+02;
tive 4; Mismatches 0;
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InterPro; IPR002160; Kunitz legume.
PROSITE; PS00283; SOYBEAN_KÜNITZ; UNKNOWN_1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                        740 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1999 (TrEMBLrel. 10, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99021743; PubMed=9804551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1999 (TrEMBLrel. 10, Le
01-JUN-2001 (TrEMBLrel. 17, Le
Hypothetical 88.3 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          falciparum.";
Science 282:1126-1132(1998).
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                                                                                                                             63.9%;
85.7%;
                                                                                                                       Query Match
Best Local Similarity 85.7
Matches 6; Conservative
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Gaps

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Hordeum vulgare (Barley).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, Pooideae,
Triticeae, Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CV. HIMALAYA;
MEDLINE=9829840; PubMed=9634587;
RObertson M., Swain S.M., Chandler P.M., Olszewski N.E.;
"Identification of a negative regulator of gibberellin action, HvSPY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=3D7;
MEDLINE=99376085; PubMed=10448855;
Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,
Churcher C.M., Craig A., Davies R.M, Devlin K., Feltwell T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFC0110w, MAL3P1.2 protein.
PFC0110W, MAL3P1.2.
Plasmodium falciparum (isolate 3D7).
Eukaryota, Alvedata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 944;
                                                                                                                                                                                                                            Length 932;
                  STRAIN=CV. VR; TISSUE=ANTHERS;
ITANAIA=CV. VR; TISSUE=ANTHERS;
Submitted (JUL-198) to the EMBL/GenBank/DDBJ databases.
EMBL; Y17720, CAA76634.1; -.
InterPro; IPR001440; TPR.
Pfam; PR00515; TPR; 10.
SMART; SM00028; TPR; 0.
SEQUENCE 932 AA; 103939 MW; 4F0896631302D95D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 38; DB 10; Length 94
Pred. No. 2.7e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in barley.";
Plant Call 10:995-1007(1998).
EMBL, AF035820; AAC36055.1; -.
InterPro; IPR001440; TPR.
InterPro; PF00015; TPR; 11.
SMART; SM00028; TPR; 9.
SEQUENCE 944 AA; 103828 MW; CBEAD8BODICE2F88 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Gibberellin action negative regulator SPY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                            62.3%; Score 38; DB 10; L
77.8%; Pred. No. 2.7e+02;
iive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       944 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 62.3%;
Best Local Similarity 77.8%;
Matches 7; Conservative
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01-NOV-1998 (TrEMBLrel. 08,
01-OCT-2000 (TrEMBLrel. 15,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                      Local Similarity 77.8
les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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179 AYYNLGVVY 187
                                                                                                                                                                                                                                                                                                                                                                     193 AYYNLGVVY 201
                                                                                                                                                                                                                                                                                                                           3 AYYRYGVVY 11
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    FROM N.A.
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Matches
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                                                      STRAIN=CV. COLUMBIA;
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,
Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome 3 BAC F24K9 genomic sequence.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lycopersicon esculentum (Tomato).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots;
Asteridae, euasterids I, Solanales, Solanaceae, Solanum.
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, euasterids I, Solanales, Solanaceae, Petunia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. Greeb T., Schmitz G., Theres K.; Tech T., Schmitz G., Theres K.; Spindly and Procera encode different components of the GA signal transduction pathway in tomato.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38; DB 10; Length 931;
Pred. No. 2.7e+02;
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                                                                                                                                                                                                                          EMBL; AC008153; AAG51433.1; -.
InterPro; IPR01440; TPR.
Pfam; PF00515; TPR; 11.
SMART; SM0028; TPR; 9.
SEQUENCE 914 AA; 101429 MW; A881D84BB5C33493 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in tomato.";
to the EMBL/GenBank/DDBJ databases
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
Proc. Natl. Acad. Sci. U.S.A. 93:9292-9296(1996)
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77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 77.50,
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Petunia hybrida (Petunia).
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nes 7; Conservative
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                                               SEQUENCE FROM N.A
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Q8RVB2

Matches

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RESULT 13
08RVB2
AC QBRVB
AC QBRVB
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DC SPER
OC SPER
OC SPER
OC SPER
COC SPER
RN [1]
RP Greb
RR Greb

Gaps

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RESULT 14 082039 AC 08203 AC 08203 DT 01-NO DT 01-NO DT 01-NO DT SPIND GN SPY. OS Eukar OC Sperm OC Sperm OC Abter OX ABLER

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Score 37; DB 9; Length 79; Pred. No. 26; 1; Mismatches 1; Indels

-. 5B35665968154089 CRC64;

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Mediavilla J., Jain S., Kriakov J., Ford M.E., Duda R.L., Jacobs W.R., Hendrix R.W., Hatfull G.F.;
"Genome organization and characterization of mycobacteriophage bxbl.";
Mol. Microbiol. 38:955-970(2000).
EMBL. AF271693, AAG59785.1;
SEQUENCE 79 AA, 9138 MW; 5B35665968154089 CRC64;
                                                                                                                                                           60.7%;
llarity 75.0%;
Conservative
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                                                                                                                                                                                  Best Local Similarity
Matches 6; Conserva
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hes 5; Conserv
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                                                                                                                                                             Query Match
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"The complete nucleotide sequence of chromosome 3 of Plasmodium
         Hornsby T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
NCBI_TaxID=148603;
Gentles S., Gwilliam R., Hamlin N., Harris D., Holroyd S., Horns Horrocks P., Jagels K., Jassal B., Kyes S., McLean J., Moule S., Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A., Rutter S., Skelton J., Squares R., Squares S., Sulston J.E., Whitehead S., Woodward J.R., Newbold C., Barrell B.G.; "The complete nucleotide sequence of chromosome 3 of Plasmodium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium falciparum (isolate 3D7).
Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                             Score 38; DB 5; Length 1416;
Pred. No. 4.3e+02;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.3%; Score 38; DB 5; Length 1417; 50.0%; Pred. No. 4.3e+02;
                                                                                                                               falciparum .";
Nature 400:532-538(1999).
EMBL; Z97348; CAB10571.3; -.
SEQUENCE 1416 AA; 167488 MW; 1E15EF2D1CD91BB5 CRC64;
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SEQUENCE 1417 AA; 167241 MW; AB7AA0E54B5B1130 CRC64;
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1-NOV-1998 (TEBBLrel. 08, Created)
01-MAY-1999 (TEBMBLrel. 10, Last sequence update)
01-DEC-2001 (TEBMBLrel. 19, Last annotation update)
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Last annotation update)
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SEQUENCE FROM N.A.
MEDLINE=20572070; PubMed=11123671;
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                                                                                                                                                                                                                                               62.3%;
50.0%;
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Nature 400:532-538(1999).
                                                                                                                                                                                                                                                                                           4; Conservative
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863 FYKYGIIY 870
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Best Local Similarity
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SEQUENCE FROM N.A.
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10 77310
10 77310
10 77311
AC 077311
DT 01-DE
DE PFC01-DE
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098041
1D 098044
AC 09804
DT 01-JU
DT 01-JU
DT 01-DE
DE GP80.
GN 80.
OS WYCOB
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                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
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209 AA; 23902 MW; 37D0A0EA7FB1E62D CRC64;
                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Xf2400.
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50.0%; Pred. No. 76;
ive 3; Mismatches 2;
209 AA
                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20365717; PubMed=10910347;
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PRELIMINARY;
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MEDLINE=99384086; PubMed=10453006;
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Q9SE35
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                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brachydanio rerio (Zebrafish) (Zebra danio).
Brukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                             Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: CYTOPLASMIC AND NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY T1B; ALSO KNOWN AS THE PROTEASOME B-TYPE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: THE PROTEASOME IS COMPOSED OF AT LEAST 15 NON IDENTIC SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60.7%; Score 37; DB 13; Length 218; 70.0%; Pred. No. 80; 2; Indels iive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218 AA; 23715 MW; F59664F48779C0E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Proteasome subunit beta 5 (Fragment).
                                                                                                                (TrEMBLrel. 06, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
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                                                         218 AA
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InterPro; IPR000243; Proteasome_B.
InterPro; IPR001353; Protsme_protease.
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                                                                                              Created)
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PROSITE; PS00854; PROTEASOME_B; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hydrolase; Protease; Proteasome
                                                                                                                                                  Proteasome subunit X (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00227; proteasome; 1.
                                                                                            01-JUN-1998 (TrEMBLrel. 06,
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Matches 7; Conservative
                                                       PRELIMINARY;
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SEQUENCE FROM N.A.
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                                                                                                                01-JUN-1998
01-MAR-2002
                                                                                                                                                                        PSMB5 OR X.
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Q9PUS4;
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                 RESULT 20
OS7331
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Q9PUS4
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Murray B.W., Sueltmann H., Klein J.,
"Analysis of a 26-kb region linked to the mbc in zebrafish: genomic organization of the proteasome component beta/Transporter associated with antigen processing-gene cluster and identification of five new proteasome beta subunit genes.",
J. Immunol. 163:2657-2666(1999).
-!-FUNCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH ARG, PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT NEUTRAL OR SLIGHTLY BASIC PH. THE PROTEASOME HAS AN ATP-DEPENDENT PROTEOLYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                             PROTECLYTIC PATHWAY.
SUBUNIT: THE PROTEASOME IS COMPOSED OF AT LEAST 15 NON IDENTICAL
SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- SUBCELLULAR LOCATION: CYTOPLASMIC AND NUCLEAR (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY T1B; ALSO KNOWN AS THE PROTESAGNE B-TYPE FAMILY.

EMBL; AF155578; AAD53518.1; -.

HSSP; P30656; 1RYP.
                                                                                                                                                                                                                                                                                                        ACTIVITY (BY SIMILARITY).
PATHWAY: INVOLVED IN AN ATP/UBIQUITIN-DEPENDENT NON-LYSOSOMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, stramenopiles, Bacillariophyta, Bacillariophyceae,
Bacillariophycidae, Bacillariales, Bacillariaceae, Cylindrotheca
NCBI_TaxID=2853;
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MEDIINE=200181313; PubMed=10550045;
Kroeger N., Deutzmann R., Sumper M.;
Froeger N., Deutzmann R., Sumper M.;
Polycationic peptides from diatom biosilica that direct silica nanosphere formation.";
Science 286:1129-1132(1999).
Science 286:1129-1132(1999).
EMBI, AFI91634; AAFI65940.1; -
SEQUENCE 265 AA; 27500 MW; E628FAF40E1B051B CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
Silaffin precursor protein sillp.
SIL1.
Cylindrotheca fusiformis (Marine diatom).
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75.0%; Pred. No. 99;
live 1; Mismatches 1;
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InterPro; IPR001353; Protsme_protease.
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PROSITE; PS00854; PROTEASOME_B; 1.
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112 SGSYYSYG 119
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Best Local Similarity
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EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
BMBL, 329970; CABL6777.1; -.
EMBL; AL161591; CAB80387.1; -.
InterPro; IPR001440; TPR.
Pfam; PF00015; TPR, 3.
Hypothetical protein.
SEQUENCE 384 AA; 41370 MW; SA46D0EEE92557DD CRC64;
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                                                                                                                                                                                                                                            6; Conservative
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124 AYYRYGL 130
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Matches 6; Conserv
                                                                                                                                                                                                                                                                                   3 AYYRYGV 9
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01-JUN-2002
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Q9LEB4
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                                                                                                                                                                                                                                                                                                                                             Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z., Favello A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T., Hallsworth K., Hawkins J., Hiller L., Johnston D., Johnston D., Largeller P., Le T., Mardis E., Menezes S., Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L., Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Vaudin M., Wilson R., Waterston R.; Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Chalwatzis N.;
                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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60.0%; Pred. No. 1.2e+02;
... ...marches 2; Indels
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Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, 108372; AAB64788.1; -.
SGD; SO002760; YDR352W.
SEQUENCE 317 AA; 35179 MW; F6A41A2175E05C75 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Materston R.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
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                                                                                     (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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                                               317 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1998 (TrEMBLrel. 05,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GAYYRYGVVY 11
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                                                                                                                                                    Similar to YBR147W YDR352W OR D9476.6
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=S288C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                            NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                              STRAIN-S288C;
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                                                                                          01-NOV-1996
                                                                                                          01-NOV-1996
01-JUN-2002
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                                               006328
RESULT 23
206328
10 006322
AC 006322
DT 01-NO ODT 01-NO 
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023165
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-20555308; PubMed=11105760;
Lorkovic Z.J., Wieczorek Kirk D.A., Klahre U., Hemmings-Mieszczak M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                   Gaps
                                                                                                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, euasterids I; Solanales, Solanaceae, Nicotiana.
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Length 384;
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60.7%; Score 37; DB 10; Length 38
85.7%; Pred. No. 1.5e+02;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pram; rrvv...,
PROSITE; PSSO102; RRM; 3.
PROSITE; PSSO0102; RRM; 3.
PROSITE; PSSO030; RRM RNP 1; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                             Nicotiana plumbaginifolia (Leadwort-leaved tobacco).
                                                                                                                                                                                                                                  (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 52.3 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60.7%; Score 37; DB 10; 70.0%; Pred. No. 1.6e+02;
                                                                                                                                                                                                    409 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
EGF-like domain; Glycoprotein; Hydrolase; Serine protease.
SEQUENCE 560 AA; 62671 MW; 5C1907230784ACD4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 37; DB 4; Length 560;
Pred. No. 2.3è+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     574 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell surface glycoprotein (S-layer protein)
MTH719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Methanobacterium thermoautotrophicum
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                                        PEAN, PP00008; EGF; 3.
PEAN, PP00008; EGF; 3.
PEAN, PP00008; LTYDSin; 1.
PEINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00122; CHYMOTRYPSIN.
PRODOM; PR00139; KRINGLE.
SMART; SM00130; KR, 1.
SWART; SM00130; KR, 1.
SWART; SM00120; EGF, 1; 3.
PROSITE; PS01186; EGF_ 1; 3.
PROSITE; PS00021; KRIGLE.; 1.
PROSITE; PS00021; KRIGLE.; 1.
PROSITE; PS50021; KRIGLE.; 1.
PROSITE; PS50021; KRIGLE.; 1.
PROSITE; PS50021; KRIGLE.; 1.
PROSITE; PS50021; KRIGLE.; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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MEDLINE=98037514; PubMed=9371463;
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54.5%;
InterPro; IPR000001; Kringle.
InterPro; IPR001254; Ser_prot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66.7%;
Fines 6; Conservative
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504 SGGWYRHGRLY
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01-JUN-2002
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026815
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Q8WUB4
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                                                                                                                                                                                                                                                                                             A Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,
A Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,
Lee J.M., Onodera C.S., Quach H.L., Tang C., Torliumi M., Wu H.C.,
A Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R.,
A Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
A Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M.,
A Narusaka M., Nguyen M., Paln C.J., Sakurai T., Satou M., Seki M.,
A Theologis A.,
Theologis A.,
I "Full Length CDNA of gene AT437210 (GI:7270704).";
L Submitted (NOV-2001) to the BMBL/GenBank/DDBJ databases.
R EMBL, AR770189; AAK44004.1; -
R EMBL, AX062946; AAL33778.1; -
R InterPro; IPR001440; TPR.,
R InterPro; IPR00151 TPR.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                        Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Goldsmith A.D., Lee J.M., Quach H.L., Tang C.C., Toriumi M., Yu G., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J. Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E. Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinnozaki K., Davis R.W., Ecker J.R., Theologis A., Full Length cDNA of gene Ar4g37210 (GI:7270704)."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=96425001; Pubmed=8827452;
Choi-Miura N.H., Tobe T., Sumiya J., Nakano Y., Sano Y., Mazda T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Purification and characterization of a novel hyaluronan-binding protein (PHBP) from human plasma: it has three EGF, a kringle and serine protease domain, similar to hepatocyte growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biochem. 119:1157-1165(1996).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.7%; Score 37; DB 10; Length 492; 85.7%; Pred. No. 2e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 protein.
492 AA; 52275 MW; 25ED16561586AD01 CRC64;
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Last annotation update)
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InterPro, IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D49742; BAA08576.1; -. EMBL; S83182; AAB46909.1; -. HSSP; P00763; 1DPO.
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01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HGF activator like protein.
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Les 6; Conservative
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                     SEQUENCE FROM N.A.
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MEROPS; S01.033;
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Q14520; O00663
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SEQUENCE 49
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Archaea, Euryarchaeota, Methanobacteria, Methanobacteriales, Methanobacteriaceae, Methanothermobacter.
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Pred, No. 2.4e+02;
Tredinthes 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 deltaH: functional analysis and comparative genomics.";
J. Bacteriol. 179:7135-7155(1997).
EMBL; AE000851; AAB85224.1; -.
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Kaneko O., Tsuboi T., Shirano M., Tachibana M., Ling I.T., Howell S., Cao Y.M., Holder A.A., Torii M.;
"The high molecular mass rhoptry protein, RhopHl, is coded by a member of the CLAG multigene family in Plasmodium falciparum and P. yoelii."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY. EMBL, AB060735; BAB70677.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
NCBI_TaxID=5861;
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                                                                                                  Zverlov V.V., Schwarz W.H.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ275974; CAB76935.1; -.
HSSP; P26221; ITF4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            742 AA; 82181 MW; D901768CEF2C36F8 CRC64;
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Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative gag-pol polyprotein.
                                                                                                                                                                                        InterPro; IPR01956; CBD 3.
InterPro; IPR002105; DocKerin_1.
InterPro; IPR002105; DocKerin_1.
InterPro; IPR0021048; EP-hand.
InterPro; IPR001701; GH 9.
Pfam; PP00442; CBM 3; 1.
Pfam; PP00444; DocKerin_1, 2.
PROSTIE; PS00048; CLÖS CELIULOSOME_RPT; 1.
PROSTIE; PS000592; GLYCOSYL HYDROL_F9 1; PROSTIE; PS00592; GLYCOSYL HYDROL_F9 1; 1.
PROSTIE; PS00592; GLYCOSYL HYDROL_F9 1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 85.7
ses 6; Conservative
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Matches 5; Conservative
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847 YYKFGVLY 854
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PYRHOPHlA-P.
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          NCBI_TaxID=1515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycosidase;
SEQUENCE 74
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Q95YI8;
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Q95Y18
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Q8S6N1
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Bellacosa A.A.B., Testa J.J.R.,
"Isolation, characterization and mapping to human chromosome 11q24-25
of a gene, TMC, encoding a highly conserved putative transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                 01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 80.5 kDa protein.
Homo sapiens (Human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60.7%; Score 37; DB 4; Length 705; 75.0%; Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
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                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC020965; AAH20965.1; -.
InterPro; IPR003674; OTase_STT3.
Pfam; PF02516; STT3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                            Hyporhetical protein.
SEQUENCE 705 Aa; 80529 MW; 71426CA5598B51C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L47337; AAL77539.1; -. SEQUENCE 705 AA; 80603 MW; C5A48A1E92A89250 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Transmembrane protein.
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1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Endo-1,4-glucanase (EC 3.2.1.4)
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Best Local Similarity 75.v.,
G; Conservative
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644 YYRFGQVY 651
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                                                                                                                                                                                                                                     SEQUENCE FROM N.A. TISSUE=LUNG;
                                                                                                                                                                                        NCBI_TaxID=9606;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                     MEDLINE=20272150; PubMed=10810093;
Lai C.-H., Chou C.-Y., Ch'ang L.-Y., Liu C.-S., Lin W.-C.;
Lai C.-H., Chou C.-Y., Ch'ang L.-Y., Liu C.-S., Lin W.-C.;
Lai Carlification of Novel Human Genes Evolutionarily Conserved in Genoral Edgans by Comparative Proteomics.";
Genome Res. 10:703-713(2000).
EMBL, AF132963; AAD27738.1; -.
InterPro; IPR001303; Aldolase_II.N.
Pfam; PF00596; Aldolase_II; 1.
SEQUENCE 242 AA; 270I2 MW; 7B99194024C77D5B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 242;
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
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Submitted (MAY-2001,
EMBL, BC008440; AAH08440.1; -
InterPro; IPR001303; Aldolase_II_N.
Pfam; PF00596; Aldolase_II; 1.
Pfam; PF00596; Aldolase_II; 1.
Pfam; PF00596; Aldolase_II; 1.
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Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2002 (TrEMBLrel. 20,
   01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similar to CGI-29 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                    Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149 SGGYYRY 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGI-29 protein.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 SGGYYRY 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=BONE MARROW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SGAYYRY 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                  NCBI_TaxID=9606;
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                                                                      CGI-29 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002
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Q96HK2
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Q96GX9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                            Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M., Overtcon II L.L., Barra J.J., Tsitrin T., Krol M.I., Jarrahi B.B., Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S., Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J., White O., Salzbarg S.L., Fraser C.M.; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
OSJNBA0073L01.17.
Orza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37; DB 10; Length 1787;
Pred. No. 8.3e+02;
2; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.0%; Score 36; DB 11; Length 241; 85.7%; Pred. No. 1.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1787 AA; 202958 MW; CBDFE5D6D7F0260E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sha S., Aoki Y., Nishi Y.;
"A cDNA sequence from murine monocyte-macrophage.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
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Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; ABCASS; BAA78906.1; -.
EMBL; BCO28434; AAH28434.1; -.
MGD; MGI:1926788; Mmrppl9.
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Pfam; PF00596; Aldolase II; 1.
SEQUENCE 241 AA; 26949 MW; 4366CF4AD2239DB8 CRC64;
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Last annotation update)
19).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 62.5
Matches 5; Conservative
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                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 YYRYGVVY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148 SGGYYRY 154
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                                                                                                                                                                NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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Q9Y318
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099WVO5
AC 099WVQ
DT 01-NO
DT 01-JU
DE MWRP1
DE MWRP1
DE MWRP1
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Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L., Kagan Y., Chaga O., Goltsman E., Bernal A., Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R., Fonstein M., Kyrpides N., Overbeek R.; Grome sequence and analysis of the oral bacterium Fusobacterium nucleatum strain ATCC 2586."

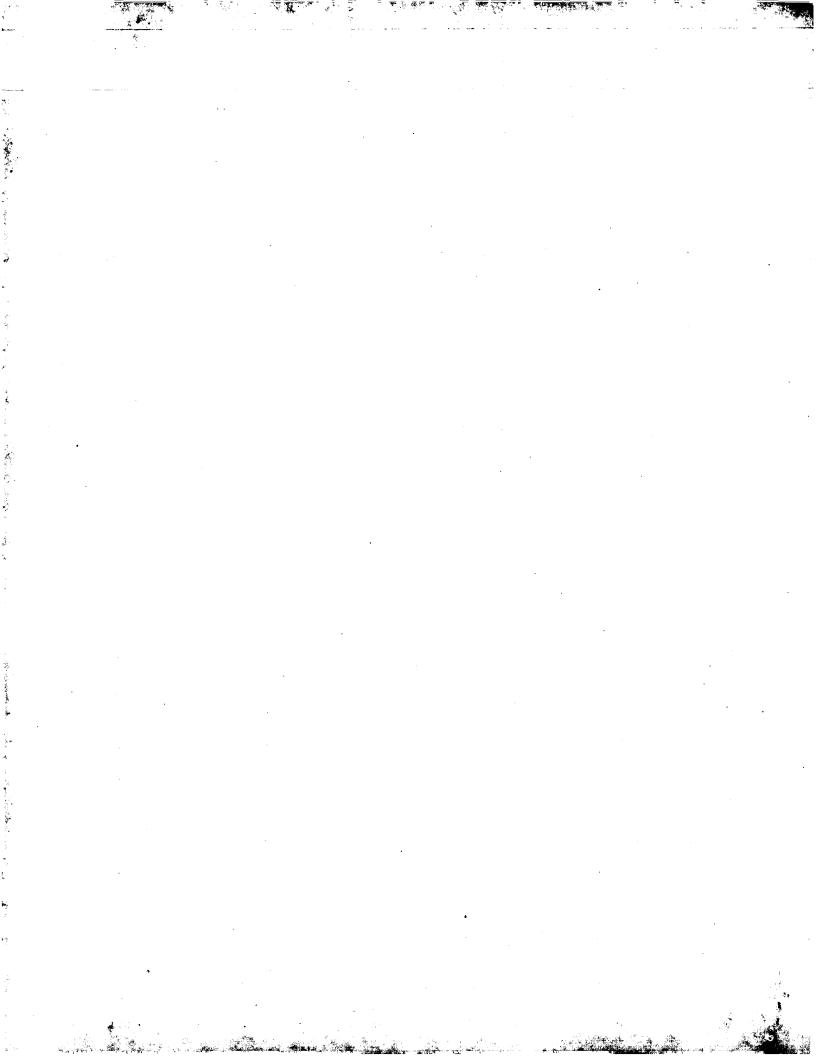
J. Bacteriol. 184:2005-2018(2002).

EMBL; AB010622; AAL95363.1; -.
Weissenbach J., Vivares C.P.; "Genome sequence and gene compaction of the eukaryote parasite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 36; DB 16; Length 339;
Pred. No. 2e+02;
                                                                                                                                                                                                                                                                     Length 252;
                                                                                                                                                                                                                                   Score 36; DB 5; Length 232
Pred, No. 1.46+02;
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                                                                                               Nature 414:450-453(2001).
EMBL, ALS90447; CAD25586.1; -.
Hypothetical protein.
SEQUENCE 252 AA; 28571 MW; AA3318F2EFBBB286 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             339 AA; 36234 MW; CF1CFBDC4A878111 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-UNN-2002 (TrEMBLrel. 21, Last sequence update) 01-UNN-2002 (TrEMBLrel. 21, Last annotation update) Galactoside transport system permease protein mglC.
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Bacteria; Fusobacteria; Fusobacterium.
NCBI_TaxID=76856;
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01-JUN-2002 (TrEMBLrel. 21, Last seq
01-JUN-2002 (TrEMBLrel. 21. Last ann
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MEDLINE=21886394; PubMed=11889109;
                                                                                                                                                                                                                                                                  59.0%;
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                                                                   Encephalitozoon cuniculi.";
                                                                                                                                                                                                                                       Query Match
Best Local Similarity 60.0
ماست 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                        123 GRYFKCGVVY 132
                                                                                                                                                                                                                                                                                                                                                                                                2 GAYYRYGVVY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 SGAYYAFG 248
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Best Local Similarity
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SEQUENCE 339 AA
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F., Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker P., Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
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Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.
NCBI_TaxID=6035;
                                                                                                                                                                                                                                                                                                                                  1; Indels
                    Strausberg R.;
Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC009077; AAH00077.1; -1.
InterPro; IPR001303; Aldolase II. N.
Pfam; PF00596; Aldolase II. 1.
Pfam; PF00596; Aldolase II.; 1.
SEQUENCE 242 AA; 27125 MW; 9B8D5D1435D6775A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC017594; AAH17594.1; -.
InterPro; IPR01013; Aldolase_II_N.
Pfam; PF00565; Aldolase_II; I.
Hypothetical protein.
SEQUENCE 242 AA; 27215 MW; F8C4A371E3C63FC2 CRC64;
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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Pred. No. 1.4e+02;
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01-JUN-2002 (TrEMBLrel. 21, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
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MEDLINE-21576510; PubMed-11719806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, Cre 01-MAR-2002 (TrEMBLrel. 20, Las 01-JUN-2002 (TrEMBLrel. 21, Las Hypochetical 27.2 kDa protein. Homo sapiens (Human).
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85.7%;
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Matches 6; Conservative
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Matches 6; Conservative
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Q88V24
AC Q88V24
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Gaps

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Humanised 1D10 ant VH and VL of MAb P P4-15 single chain

Light (kappa) chai

8019 VK antibody Mouse MAb 2G12 L

Recombinant mouse Murine CCR5xCD3 bi

Recombinant mouse

Anti-placental alk

3B10xP5-2 bispeci

Human anti-placent Light chain variab TROOOS Human kappa Anti-human gp39 MA Humanised MAD 39-1 Murine 1588 light Moncelonal antibod Monoclonal antibod

Scoring table:

Searched:

Minimum DB Maximum DB

Database

Perfect score:

Seguence:

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Run on:

Mouse monoclonal a Mouse and human ch Mouse and human ch Mouse and human ch Mouse and human ch

Human monoclonal a Human monoclonal a

monoclonal a Monoclonal antibod

Human

IgE receptor chain variab

chain variab

Light

Mouse anti-human CDR1 from murine

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PIP3; phosphatidylinositol-3,4,5-triphosphate; variable region; CDR1; immunogen; antibody; light chain; complementarity determining region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murine PIP3 recognizing Mab variable region light chain CDR1 region.
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AAW03721
AAW03725
AAY92161
AAY92157
ABB05962
ABB05963
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ABB05996
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AAW27350
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AAE22193
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AAR11987
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ABB05992
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ABB05994
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(IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY87660 standard; Protein; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 10; Page 13; 15pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98JP-0252921
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JP2000083664-A.
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 RESULT 1
AAY87660
ID AAY8
  Murine PIP3 recogn
Murine MC-1 antibo
Murine MC-1 antibo
Anti-DNA antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                    July 18, 2003, 15:01:44; Search time 37.18 Seconds (without alignments) 39.423 Million cell updates/sec
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| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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| SIDSZ/gcgdata/geneseqg-embl/AA1982.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
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             GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                         Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                908470 segs, 133250620 residues
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Maximum Match 100%
Listing first 45 summaries
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AAE22197
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AAW05822
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Score

Result Š. 26432

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This invention describes a novel antibody specifically recognizing phosphatidylinositol-3,4,5-triphosphate (PIP3). The antibody of the invention is used in immunogenic compositions in which a dead Salmonella genus microbe is used as an adjuvant and mixed with PIP3. The antibody can be used in an immunoassay containing a step in which the above antibody or its variable region is reacted with PIP3 present in a sample and the bond based on their immunological reaction. The method can determine PIP3 easily in a high sensitivity. This sequence represents the murine PIP3 recognizing monoclonal antibody variable region heavy chain complementarity determining region, CDR1 described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel antibody specifically recognizing phosphatidylinositol-3,4,5-triphosphate (PIP3). The antibody of the invention is used in immunogenic compositions in which a dead Salmonella genus microbe is used as an adjuvant and mixed with PIP3. The antibody can be used in an immunoassay containing a step in which the above antibody or its variable region is reacted with PIP3 present in a sample and the bond based on their immunological reaction. The method can determine PIP3 easily in a high sensitivity. This sequence represents the murine PIP3 recognizing monoclonal antibody variable region light chain described in the method of the invention.
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murine PIP3 recognizing Mab variable region light chain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIP3; phosphatidylinositol-3,4,5-triphosphate; variable region; immunogen; antibody; light chain.
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                                                                                                                                                                                                                                                      Length 11;
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                                                                                                                                                                                                                                                     100.0%; Score 57; DB 21;
100.0%; Pred. No. 0.00018;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (FUKU/) FUKUI Y.
(IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; Page 12; 15pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98JP-0252921
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Best Local Similarity
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                                                                                                                                                                                     the invention.
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The invention relates to the use of an antibody and/or chemokine construct that binds a chemokine receptor for preparing a pharmaceutical composition for eliminating cells latently infected with a primate immunodeficiency virus (e.g. human immunodeficiency virus (HIV-1). They are used in gene therapy and as vaccines. The antibody and/or chemokine construct is also used for preparing a pharmaceutical composition for treating, preventing and/or alleviating immunological disorders including autoimmune diseases (e.g. multiple sclerosis, type I diabetes and inflammation, atopic dermatitis and psoriasis), inflammatory diseases (e.g. skin inflammatory diseases (chronic arthritis), inflammatory couch as inflammatory bowel diseases and inflammatory bowel diseases and inflammatory bowel diseases and inflammatory bowel diseases and arthritism inflammatory in the manual diseases and inflammatory howel diseases and inflammatory bowel diseases and inflammatory in the manual diseases and inflammatory bowel diseases and suffared ward transplant rejections. The present sequence is murine Mc-1 antibody light chain variable domain (VL) complementarity determining region 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of an antibody and/or chemokine construct that binds to a chemokine receptor, for eliminating cells latently infected with primate immunodeficiency virus, or treating, preventing and alleviating immune
                                                                                                                                                                                                                                                                                               Chemokine construct; human immunodeficiency virus 1; allergic disease;
                                                                                                                                                                                                                                                                                                               skin disease, immunological disorder; autoimmune disease; psoriasis; multiple sclerosis; rheumatoid arthritis; inflammatory bowel disease; diabetes; skin inflammation; attopic dermatitis; inflammatory disease; inflammatory renal disease; HIV-1; transplant rejection; murine; CDR1; light chain variable domain; VL; complementarity determining region 1;
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100.0%; Pred. No. 0.0042;
iive 0; Mismatches 0;
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                                                                                                                                      AAE22197 standard; peptide; 11 AA.
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                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mack M, Schloendorff D,
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1 RASENIYSYLP 11
                      24 RASENIYSYLP 34
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nes 10; Conserv
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                                                                                                                                                                               AAE22197;
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100.0%; Score 57; DB 21; Length 107; 100.0%; Pred. No. 0.0023; ive 0; Mismatches 0; Indels (

Query Match
Best Local Similarity 100.
Matches 11; Conservative

AAW04587 standard; Protein; 99 AA.

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The invention relates to the use of an antibody and/or chemokine construct that binds a chemokine receptor for preparing a pharmaceutical composition for eliminating cells latently infected with a primate immunodeficiency virus (e.g. human immunodeficiency virus (HIV-1). They are used in gene therapy and as vaccines. The antibody and/or chemokine construct is also used for preparing a pharmaceutical composition for treating, preventing and/or alleviating immunological disorders including autoimmune diseases (e.g. multiple sclerosis, type I diabetes and rheumacoin architis), allergic diseases, skin diseases (e.g. skin inflammation, atopic dermatitis and psoriasis), inflammatory diseases such as inflammatory joint diseases (chronic arthritis), inflammatory renal diseases and inflammatory bowel diseases and graft versus host and transplant rejections. The present sequence is murine MC-1 antibody light chain variable domain (WJ) II). This antibody is specific for human chemokine receptor 5 (CCRS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of an antibody and/or chemokine construct that binds to a chemokine receptor, for eliminating cells latently infected with primate immunodeficiency virus, or treating, preventing and alleviating immune
                                                                                                                                                                       skin disease; immunological disorder; autoimmune disease; psoriasis; multiple sclerosis; rheumatoid arthritis; inflammatory bowel disease; diabetes; skin inflammation; atopic dermatitis; inflammatory disease; inflammatory renal disease; HIV-1; transplant rejection; CCR5; murine; MC-1 antibody; VL; light chain variable domain; chemokine receptor 5.
                                                                                                                                                   Chemokine construct; human immunodeficiency virus 1; allergic disease;
                                                                                                               Murine MC-1 antibody light chain variable domain (VL)(1) #2.
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100.0%; Pred. No. 0.045;
tive 0; Mismatches 0; Indels
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AAE22190 standard; Protein; 92 AA
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                                                                          (first entry)
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                                                                          25-JUL-2002
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-DNA antibody which specifically binds DNA hairpin - useful to develop prods. for diagnosis and treatment of disorders, e.g. glomerulonephritis or systemic lupus erythematosus
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Calf thymus DNA was used to immunise a MRL-ipr mouse, spleen cells from which were then fused with Sp2/0 myeloma cells to give hybridomas producing the anti-DNA MAD. 15d8 was found to react strongly with single stranded DNA and poly(dT), and weakly with poly(dG).
                                                                                                                                                                                                                       Light chain; variable region; anti-DNA; monoclonal; antibody; MAb 1568; hairpin; diagnosis; inflammatory glomerulonephritis; systemic lupus erythematosus; screening; treatment; prevention; SLE; disease.
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                                                                                                                                                                   Anti-DNA antibody 15d8 light chain variable region.
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100.0%; Pred. No. 0.049;
tive 0; Mismatches 0
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'label= framework_II
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/label= J_region
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/label= CDR_III
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/label= CDR_I
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Best Local Similarity 100.
Matches 10; Conservative
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'label=
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N-PSDB; AAT43739.
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Local Similarity

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RESULT 5 AAW04587

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Glick GD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorders associated with the pathological complexation of DNA, e.g. inflammatory glomerulonephritis and systemic lupus erythematosus. It can also be used to generate reagents to screen for pharmaceutical agents, and treat and/or prevent an above disorder.

Calf thymus DNA was used to immunise a MRL-lpr mouse, spleen cells from which were then fused with Sp2/0 myeloma cells to give hybridomas producing the anti-DNA MAD. 9f11 was found to react poly (dG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    - useful to
                                                                                                                                    MAD 9f11; hairpin; diagnosis; inflammatory glomerulonephritis;
systemic lupus erythematosus; screening; treatment; prevention;
                                                                                                                            chain; variable region; anti-DNA; monoclonal; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-DNA antibody which specifically binds DNA hairpin -develop prods. for diagnosis and treatment of disorders, glomerulonephritis or systemic lupus erythematosus
                                                                                                           Anti-DNA antibody 9f11 light chain variable region.
                                                                                                                                                                                                                                                                 59..90
/label= framework_III
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                                                                                                                                                                                                                                                                                              103..115 -
/label= J_region
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/label= CDR_III
                                                          AAW04596 standard; Protein; 99
                                                                                                                                                                                                                                                12..58
/label= CDR_II
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                                                                                           (first entry)
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/label= (
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         RASENIYSYL 10
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                                                                                                                                                      SLE; disease
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                                                                                           12-AUG-1997
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Region
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MAb 9f
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                                                                                                                                                                                                                                                                                                                                                                                                                                                MAD 15b10; hairpin; diagnosis; inflammatory glomerulonephritis; systemic lupus erythematosus; screening; treatment; prevention;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Light chain; variable region; anti-DNA; monoclonal; antibody;
                                   Length 99;
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                                                                            0; Indels
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                                   DB 18;
0.049;
                                   Score 50; DB 1
Pred. No. 0.04
0; Mismatches
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/label= framework_III
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                     87.7%; Scc..
100.0%; Pre
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/label= J_region
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/label= CDR_III
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/label= CDR_II
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/label= CDR_I
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                                                                                Conservative
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/label=
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                Query Match
Best Local Similarity
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                                                                                                                                             16 RASENIYSYL
99 AA;
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(IOWA-) IOWA IMMUNOTHERAPY INVESTIGATORS.
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                                                  Calf thymus DNA was used to immunise a MRL-1pr mouse, spleen cells from which were then fused with Sp2/0 myeloma cells to give hybridomas producing the anti-DNA MAD. 15b10 was found to react strongly with single stranded DNA and poly(dT), and weakly with poly(dG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Light chain; variable region; anti-DNA; monoclonal; antibody; MAb 5f3; hairpin; diagnosis; inflammatory glomerulonephritis; systemic lupus erythematosus; screening; treatment; prevention;
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pharmaceutical agents, and treat and/or prevent an above
                                                                                                                                                                                                                                                                                  87.7%; Score 50; DB 18; Length 99; 100.0%; Pred. No. 0.049; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-DNA antibody 5f3 light chain variable region.
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/label= framework_III
91.102
/label= CDR_III
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/label= framework II
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/label= J_region
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/label= CDR_II
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23..27
/label= CDR_I
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Best Local Similarity luv.
The conservative of the con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-011854/01.
N-PSDB; AAT43743.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 RASENIYSYL
                                                                                                                                                                                                                                99 AA;
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                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW04598;
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The present sequence is the light chain variable region of the anti-DNA monoclonal antibody (MAb) 5f3, which has a high affinity for single stranded DNA, low or no affinity for double stranded DNA and specifically binds a DNA hairpin. The MAb can be used diagnose
                                                                                                                                                                                                      disorder. Calf thymus DNA was used to immunise a MRL-lpr mouse, spleen cells from which were then fused with \mathrm{Sp2/0} myeloma cells to give hybridomas producing the anti-DNA MAb.
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                                                                                                disorders associated with the pathological complexation of DNA, e.g. inflammatory glomerulonephritis and systemic lupus erythematosus. It can also used to generate reagents to screen for pharmaceutical agents, and treat and/or prevent an above
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                                                                                                                                                                                                                                                                                                                                                                                  Length 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B-cell lymphoma; humanised antibody; bispecific antibody; myeloma; leukaemia; hybridoma; monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Humanised 1D10 antibody light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                               87.7%; Score 50; DB 18;
100.0%; Pred. No. 0.049;
ive 0; Mismatches 0
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|abel= CDR1
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/label= CDR2
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Best Local Similarity 100.
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/note=
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/note≃
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Chimeric Mus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Light chain; variable region; anti-DNA; monoclonal; antibody; 9f11 group; hairpin; diagnosis; inflammatory glomerulonephritis; systemic lupus erythematosus; screening; treatment; prevention;
                                                                              New bispecific antibody reactive with both T or NK cells and malignant B cells - also their humanised forms and hybridomas producing them, useful for treating or preventing leukaemia,
                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                    87.7%; Score 50; DB 17; Length 107; 100.0%; Pred. No. 0.053; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-DNA antibody 9f11 group light chain variable region.
                            Weiner G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    framework_III
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/label= framework_II
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/label= CDR_III
98..107
/label= J_region
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                                                                                                                                                  Claim 14; Fig 4a; 85pp; English.
(PROT-) PROTEIN DESIGN LABS INC
                          Tso JY,
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/label= CDR_II
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/label= CDR_I
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/label= i
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nes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               24 RASENIYSYL 33
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                          Gingrich R, Link BK,
                                                                                                                       lymphoma and myeloma
                                                   WPI; 1996-412742/41
                                                                                                                                                                                                                                                                                                                                             107 AA;
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                                                                                                                                                                                                                                                                                                                                               Sequence
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Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                 The present sequence is the light chain variable region of the group 9f11 putative consensus anti-DNA monoclonal antibody (MAb), which has a high affinity for single stranded DNA, low or no affinity for double stranded DNA and specifically binds a DNA hairpin. The MAb can be used diagnose disorders associated with the pathological complexation of DNA, e.g. inflammatory glomerulonephritis and systemic lupus erythematosus. It can also be used to generate reagents to screen for pharmaceutical agents, and treat and/or prevent an above disorder.

The sequence was derived by aligning homologous anti-DNA MAb, whose sequences have been published, as well as several MAb of other specificities obtained from a database search.
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                                                                                                                                                                             - useful
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                                                                                                                                                                         Anti-DNA antibody which specifically binds DNA hairpin - usef
develop prods. for diagnosis and treatment of disorders, e.g.
glomerulonephritis or systemic lupus erythematosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murine MC-1 antibody light chain variable domain (VL)(1) #1.
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100.0%; Pred. No. 0.053;
iive 0; Mismatches 0
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   96WO-US07113
                                  95US-0443540
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05-SEP-2001; 2001US-0948004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 87.7
Best Local Similarity 100.
Matches 10, Conservative
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                                                                                               Swanson PC;
                                                              (UNMI ) UNIV MICHIGAN
                                                                                                                               WPI; 1997-011854/01.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 AA;
                                                                                                                                               N-PSDB; AAT43808
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16-MAY-1996;
                                  18-MAY-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                               Glick GD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE22189;
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The invention relates to the use of an antibody and/or chemokine construct that binds a chemokine receptor for preparing a pharmaceutical composition for eliminating cells latently infected with a primate immunodeficiency virus (e.g. human immunodeficiency virus (HIV-1). They are used in gene therapy and as vaccines. The antibody and/or chemokine construct is also used for preparing a pharmaceutical composition for treating, preventing and/or alleviating immunological disorders including autoimmune diseases (e.g. multiple sclerosis, type I diabetes and rheumatoin, atopic dermatitis and psoriasis, inflammatory diseases such as inflammatory joint diseases (chronic arthritis), inflammatory renal diseases and inflammatory bowel diseases and graft versus host cand transplant rejections. The present sequence is murine MC-1 antibody light chain variable domain (WJ)[1]. This antibody is specific for human chemokine receptor 5 (CRS).
                                         Use of an antibody and/or chemokine construct that binds to a chemokine receptor, for eliminating cells latently infected with primate immunodeficiency virus, or treating, preventing and alleviating immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              compound; therapeutic; antibody; SICS; 8019;
                                                                                                                                                                                                                                                                                                                                                                                                                                Match 87.7%; Score 50; DB 23; Length 107; Local Similarity 100.0%; Pred. No. 0.053; es 10; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pavlinkova G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW46483 standard; protein; 109 AA.
                                                                                                                       Example 2; Page 49; 117pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KENT ) UNIV KENTUCKY RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97WO-US12223.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96US-0681432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antigen; immuno-conjugate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diagnosis, photoaffinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RASENIYSYL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 RASENIYSYL 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kohler H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-120935/11.
WPI; 2002-362240/39.
N-PSDB; AAD35248.
                                                                                                                                                                                                                                                                                                                                                                                                  107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8019 VK antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9803870-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BE,
                                                                                            disorders
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW46483;
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haley
                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
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Gaps

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conditions, particularly a single 2-5 minute photoactivation results in almost 100% attachment (contrast conditions usually required to attach

molecules to antibodies.

This is the amino acid sequence of 8019 VK antibody. The invention relates to the site-specific photo-attachment of a nucleic photoaffinity compound to an antibody which comprises reacting them under conditions that promote attachment of the photoaffinity compound to at least 1 nucleotide binding site in the antibody. Also claimed are: photoaffinity compound-antibody conjugates produced this way, and immuno-conjugates comprising cytotoxic or therapeutic agent site-specifically attached to the photoaffinity compound in the conjugate. When the conjugate is labelled it is used for detection or quantitation of an antigen (Ag) by any standard immunoassay format, while immuno-conjugates are used therapeutically, e.g. in cases tumours, infections or genetic diseases, or as imaging agents. The photoaffinity compounds are attached under mild, physiological

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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New chimeric mouse human antibodies - used in treatment, diagnosis and prophylaxis of HIV infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              þe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The mouse VL gene product may be used to produce chimeric mouse-human Abs against HIV-1 comprising human Ig constant regions and murine variable regions. These novel sequence are useful in treatment, diagnosis and prophylaxis of HIV infections, and may be produced by a bacterial, yeast or mammalian expression system.
                                                                                                                                                                                                                         ö
                                                                                                                                                                                                    Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 126;
                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Robinson RR;
                                                                                                                                                                                                   87.7%; Score 50; DB 19;
100.0%; Pred. No. 0.054;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.7%; Score 50; DB 12; 100.0%; Pred. No. 0.064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ghosh-Dastidar P,
                                                                                                                                                                                                                                                                                                                  AAR12235 standard; Protein; 126 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 8; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                            Mouse MAb 2G12 L chain V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90WO-US06627.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89US-0433703
                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                        10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Better MD, Horwitz AH,
                                                                                                                                                                                                                                            1 RASENIYSYL 10
                                                                                                                                                                                                                                                         WPI; 1991-178106/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                 109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (XOMA-) XOMA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAQ12015.
                                                                                                                                                                                                                                                                                                                                                                                                HIV-1; chimera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-NOV-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                          19-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9107494-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-1991.
                                                                                                                                                                                  Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                      AAR12235
                                                                                                                                                                                                                                                                                                                                                                                                                      Mus sp.
                                                                                                                                                                                                                        Matches
$$99999999999999
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Conjugates formed by site-specific attachment of nucleic photo-affinity agents to antibodies - useful as immunoassay reagents for detecting antigen, also immuno-therapeutic complex also containing cytotoxin for treating cancer, infection or genetic

Disclosure; Figure 12c; 75pp; English

disease

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Humanised 1D10 antibody light chain.
                                                                 Chimeric Mus sp.
                                                                                                                                                                                                                                     29-FEB-1996;
                                                                                                                                                                                               WO9626964-A1
                                                                                                                                                                                                                                                       01-MAR-1995;
                                                                                                                                                                                                                  06-SEP-1996.
                                                                                                                                                                                                                                                                                                     Gingrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR53148
                                                                                             Domain
                                                                                                              Region
                                                                                                                                 Region
                                                                                                                                                   Region
                                                                                                                                                                     Domain
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 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      This is the light (kappa)-chain variable (V) region of a mouse monoclonal antibody (MAb), 2G12, and is specific for an HIV-1 viral antigen. It is used in the construction of a chimeric MAb comprising heavy and light chains having murine V regions and human C regions. The chimeric MAbs are more effective than murine MAb 2G12 since they have an increased compatibility in humans. The heavy and light chain V-regions are joined by manipulating their respective joining (J) regions, to generate restriction enzyme recognition sites. The chimeric MAbs can be used as immunoconjugates, in association with e.g. toxins for HIV treatment. They can also be used in diagnosis of HIV.
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                                                                                                                                                                                                                                                                                                                                                            New chimeric mouse-human antibodies - used to detect, kill and remove HIV-1 antigen from sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.7%; Score 50; DB 12; Length 127;
100.0%; Pred. No. 0.065;
tive 0; Mismatches 0; Indels
                                                                                                                                          Light (kappa) chain variable region of murine 2G12 immuno-
0; Indels
                                                                                                                                                                                                                                                                                                               Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR;
                                                                                                                                                                     Chimeric antibodies; immunoconjugates; HIV; AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Prec. ....
Mismatches
                                                                                    AAR12357 standard; Protein; 127 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW05828 standard; Protein; 214 AA.
                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, fig 8; 107pp; English.
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                                                                                                                                                                                                                                                                 89US-0433730
                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Conservative
10; Conservative
                                                                                                                                                                                                                                                                                            (GREC ) GREEN CROSS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RASENIYSYL 10
                   1 RASENIYSYL 10
                                44 RASENIYSYL 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RASENIYSYL 53
                                                                                                                                                                                                                                                                                                                                 WPI; 1991-178044/24.
N-PSDB; AAQ12059.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127 AA:
                                                                                                                                                                                                                                                                                   (XOMA-) XOMA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-JAN-1997
                                                                                                                                                                                                                                               13-NOV-1990;
                                                                                                                                                                                                                                                                 13-NOV-1989;
                                                                                                                        15-AUG-1991
                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                             30-MAY-1991.
                                                                                                                                                                                                          WO9107493-A
                                                                                                      AAR12357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW05828;
                                                                                                                                                  globulin.
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Matches
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AAW05828
ID AAW0
XX
AC AAW0
XX
DT 27-J
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The humanised 1D10 antibody light chain (AAW05828) includes a variable region (see also AAW05822) consisting of human R3 5HG light chain variable region (tramework and complementarity determining regions from the murine 1D10 antibody specific for a 28/32 kDa antigen found on the surface of malignant B-cells. It can be coexpressed with humanised 1D10 heavy chain (see also AAW05829) in mammalian host cells. Bispecific antibodies can be constructed that include a first binding fragment comprising humanised M291 heavy and light chain variable regions (see also AAW05826, AAW05830), and a second binding fragment comprising humanised 1D10 heavy and light chain variable regions. Such antibodies are reactive with both T or NK cells and malignant B cells, and have therapeutic and diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New bispecific antibody reactive with both T or NK cells and malignant B cells - also their humanised forms and hybridomas producing them, useful for treating or preventing leukaemia, lymphoma and myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 17; Length 214; 0.12;
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B-cell lymphoma; humanised antibody; bispecific an myeloma; houkaemia; hybridoma; monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                108..214
/label= Human_C-kappa_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IOWA-) IOWA IMMUNOTHERAPY INVESTIGATORS
                                                                                                                                                                                                  ..107
label= Variable domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 50;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Weiner
                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR53148 standard; Protein; 243 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87.7%; £
100.0%;
                                                                                                                                                                                                                                                                                                                                                               89..97
/label= CDR3
                                                                                                                                                                                                                                                   24..33
/label= CDR1
                                                                                                                                                                                                                                                                                                                                   = CDR2
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Best Local Similarity 100
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                         49..55
/label=
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                                                                                     Chimeric Homo sapiens;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Link BK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-412742/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RASENIYSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    214 AA;
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Human; NKG2D; NKG2D receptor complex; cancer; infectious disease; tumour; autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary; intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix; prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; Fy sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DAP10; helminth; cytostatic; antimicrobia!; immunomodulatory; 1182D10; 6H7E7; 8G7C10; 6E5A7; 1182D10; 6H7E7; P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; A10xP4-7; B4-14; P4-15; P5-2; P5-3; P4-14;

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AAU72864 standard; Protein; 256 AA

(first entry)

26-FEB-2002

AAU72864;

P4-15 single chain Fv.

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This sequence is encoded by the Fabbabb Liggment or the planshing pULI40 and represents the heavy Chain and light chain variable regions (WH and VL) of the monoclonal antibody (MAD) PR1. The CDNA encoding this sequence was derived by PCR amplification of reverse transcribed PR1-hybridoma RNA using the primer sequences given in AAG64477-81. The VH and VL complementarity determining regions (CDRs) are used in the construction of the MAD of the invention which competes with PR1 for binding to a prostate call of the invention which competes with PR1 for binding to a prostate call of a patient suffering from prostate cancer. It can also be used for the diagnosing the presence of prostate cancer in an individual and for the diagnosing the presence of prostate cancer in a conviction abnormal growth of prostate cells, eg. benign prostate cancer in the hyperplasia. The MAD reacts strongly with prostate cancer cells but only weakly with a few other normal human tissues. The effect of the relation of the cancer cells of the relation of the cancer cells of the cancer cells of the cancer of the cancer cells of the cancer of the cancer of the control of the cancer of the ca
                                                                                                                          PE38KDEL; plasmid; pUL140; heavy; chain; light; variable region; VH; VL; monoclonal antibody; MAb; PR1; PCR; amplify; PR1-hybridoma RNA; primer; complementarity determining regions; CDR; drug; cytotoxin; prostate cell associated antigen; radioisotope; PCAA; prostate; cells; cancer; diagnosis; benign prostate hyperplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence is encoded by the PE38KDEL fragment of the plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monoclonal antibody specific for prostate cells - used in the diagnosis and treatment of conditions involving abnormal growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prostate cells, esp prostate cancer.
                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Fig 1; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                        1..118
/label= PR1 VH
                                                                                                                                                                                                                                                                                                                                                                                                                         119..133
/label= Linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134..243
/label= PR1 Vl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93WO-US09166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (USSH ) US SEC DEPT HEALTH.
                           (first entry)
                                                                            VH and VL of MAb PR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1994-151334/18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAQ64476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-OCT-1992;
                           07-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-APR-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9409150-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pastan IH;
                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
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The invention relates to a multifunctional polypeptide comprising a domain with a binding site that specifically recognises an extracellular group of the NKG2D receptor complex and a second domain which functions as a receptor or ligand. The polypeptide and its associated polymercecide are used for the polypeptide and its associated polymercecide are used for the preparation of a pharmaceutical composition for the treatment of cancer, infections and/or autoimmune composition. The cancer may be a tumour of the head and neck, stomach, oesophagus, colon, liver, intrahapatic bile ducts, pancreas, lung, larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid, larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid, larynx, breast, ovary, uterus, caused by viruses, bacteria, fungi, protozoa or helminths. The autoimmune diseases include multiple clerosis, Grave's disease, ankylosing spondylitis, acute anterior uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent diabetes mellitus, rheumatoid arthitis, pemphigus vulgaris and autoimmune hepatitis. Sequences AAU72820-AAU72875 represent the NKG2D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor and the polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 7; Fig 16; 114pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.vv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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Multifunctional polypeptides comprising binding sites that specifically recognise extracellular groups of the NKG2D receptor complex and domains which function as receptors or ligands, useful for treating

cancers and infectious diseases -

G, Lutterbuese R, Borschert K, Kischel R;

Riethmueller Hofmeister R;

Kufer P, Mayer M,

(KUFE/) KUFER P.

WPI; 2002-055119/07. N-PSDB; AAS97138.

26-MAR-2001; 2001WO-EP03414. 24-MAR-2000; 2000EP-0106467.

WO200171005-A2 Homo sapiens.

27-SEP-2001.

ö RASENIYSYL 170 161 g

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Gaps

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87.7%; Score 50; DB 15; Length 243; 100.0%; Pred. No. 0.13; ive 0; Mismatches 0; Indels

Ouery Match Best Local Similarity 100. ....has 10; Conservative

157 RASENIYSYL 166

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1 RASENIYSYL

RESULT 18

RESULT 17 AAU72864 RESULT 19

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The present sequence is the recombinant mouse anti-rotavirus antibody. It comprises of mouse heavy chain (VH) and light chain (VL) variable regions joined by a linker. The recombinant antibody encoding DNA is inserted into pCANTAB 5E expression vector (clone 11). The vector is used to transform probiotic bacteria like, Lactobacilli for expression and secretion of recombinant anti-rotavirus antibodies. The antibodies have antibacterial and antiviral activity. Antibody-expressing probiotic bacteria can be administered for treatment of gastrointestinal (GI) tract infections and to immunise neonates, humans or immunosuppressed/immunodeficient adults acutely exposed to a bolus of GI pathogen.
                                                                                                                                         Recombinant anti-rotavirus antibody; mouse; heavy chain variable region; Wl; light chain variable region; VL; pCANTAB 5E vector; treatment; probiotic bacteria; antibacterial; antiviral; gastrointestinal tract; immunise; neonate; immunosuppressed; immunodeficient; di pathogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Composition for supplementing or replacing an immune response against gastrointestinal pathogens in e.g. newborn infants, comprises probiotic microorganisms expressing antibodies specific for the gastrointestinal
                                                                                                                                                                                                                                                                                                                                                                                   254..266 / Labels E_tag_domain / labels E_tag_domain / notes - Enables immunodetection and immunoaffinity purification of the recombinant antibody"
                                                                                                                                                                                                                                                                                                       /label= Mouse_Heavy_chain_variable_region
                                                                                                                                                                                                                                                                                                                                                152. 250
/label= Mouse_Light_chain_variable_region
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                                                                                                              Recombinant mouse anti-rotavirus antibody (Clone 11)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mueller GC,
                                                                                                                                                                                                                                                                                                                      117..151
/label= Linker_region
                                                                                                                                                                                                                                                                        cocation/Qualifiers
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                  AAY44972 standard; Protein; 268 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US17296
                                                                                (first entry)
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N-PSDB; AAZ50508.
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                                                                              23-MAY-2000
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                                                                                                                                                                                                                        Synthetic
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                                                                                                                                                                                                                                         Mus sp
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                                                                                                                                                                                                                                                                                                                                                                                    Domain
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                                                                                                                                      Recombinant anti-rotavirus antibody; mouse; heavy chain variable region; Wl; light chain variable region; VL; pCANTAB SE vector; treatment; probiotic bacteria antibacterial; antiviral; gastrointestinal tract; immunise; neonate; immunosuppressed; immunodeficient; GI pathogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Composition for supplementing or replacing an immune response against gastrointestinal pathogens in e.g. newborn infants, comprises probictic microorganisms expressing antibodies specific for the gastrointestinal
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/note= "Enables immunodetection and immunoaffinity
purification of the recombinant antibody"
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                                                                                                                                                                                                                                                                                               'label= Mouse_Heavy_chain_variable_region
                                                                                                                                                                                                                                                                                                                                                             'label= Mouse_Light_chain_variable_region
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                                                                                                         Recombinant mouse anti-rotavirus antibody (Clone 22).
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                                                                                                                                                                                                                                                                                                               17..152
| label = Linker_region
                                                                                                                                                                                                                                                                  Location/Qualifiers
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                AAY44973 standard; Protein; 268 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 2; 48pp; English.
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                                                                            (first entry)
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N-PSDB; AAZ50509.
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                                                                            23-MAY-2000
                                                                                                                                                                                                                    Synthetic.
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Region
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Matches
AAY44973
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87.7%; Score 50; DB 21; Length 268; 100.0%; Pred. No. 0.15; ive 0; Mismatches 0; Indels

Local Similarity 100. Les 10; Conservative

Matches

Query Match

RASENIYSYL 10 |||||||||| RASENIYSYL 175

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AAU72873 standard; Protein; 503 AA

AAU72873

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The invention relates to the use of an antibody and/or chemokine construct that binds a chemokine receptor for preparing a pharmaceutical composition for eliminating cells latently infected with a primate immunodeficiency virus (e.g. human immunodeficiency virus (HIV-1). They are used in gene therapy and as vaccines. The antibody and/or chemokine construct is also used for preparing a pharmaceutical composition for treating, preventing and/or alleviating immunological disorders including autoimmune diseases (e.g. multiple sclerosis, type I diabetes and rheumatoin, atopic dermatitis and psoriasis), inflammatory diseases (c.g. multiple sclerosis, type I diabetes such as inflammatory joint diseases (chronic arthritis), inflammatory as inflammatory bowel diseases and inflammatory bowel diseases and graft versus host and transplant rejections. The present sequence is CRRxCD3 bispecific and transplant rejections. The present sequence is CRRxCD3 bispecific single chain antibody construct. This antibody construct comprises of murine MC-1 antibody specific for human chemokine receptor 5 (CCR5) and M and WL domains of an antibody specific for a CD3 antigen joined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of an antibody and/or chemokine construct that binds to a chemokine receptor, for eliminating cells latently infected with primate immunodeficiency virus, or treating, preventing and alleviating immune
                                                                                                                                                                                Chemokine construct; human immunodeficiency virus 1; allergic disease; skin disease; immunological disorder; autoimmune disease; psoriasis; multiple sclerosis; rheumatoid arthritis; inflammatory bowel disease; diabetes; skin inflammation; atopic dermatitis; inflammatory disease; inflammatory renal disease; HIV-1; transplant rejection; CCRSxCD3; antibody; chemokine receptor 5; CD3 antigen; chimeric; murine.
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                                                                                                                                             Murine CCR5xCD3 bispecific single chain antibody construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spring M;
                     AAE22193 standard; Protein; 495 AA.
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05-SEP-2001; 2001US-0948004
                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                             Chimeric - Mus sp.
Chimeric - Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                      WO200220615-A2.
                                                                                                     25-JUL-2002
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                                                             AAE22193;
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The invention relates to a multifunctional polypeptide comprising a domain with a binding site that specifically recognises an extracellular compain with a binding site that specifically recognises an extracellular group of the NKG2D receptor complex and a second domain which functions of a receptor or ligand. The polypeptide and its associated composition for the treatment of cancer, infections and/or autoimmune compositions. The cancer may be a tumour of the head and neck, stonach, coephagus, colon, liver intraheptic bile ducts, pancreas, lung, conditions. The cancer may be a tumour of the head and neck, stonach, coephagus, colon, liver intraheptic bile ducts, pancreas, lung, larymx, breast, ovarry, uterus, cervix, prostate, kidney, testis, thyroid, larymx, breast, ovarry, uterus, cervix, prostate, kidney, testis, thyroid, complete or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma. The infectious diseases can be caused by viruses, bacteria, fungi, protozoa or helminchs. The autoimmune diseases include multiple sclerosis, Grave's disease, ankylosing spondylitis, acute anterior cueitis, soluciamune hepatitis. Sequences AAU72820-AAU72875 represent the NKG2D receptor and the polypeptides of the invention.
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                                                                                                                                     Human; NKG2D; NKG2D receptor complex; cancer; infectious disease; tumour; autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary; intrahepatic bille duct; pancreas; lung; larynx; breast; uterus; cervix; prostate; kidney; testis; chyorid; bladder; brain; melanoma; myeloma; Fascoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DAP10; helminth; cytostatic; antimicrobial; immunomodulatory; 1182D10; 6H7E7; 8G7C10; 6E5A7; 1182D10; 6H7E7; 8G7C10; 6E5A7; 1182D10; 6H7E7; P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; 3810xP4-3; B4-14; P5-3 tetramerisation domain; 3810xP5-2; 3810xP5-23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Multifunctional polypeptides comprising binding sites that specifically recognise extracellular groups of the NKG2D receptor complex and domains which function as receptors or ligands, useful for treating cancers and infectious diseases
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                                                                                                  3B10xP5-2 bispecific single chain Fv.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAR-2001; 2001WO-EP03414.
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Hofmeister R;
                                                          (first entry)
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N-PSDB; AAS97147.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                          26-FEB-2002
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Mayer M,
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                 AAU72873;
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Gaps

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Local Similarity

RASENIYSYL 10 24 RASENIYSYL 33

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RESULT

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The murine anti-PLAP VK gene (AAQ11845) contains 3 CDRs which are use to reshape the human anti-PLAP VK gene. The murine anti-PLAP VK gene (AAQ11845) CDRs were used to reshape the human anti-PLAP gene VK (AAQ11847). The specific binder for human PLAP contains at least one of the former 3 CDRs and/or at least one of the latter CDRs. The produced antibodies are more readily tolerated when administered to a human patient. Antibody reagents can be used to identify, e.g. by serum testing or imaging, and/or to treat PLAP-producing cancers. Buch cancers can occur as, e.g. breast cancer, ovarian cancer and colon cancer or can manifest themselves as liquids such as pleural
                                                                                                              Placental alkaline phosphatase; antibody; cancer; light chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phosphatase - for treating and diagnosing cancers e.g. breast, ovarian and colon cancers and pleural effusions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic specific binder for human placental alkaline
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0.2;
                                                                              Human anti-placental alkaline phosphatase Vk.
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Pred. No.
                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                            50..56
/label= CDR2
                                                                                                                                                                                                               24..34
/label= CDR1
                                                                                                                                                                                                                                                                              89..97
/label= CDR3
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90.0%;
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89GB-0026045.
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                                             (first entry)
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Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                                                                               Homo sapiens.
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17-NOV-1989;
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                                            31-JUL-1991
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                                                                                                                             PLAP; CDR
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               AAR11987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The murine anti-PLAP Vk gene contains 3 CDRs which are used to reshape the human anti-PLAP Vk gene (AAQ11848). The murine anti-PLAP Vk gene (AAQ11845) CDRs were used to reshape the human anti-PLAP gene Vk (AAQ11847). The specific binder for human PLAP contains at least one of the former 3 CDRs and/or at least one of the latter CDRs. The produced antibodies are more readily tolerated when administered to a human patient. Antibody reagents can be used to identify, e.g. by serum testing or imaging, and/or to treat PLAP-producing cancers. Such cancers can occur as, e.g. breast cancer, ovarian cancer and colon, cancer or can manifest themselves as liquids such as pleural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic specific binder for human placental alkaline phosphatase - for treating and diagnosing cancers e.g. breast, ovarian and colon cancers and pleural effusions
                                                                                                                                                                                              Placental alkaline phosphatase; antibody; cancer; light chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 47; DB 12; Length 107;
Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                              Anti-placental alkaline phosphatase Vk.
                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                             AAR11985 standard; Protein; 107 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Fig 2; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82.5%;
90.0%;
                                                                                                                                                                                                                                                                                             24..34
/label= CDR1
                                                                                                                                                                                                                                                                                                                               50..56
/label= CDR2
                                                                                                                                                                                                                                                                                                                                                            89..97
/label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90EP-0312407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90GB-0019552
89GB-0026045
                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 90.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RASENIYSYL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 RASENIYSYV 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UNIL ) UNILEVER PLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1991-157662/22.
N-PSDB; AAQ11846.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Verhoeyen ME;
                                                                                                                                                                                                                                              fus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-NOV-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-SEP-1990;
17-NOV-1989;
                                                                                                                             31-JUL-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                            29-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                            EP429242-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       effusions
                                                                                                                                                                                                                 PLAP; CDR
                                                                                             AAR11985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                               Region
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Gaps

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21-DEC-1995 (first entry)

AAR11987 standard; Protein; 107 AA.

RESULT 23 AAR11987 ID AAR1

8

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Matches

Length 107; 0; Indels

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The present invention describes a method (M1) for producing a human antibody phage display library (I), comprising: (1) providing a nonhuman transgenic animal (II) whose genome comprises human immunoglobulin genes; (2) isolating nucleic acids encoding human antibody chains (III) from lymphatic cells; and (3) forming a library of display packages whose members comprise a nucleic acid encoding (III) which is displayed from the package. The method is used for producing a human antibody display library, e.g., a Fab phage display library. The display method may be used too screen nucleic acids encoding antibody chains obtained from the contract of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Producing a human antibody phage display library comprises providing a transgenic animal whose genome comprises human immunoglobulin genes and isolating nucleic acids encoding antibody chains from lymphatic cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunised nonhuman transgenic animals, and from this a population of antibodies may be prepared. Production of a human monoclonal antibodies display library using this method means there is no need to immunise humans with antigens, and the difficulties faced with immortalising B cells are avoided. AAH29958 to AAH30066 and AAB74994 to AAB75056
                                   y; immunoglobulin; interleukin 8; ILB; immunogen;
phage display library; immunisation; transgenic animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Light chain; variable region; murine; mouse; anti-human; disease; glycoprotein 39; gp39; monoclonal; antibody; 39-1.106; hybridoma; diagnosis; inhibition; B-cell; activation; treatment; disorder; immune; autoimmune; allergic response; organ rejection; drug; graft versus host; cell imaging; tumour; targetted; delivery; targeted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 46; DB 22; Length 224; Pred. No. 0.73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-human gp39 MAb 39-1.106 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BIOS-) BIOSITE DIAGNOSTICS INC.
(GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gray J, Lonberg N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 37; Page 121-122; 161pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW03721 standard; Protein; 128 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.7%;
                                                                                                                                                                                                                                                                                                                                                                           99US-0157415.
99US-0453234.
                                                                                                                                                                                                                                                                                                                      02-OCT-2000; 2000WO-US27237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Buechler J, Valkirs G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 RASQNVYSYL 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RASENIYSYL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-335567/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224 AA;
                                   Human; antibody;
human antibody pł
                                                                                                                                                                                                     WO200125492-A1.
                                                                                                                      Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                           02-OCT-1999;
01-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-APR-1997
                                                                                                                                                                                                                                                              12-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW03721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW0372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PALIBORIES AND THE ALTONOUS AND THE PRINCE CONTRICT OF THE PALIBORIES OF MATCHINGTON OF MATCHING OF MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polypeptide(s) which bind heavy metals, esp. mercury - derived from monoclonal antibodies, used for detecting, removing, adding or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the PCR amplified nucleotides were determined. These are given in AA097489 e997510 and the deduced AA sequences in AAR79241-R79250 & AAR78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45 and in the claims are different from the descriptions in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence listings. The descriptions in the sequence listings are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hybridoma antibodies have been produced with the spleen cells of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                     Monoclonal antibody; heavy metal; mercury; variable region;
Light chain variable region for monoclonal antibody 2D5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRO005 HuMab kappa chain protein sequence 1CE8K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptide(s) which bind heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB75038 standard; Protein; 224 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 23; Page 69; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                        94US-0187407.
                                                                                                                                                                                                                                                                                                                95WO-US01199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neutralising heavy metals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 90.(
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             (BION-) BIONEBRASKA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RASENIYSYL 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wagner FW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-275415/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAQ97509
                                                                                                                                                                                                                                                                                                             27-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                        27-JAN-1994;
                                                                                                                                                                                                                                                        03-AUG-1995.
                                                                                  light chain
                                                                                                                                                                                                WO9520607-A
                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lopez O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB75038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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AAB75038
ID AAB75
XX
AC AAB75
XC
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XX
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XX
DX
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Gaps

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0; Indels

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Light chain, variable region, murine, mouse, anti-human, disease, glycoprotein 39; gp39, monoclonal, antibody, 39-1.106, hybridoma, diagnosis; inhibition; B-cell; activation; treatment; disorder; immune, autoimmune, allergic response; organ rejection; drug; graft versus host; cell imaging; tumour; targetted; delivery;
Humanised MAb 39-1.106 light chain variable region.
                                                                                                                                                                                                                                                      note= "corresponding codon TAA"
                                                                                                                                                                                                                      'note= "corresponding codon TAG"
                                                                                                                                                                                                                                                                                       note= "corresponding codon
                                                                                                                                                                                   Location/Qualifiers
                                                                                                                   targeted; humanised
                                                                                                                                                                                                                                                                       Misc-difference 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAT36018.
                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                        26-JAN-1996;
                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                      WO9623071-A2
                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aruffo AA,
Harris LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       murine anti-human glycoprotein (gp) 39 monoclonal antibody (MAb) 39-1.106 (a member of the murine kappa V subfamily). The MAb was corporated by immunising a 6-8 week old BALBC mouse with a gp39-CD8 fusion protein, and 3 days later harvesting and fusing spleen and lymph cells to mouse melanoma cells, to produce an anti-human gp39 cm MAb producing hybridoma. The MAb may be useful for diagnosing disease states, inhibiting B-cell activation and for treating immunological disorders, e.g. autoimmune disorders, allergic responses, organ rejection and graft versus host disease. It may also be used for imaging cells which express gp39 on their surface, e.g. tumour cells, and to target therapeutic agents to such cells. The MAb inhibits the CD40/gp39 interaction, therefore limiting both prim and sec. responses to T-cell dependent antigens and Ab prodn. specific to these antigens. A typical compsn. for intramuscular injection pref. contains 50 mg of MAb in 1 ml of sterile buffered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monoclonal antibodies specific for different epitope(s) on human gp39 - used for inhibiting B cell activation and for the diagnosis of various disorders, e.g. cancer, psoriasis etc..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is the light chain variable region of the
                                                                                                                                    "complementarity determining region 1"
                                                                                                                                                                    "complementarity determining region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 17; Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                     /note= "complementarity determining
                                                                                                                                                                                                                                                                                                                                                                                                          Gordon ML;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 44; DB 17
Pred. No. 0.95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         Bajorath J, Gilliland LK,
Hollenbaugh D, Siadak AW;
                                                                  /label= sig_peptide
                                                                                  21..128
/label= mat_peptide
                                  location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 89; Fig 6A; 167pp; English.
                                                                                                                                                                                                                                                                                                                                                                       (BRIM ) BRISTOL-MYERS SQUIBB CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77.2%;
90.0%;
                                                                                                                                                                                                                                                                                                     96WO-US01119
                                                                                                                                                                                                                                                                                                                                        95US-0379057
                                                                                                                                                                                       .117
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                                                                                                                     44..54
/note=
                                                                                                                                                                    /note=
109..11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1996-362694/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAT35973
                                                                                                                                                                                                                                      WO9623071-A2
                                                                                                                                                                                                                                                                                                       26-JAN-1996;
                                                                                                                                                                                                                                                                                                                                        26-JAN-1995;
                                                                                                                                                                                                                                                                      01-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                       Aruffo AA,
Harris LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                Peptide
                                                                                  Peptide
                                                                                                                     Region
                                                                                                                                                      Region
                                                                                                                                                                                     Region
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AAW03725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monoclonal antibodies specific for different epitope(s) on human gp39 - used for inhibiting B cell activation and for the diagnosis of various disorders, e.g. cancer, psoriasis etc..
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                                                                                                                                                                                                                                                                                                                                                                      Gordon ML;
/note= "corresponding codon TAA"
                                                                                                                                                                                                                                                                                                                                                                   Bajorath J, Gilliland LK,
Hollenbaugh D, Siadak AW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 13; Fig 16; 167pp; English.
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90.0%;
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nes 9; Conservative
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AAW03725 standard; Protein; 171 AA.

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(first entry)

02-APR-1997

AAW03725;

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This is a murine anti-Tie2 kinase receptor agonist monoclonal antibody 1588 light chain variable region. Tie2 is a single-transmembrane, tyrosine kinase receptor ('Tie' stands for tyrosine kinase receptor with immunoglobulin and endothelial growth factor (EGF) homology domain(s)). Anti-Tie2 antibodies may be administered to enhance angiogenesis in mammals suffering from ischemic disease, myocardial infarction or cerebral stroke or other vascular diseases such as diabetes. It may also be used to enhance endothelial cell survival and to promote haematopoietic or megakaryocyte cell proliferation (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a protein which is fused with a monoclonal antibody against an antigen present on cell surface and which
                                                                                                                                                                                                                                                                   Tie2 receptor agonist antibodies useful for promoting angiogenesis in patients suffering from strokes and myocardial infarctions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein fused with a monoclonal antibody against an antigen present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monoclonal antibody; fusion protein; antigen; cell surface; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monoclonal antibody related amino acid sequence SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 43; DB 21; Length 107; Pred. No. 1.2; 2; Mismatches 0; Indels
                                                                                                                                                               Winkler JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB05962 standard; protein; 258 AA.
                                                                                                                                                                                                                                                                                                                                  Claim 10; Page 38; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 14; Page 9; 24pp; Japanese.
                                                                                                                                                               Holmes SD, Erickson-miller CL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75.4%;
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                                                        98US-0102098.
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                 99WO-US22428.
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                                                                                                                                                                                                      WPI; 2000-293114/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match.
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 AA;
                                                                                                                                                                                                                                N-PSDB; AAA09016.
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                                                        28-SEP-1998;
                   28-SEP-1999;
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     stroke
                                                                                             Light chain; variable region; complementarity determining region; CDR 1; anti-Tibez Kinase receptor; monoclonal antibody; 15BB; angiogenetic; vascular-general; proliferative; antilschemic; cerebroprotective; cardiant; agonist; antibody inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY92161-63 are light chain CDR (complementarity determining regions) from a novel murine anti-Tie2 kinase receptor agonist monoclonal antibody 1588. Tie2 is a single-transmembrane, tyrosine kinase receptor ('Tie' stands for tyrosine kinase receptor with immunoglobulin and endothelial growth factor (EGF) homology domain(s)). Anti-Tie2 antibodies may be administered to enhance angiogenesis in mammals antibodies may be administered to enhance angiogenesis in mammals or offering from ischemic disease, myocardial infarction or cerebral stroke or other vascular diseases such as diabetes. It may also be used to enhance endothelial cell survival and to promote haematopoietic or megakaryocyte cell proliferation (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tie2 receptor agonist antibodies useful for promoting angiogenesis in patients suffering from strokes and myocardial infarctions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                    Murine 15B8 light chain variable region CDR 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Winkler JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY92157 standard; Protein; 107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 14; Page 41; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Holmes SD, Erickson-miller CL,
                                                                                                                                                                                                                                                                                                                                                                                                              (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                  99WO-US22428
                                                                                                                                                                                                                                                                                                                                                                         98US-0102098
               (first entry)
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nes 8; Conservative
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                                                                                                                                                                                                        Mus musculus
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AAY92157;

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Sequence Query Match Matches

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Gaps

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may also

can transfer a gene by combining with the gene and containing a human type single-stranded monoclonal antibody and a peptide which is the combining site for the gene. Also described is a complex of a monoclonal antibody-fused protein which is a complex of monoclonal antibody-fused protein and a method for the preparation of a monoclonal antibody-fused protein against a receptor present on cell surface in which: (1) an mRNA extracted from a hybridoma cell having productivity of said monoclonal antibody against a receptor present on cell surface is used as the template to amplify a single-stranded antibody gene of a mouse type monoclonal antibody is converted to prepare a single-stranded antibody gene of a human type monoclonal antibody is converted to prepare a single-stranded antibody gene of a human type monoclonal antibody is converted to prepare a single-stranded antibody gene of a human type monoclonal antibody; (3) a gene encoding the mine and the single-stranded antibody gene of the mine the mine the single-stranded antibody gene of the single-stranded single-stranded single-stranded single-stranded single-stranded single-stranded single-stranded single-stranded single-stranded si human type monoclonal antibody to prepare a human type single-stranded immunoporter gene; and (4) the human type single-stranded immunoporter gene; and expressed in a microbe to prepare a recombinant protein of the human type single-stranded immunoporter. Also described is a method for introducing the above complex of monoclonal antibody-fused protein through a cell surface receptor. The method is used for the preparation of a monoclonal antibody-fused protein gainst a receptor present on cell surface. The present sequence represents a specifically claimed amino acid sequence from the present invention. \$

258 AA; Sequence

Gaps . 0 73.7%; Score 42; DB 23; Length 258; 88.9%; Pred. No. 5.1; ive 0; Mismatches 1; Indels Best Local Similarity 88.9 Matches 8; Conservative Query Match

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165 RTSENIYSY 173

ABB05963 standard; protein; 258 AA

ABB05963;

(first entry) 09-MAY-2002

Monoclonal antibody related amino acid sequence SEQ ID NO:2.

Monoclonal antibody; fusion protein; antigen; cell surface; receptor.

Homo sapiens. Synthetic.

JP2001333780-A.

04-DEC-2001.

29-MAY-2000; 2000JP-0158575.

29-MAY-2000; 2000JP-0158575.

(KEIO-) GH KEIO GIJUKU

WPI; 2002-135945/18.

A protein fused with a monoclonal antibody against an antigen present Claim 15; Page 9; 24pp; Japanese. on cell surfaces -

The present invention describes a protein which is fused with a monoclonal antibody against an antigen present on cell surface and which can transfer a gene by combining with the gene and containing a human type single-stranded monoclonal antibody and a peptide which is the combining site for the gene. Also described is a complex of a monoclonal antibody-fused protein which is a complex of monoclonal antibody and a bNA, and a method for the preparation of a monoclonal

which: (1) an mRNA extracted from a hybridoma cell having productivity of said monoclonal antibody against a receptor present on cell surface is used as the template to amplify a single-stranded antibody gene of a mouse type monoclonal antibody by RCR; (2) the framework portion of the mouse type monoclonal antibody is converted to prepare a single-stranded antibody gene of a human type monoclonal antibody; (3) a gene encoding the amino acid tail is added to the single-stranded antibody gene of the human type single-stranded antibody gene of the immunoporter gene; and (4) the human type single-stranded immunoporter. Communoporter gene; and (4) the human type single-stranded immunoporter. Communoporter gene; and (4) the human type single-stranded immunoporter. Also described is a method for introducing the above complex of monoclonal antibody-fused protein through a cell surface receptor. The method is used for the preparation of a monoclonal antibody-fused protein against a receptor present on cell surface. The present sequence represents a specifically claimed amino acid sequence from the present invention. 

258 AA; Sequence

ö Score 42; DB 23; Length 258; Pred. No. 5.1; 1; Indels 0; Mismatches 73.7%; 88.9%; Query Match
Best Local Similarity 86.

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165 RTSENIYSY 173

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RESULT 32 **ABB05990** 

ABB05990 standard; Protein; 258 AA.

ABB05990;

09-MAY-2002 (first entry)

Mouse monoclonal antibody related protein sequence BB.

Monoclonal antibody; fusion protein; antigen; cell surface; receptor.

Mus sp. Synthetic.

JP2001333780-A.

04-DEC-2001.

29-MAY-2000; 2000JP-0158575.

29-MAY-2000; 2000JP-0158575

(KEIO-) GH KEIO GIJUKU.

WPI; 2002-135945/18 N-PSDB; ABA94200

protein fused with a monoclonal antibody against an antigen present on cell surfaces 

Example; Fig 9; 24pp; Japanese.

οĘ The present invention describes a protein which is fused with a monoclonal antibody against an antigen present on cell surface and which can transfer a gene by combining with the gene and containing a human type single-stranded monoclonal antibody and a peptide which is the combining site for the gene. Also described is a complex of a monoclonal antibody-fused protein which is a complex of monoclonal antibody-fused protein which is a complex of monoclonal antibody-fused protein against a receptor present on cell surface in antibody-fused protein against a receptor present on cell surface in which: (1) an mRNN extracted from a hybridoma cell having productivity of said monoclonal antibody against a receptor present on cell surface is used as the template to amplify a single-stranded antibody gene of a antibody gene of a human type monoclonal antibody; (3) a gene encoding the amino acid tail is added to the single-stranded antibody gene of the human type monoclonal antibody to prepare a human type single-stranded immunoporter gene; and (4) the human type single-stranded immunoporter gene; and microbe to prepare a recombinant protain of the human type single-stranded immunoporter. Also described is a method for introducing the above complex of monoclonal antibody-fused protein for a monoclonal antibody-fused protein surface receptor. The method is used for the preparation of a monoclonal antibody-fused protein against a receptor present on cell surface. The present sequence represents a protein sequence which is

8866666666666888

8X333333333333X8

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Gaps

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Indels

73.7%; Score 42; DB 23; Length 258; 88.9%; Pred. No. 5.1;

0; Mismatches

Local Similarity 88.5

165 RTSENIYSY 173

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1 RASENIYSY

given in an example from the present invention

Sequence

Query Match Best Loc Matches

mouse type monoclonal antibody by PCR; (2) the framework portion of the mouse type monoclonal antibody is converted to prepare a single-stranded antibody gene of a human type monoclonal antibody; (3) a gene encoding the amino acid tail is added to the single-stranded antibody gene of the human type monoclonal antibody to prepare a human type single-stranded immunoporter gene; and (4) the human type single-stranded immunoporter gene is expressed in a microbe to prepare a recombinant protein of the human type single-stranded immunoporter. Also described is a method for introducing the above complex of monoclonal antibody-fused protein of the through a cell surface receptor. The method is used for the preparation of a monoclonal antibody-fused protein sequence represents a protein sequence which is given in an example from the present invention. protein fused with a monoclonal antibody against an antigen present Gaps Monoclonal antibody; fusion protein; antigen; cell surface; receptor; Mouse and human chimeric monoclonal antibody related protein CvB. The present invention describes a protein which is fused with a ; 0 Score 42; DB 23; Length 258; Pred. No. 5.1; 0; Mismatches 1; Indels ABB05991 standard; Protein; 258 AA Example; Fig 10; 24pp; Japanese. 73.7%; 88.9%; 29-MAY-2000; 2000JP-0158575. 29-MAY-2000; 2000JP-0158575 09-MAY-2002 (first entry) Local Similarity 88.5 nes 8; Conservative Chimeric - Mus sp. Chimeric - Homo sapiens. (KEIO-) GH KEIO GIJUKU. 165 RTSENIYSY 173 1 RASENIYSY 9 WPI; 2002-135945/18. 258 AA; on cell surfaces N-PSDB; ABA94201 JP2001333780-A. 04-DEC-2001 Synthetic. ABB05991; Sequence chimeric Query Match RESULT 33 ABB05991 Matches

The present invention describes a protein which is fused with a monoclonal antibody against an antigen present on cell surface and which can transfer a gene by combining with the gene and containing a human type single-stranded monoclonal antibody and a peptide which is the combining site for the gene. Also described is a complex of a monoclonal antibody-fused protein which is a complex of monoclonal antibody-fused protein which is a complex of monoclonal antibody-fused protein against a receptor present on cell surface in which; (1) an mRNA extracted from a hybridoma cell having productivity of and monoclonal antibody against a receptor present on cell surface is used as the template to amplify a single-stranded antibody gene of a monoclonal antibody is converted to prepare a single-stranded antibody gene of a human type monoclonal antibody; (3) a gene encoding the amino acid tail is added to the single-stranded antibody gene of the Monoclonal antibody; fusion protein; antigen; cell surface; receptor; A protein fused with a monoclonal antibody against an antigen present Mouse and human chimeric monoclonal antibody related protein CaB. ABB05992 standard; Protein; 258 AA. Example; Fig 11; 24pp; Japanese. 29-MAY-2000; 2000JP-0158575. 29-MAY-2000; 2000JP-0158575. (first entry) Chimeric - Mus sp. Chimeric - Homo sapiens. (KEIO-) GH KEIO GIJUKU WPI; 2002-135945/18. N-PSDB; ABA94202. on cell surfaces -JP2001333780-A. 09-MAY-2002 04-DEC-2001 Synthetic. ABB05992; chimeric. RESULT 34 ABB05992 

monoclonal antibody against an antigen present on cell surface and which type single-stranded monoclonal antibody and a peptide which is the combining site for the gene and containing a human type single-stranded monoclonal antibody is a complex of a monoclonal antibody-fused protein which is a complex of monoclonal antibody-fused protein which is a complex of monoclonal antibody-fused protein a method for the preparation of a monoclonal antibody-fused protein against a receptor present on cell surface in which: (1) an mRNA extracted from a hybridoma cell having productivity of said monoclonal antibody against a receptor present on cell surface is used as the template to amplify a single-stranded antibody gene of a mouse type monoclonal antibody by PCR; (2) the framework portion of the mouse type monoclonal antibody is converted to prepare a single-stranded

human type monoclonal antibody to prepare a human type single-stranded immunoporter gene; and (4) the human type single-stranded immunoporter gene is expressed in a microbe to prepare a recombinant protein of the human type single-stranded immunoporter. Also described is a method for introducing the above complex of monoclonal antibody-fused protein through a cell surface receptor. The method is used for the preparation of a monoclonal antibody-fused protein surface research sequence represents a protein sequence which is given in an example from the present invention. 

258 AA; Sequence

; 0 Score 42; DB 23; Length 258; Pred. No. 5.1; 0; Mismatches 1; Indels 73.78; 88.98; 8; Conservative 1 RASENIYSY 9 Local Similarity Query Match Matches . ∂ 임

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Gaps

165 RTSENIYSY 173

RESULT 35 ABB05993

ABB05993 standard; Protein; 258 AA. ABB05993 

Mouse and human chimeric monoclonal antibody related protein DB.

(first entry)

09-MAY-2002

Monoclonal antibody; fusion protein; antigen; cell surface; receptor; chimeric.

Chimeric - Mus sp. Chimeric - Homo sapiens.

Synthetic.

JP2001333780-A.

04-DEC-2001

29-MAY-2000; 2000JP-0158575.

29-MAY-2000; 2000JP-0158575.

(KEIO-) GH KEIO GIJUKU

WPI; 2002-135945/18.

N-PSDB; ABA94203

A protein fused with a monoclonal antibody against an antigen present on cell surfaces

Example; Fig 12; 24pp; Japanese.

The present invention describes a protein which is fused with a monoclonal antibody against an antigen present on cell surface and which can transfer a gene by combining with the gene and containing a human type single-stranded monoclonal antibody and a peptide which is the combining site for the gene. Also described is a complex of a monoclonal antibody-fused protein which is a complex of monoclonal antibody-fused protein which is a complex of protein and a DNA, and a method for the preparation of a monoclonal antibody gainst a receptor present on cell surface is which; (1) an mRNA extracted from a hybridoma cell having productivity of said monoclonal antibody against a receptor present on cell surface is used as the template to amplify a single-stranded antibody gene of a mouse type monoclonal antibody by PCR; (2) the framework portrion of the mouse type monoclonal antibody by PCR; (3) the framework portrion of the antibody gene of a human type monoclonal antibody to prepare a single-stranded antibody gene of the human type single-stranded immunoporter gene; and (4) the human type single-stranded immunoporter

ö gene is expressed in a microbe to prepare a recombinant protein of the human type single-stranded immunoporter. Also described is a method for introducing the above complex of monoclonal antibody-fused protein through a cell surface receptor. The method is used for the preparation of a monoclonal antibody-fused protein against a receptor present on cell surface. The present sequence represents a protein sequence which is given in an example from the present invention. Monoclonal antibody; fusion protein; antigen; cell surface; receptor; Gaps Mouse and human chimeric monoclonal antibody related protein BC. ö Length 258; 1; Indels 23; Mismatches Score 42; Pred. No. ABB05994 standard; Protein; 258 AA. . 0 73.7%; 88.9%; (first entry) Query Match Best Local Similarity 88.2 Lea 8; Conservative Chimeric - Mus sp. Chimeric - Homo sapiens. | ||||||| 165 RTSENIYSY 173 σ 1 RASENIYSY 258 AA; 09-MAY-2002 Synthetic. ABB05994; Sequence chimeric 8830000088 ò 셤

protein fused with a monoclonal antibody against an antigen present on cell surfaces

29-MAY-2000; 2000JP-0158575. 29-MAY-2000; 2000JP-0158575

JP2001333780-A.

04-DEC-2001

(KEIO-) GH KEIO GIJUKU

WPI; 2002-135945/18

N-PSDB; ABA94204

Example; Fig 13; 24pp; Japanese.

une present invention describes a process and which can transfer a gene by combining with the gene and containing a human trype single-stranded monoclonal antibody and a peptide which is the combining site for the gene. Also described is a complex of a monoclonal antibody-fused protein which is a complex of monoclonal antibody-fused protein which is a complex of monoclonal antibody-fused protein and a method for the preparation of a monoclonal protein and an each of for the preparation of a monoclonal antibody-fused protein against a receptor present on cell surface in which: (1) an mRNA extracted from a hybridoma cell having productivity of said monoclonal antibody as ingle-stranded antibody gene of a mouse type monoclonal antibody is converted to prepare a single-stranded antibody gene of a human type monoclonal antibody to prepare a single-stranded nutloody gene of a human type monoclonal antibody to prepare a human type single-stranded immunoporter gene; and (4) the human type single-stranded immunoporter gene is expressed in a microbe to prepare a recombinant protein of the human type single-stranded immunoporter. See in munoporter a recombinant protein of the human type single-stranded immunoporter. The present invention describes a protein which is fused with a

Gaps

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73.7%; 88.9%;

Query Match 73.7 Best Local Similarity 88.9 Matches 8; Conservative

165 RTSENIYSY 173

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given in an example from the present invention.

258 AA;

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introducing the above complex of monoclonal antibody-fused protein through a cell surface receptor. The method is used for the preparation of a monoclonal antibody-fused protein against a receptor present on cell surface. The present sequence represents a protein sequence which is given in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A protein fused with a monoclonal antibody against an antigen present
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                                                                                                                                                                                                                                                                 Human monoclonal antibody related protein sequence CvC.
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                                                                                 73.7%;
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The present interaction describes a process which is these which a monoclonal antibody against an antigen present on cell surface and which can transfer a gene by combining with the gene and containing a human corporation and a monoclonal antibody and a peptide which is the combining site for the gene. Also described is a complex of a monoclonal antibody-fused protein which is a complex of monoclonal antibody-fused protein against a receptor present on cell surface in which: (1) an mRNA extracted from a hybridoma cell having productivity of said monoclonal antibody against a receptor present on cell surface is used as the template to amplify a single-stranded antibody portion of the mouse type monoclonal antibody by CK: (2) the framework portion of the mouse type monoclonal antibody by CK: (2) the framework portion of the complex to a minody gene of a human type monoclonal antibody; (3) a gene encoding the amino acid tail is added to the single-stranded antibody gene of the fuman type monoclonal antibody to prepare a human type single-stranded immunoporter gene; and (4) the human type single-stranded immunoporter gene; and microbal antibody to prepare a human type single-stranded immunoporter gene; through a cell surface receptor. The method is used for the preparation of the human type single-stranded immunoporter. Also described is a method for introducing the above complex of monoclonal antibody-fused protein a preparation of a monoclonal antibody-fused protein against a receptor present on cell curface. The present sequence represents a protein sequence which is surface. The present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A protein fused with a monoclonal antibody against an antigen present
                                                                                                                                                                                                                                                                       Monoclonal antibody; fusion protein; antigen; cell surface; receptor.
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                                                                                                                                                                                                               Human monoclonal antibody related protein sequence CaC.
                         ABB05996 standard; Protein; 258 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example, Fig 15; 24pp; Japanese.
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ABB0599
                                                           monoclonal antibody against an antigen present on cell surface and which can transfer a gene by combining with the gene and containing a human cype single-stranded monoclonal antibody and a peptide which is the combining site for the gene. Also described is a complex of a monoclonal antibody-fused protein which is a complex of monoclonal antibody-fused protein which is a complex of monoclonal antibody-fused protein which is a receptor present on cell surface in which: (1) an mRNA extracted from a hybridoma cell having productivity of said monoclonal antibody against a receptor present on cell surface in which: (1) an mRNA extracted from a hybridoma cell having productivity of said monoclonal antibody painst a receptor present on cell surface is used as the template to amplify a single-stranded antibody gene of a mouse type monoclonal antibody is converted to prepare a single-stranded antibody gene of a human type monoclonal antibody to prepare a human type single-stranded immunoporter. See the amino acid tail is added to the single-stranded infamunoporter gene is expressed in a microbe to prepare a recombinant protein of the human type single-stranded immunoporter. Also described is a method for introducing the above complex of monoclonal antibody-fused protein against a receptor present on cell through a cell surface receptor. The method is used for the preparation of a monoclonal antibody-fused protein against a receptor present on cell surface. The present sequence represents a protein sequence which is
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monoclonal antibody against an antigen present on cell surface and which can transfer a gene by combining with the gene and containing a human can transfer a gene by combining with the gene and containing a human combining site for the gene. Also described is a complex of a monoclonal antibody-fused protein which is a complex of monoclonal antibody-fused protein which is a complex of monoclonal antibody-fused protein against a receptor present on cell surface in which: (1) an mRNA extracted from a hybridoma cell having productivity of said monoclonal antibody gainst a receptor present on cell surface is used as the template to amplify a single-stranded antibody gene of a monose type monoclonal antibody is converted to present on cell surface is used as the template to amplify a single-stranded antibody gene of the mouse type monoclonal antibody is converted to prepare a single-stranded intibody gene of the amino acid tail is added to the single-stranded antibody gene of the amino acid tail is added to the single-stranded immunoporter gene; and (4) the human type single-stranded immunoporter gene; and microbe to prepare a human type single-stranded immunoporter gene; and microbe to prepare a recombinant protein of the human type single-stranded immunoporter.

C introducing the above complex of monoclonal antibody-fused protein through a cell surface receptor The method is used for the preparation chrowing a cell surface receptor. The method is used for the preparation chrown and antibody-fused protein antibody-fused protein or cell surface receptor. The method is used for the preparation or cell surface receptor.
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Pred. No. 5.1;
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       73.7%;
88.9%;
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monoclonal antibody against an antigon present on cell surface and which can transfer a gene by combining with the gene and containing a human crype single-stranded monoclonal antibody and a peptide which is the combining site for the gene. Also described is a complex of a monoclonal containing an integration which is a complex of monoclonal antibody-fused protein which is a complex of monoclonal antibody-fused protein against a receptor present on cell surface in which: (1) an mRNA extracted from a hybridoma cell having productivity of said monoclonal antibody against a receptor present on cell surface is used as the template to amplify a single-stranded antibody gene of a monoclonal antibody is converted to prepare a single-stranded antibody gene of the minoclonal antibody is converted to prepare a single-stranded antibody gene of a human type monoclonal antibody is converted to prepare a single-stranded antibody gene of the human type monoclonal antibody is antibody gene of the human type monoclonal antibody is antibody gene of the human type monoclonal antibody is antibody gene of the human type monoclonal antibody is antibody gene of the human type monoclonal antibody is antibody gene of the human type monoclonal antibody is antibody gene of the human type monoclonal antibody is converted to prepare a single-stranded antibody gene of the human type monoclonal antibody is antibody gene of the human type monoclonal antibody is antibody gene of the human type monoclonal antibody is antibody gene of the human type monoclonal antibody is antibody gene of the single-stranded monoclonal antibody is an of the human type monoclonal antibody is an into antibody gene of the single-stranded monoclonal antibody is converted to prepare a single-stranded monoclonal antibody is converted to prepare a single-stranded monoclonal antibody is converted to prepare a single-stranded monoclonal antibody gene of the human type monoclonal antibody gene of the human type monoclonal antibody gene of the human type monoclonal antibod
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                                                                                                                                                                                                                                                                                                                                Monoclonal antibody related protein sequence pBH.
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: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
       GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                      US-09-257-069-8
US-09-881-037-35
US-08-881-037-35
US-08-881-037-34
US-08-881-037-34
US-08-881-037-55
US-08-881-037-71
US-08-881-037-71
US-08-881-037-71
US-08-881-037-72
US-08-881-037-72
US-08-881-037-72
US-08-397-411-2
US-08-397-411-2
US-08-397-411-2
US-08-397-411-2
US-08-397-411-2
US-08-377-411-2
US-08-377-411-2
US-08-377-411-2
US-08-377-411-2
US-08-377-411-2
US-08-379-057-28
US-08-379-057-21-62
                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -08-553-501A-62
-08-765-783A-81
                                                                                                                                     262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                    protein search, using sw model
                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                   seq length: 0
seq length: 200000000
                                                                                               1 RASENIYSYLP 11
                                                                               US-10-007-790-8
57
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Match Length DB
                                                                                                                                                                                                                                                                                                                                                       Perfect score:
                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                         Score
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                                                                                                                                                                  Minimum DB
Maximum DB
                                    OM protein
                                                                                                 Sequence:
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                                                   Run on:
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Gaps
                            884,
886,
857,
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Sequence
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i Sequence 4, Application US/09257069

j Patent No. 6348830

i GENERAL INFORMATION:
 GENERAL INFORMATION:
 APPLICANT: Medical & Biological Laboratories Co., Ltd.
 TITLE OF INVENTION: Monoclonal Antibody Specific for TITLE OF INVENTION: Monoclonal Antibody Specific for TITLE OF INVENTION: MONBER: US/09/257,069
 CURRENT APPLICATION NUMBER: US/09/257,069
 CURRENT FILING DATE: 1998-09-07
 PRIOR APPLICATION NUMBER: US/09/257,069
 PRIOR PILING DATE: 1998-09-07
 PRIOR FILING DATE: 1998-09-07
 NUMBER OF SEQ ID NOS: 10
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 4
 LENGTH: 107
 TYPE: PRT
 ORGANISM: Mus musculus
 US-09-257-069-4
                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/09257069
Patent No. 6346380
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Monoclonal Antibody Specific for TITLE OF INVENTION: Phosphatidylinositol-3,4,5-Triphosphate; FILE REPERENCE: M3-008-US
CURRENT APPLICATION NUMBER: US/09/257,069
CURRENT APPLICATION NUMBER: US/09/257,069
FRIOR APPLICATION NUMBER: J999-02-4
PRIOR FILING DATE: 1998-09-07
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 57; DB 4; I
Pred. No. 0.00014;
          US-09-205-231-87

US-08-553-501A-84

US-08-553-501A-86

US-09-205-231-86

US-09-205-231-86

US-08-553-501A-55

US-08-553-501A-55

US-09-205-231-55

US-09-205-231-55

US-08-205-231-57

US-08-100-73

US-08-100-73

US-08-921-100-73
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US-08-880-142-77
US-08-902-201-73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
CORGANISM: Mus musculus
US-09-257-069-8
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87.7%; Score 50; DB 3; Length 99; 100.0%; Pred. No. 0.031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                       COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037
FLING DATE: 23-JUN-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION DATA
APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION: 330
ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, ANCOINEER: 34,202
REFERENCE/DOCKET NUMBER: 203442110710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
CORPUTER: IBM PC compatible
CORPUTER: BATENTIN RC SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 33, Application US/08881037
Patent No. 6080588
GENERAL INFORMATION:
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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FILING DATE: 23-UNN-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-MAY-1995
                     & Foerster
                   E: Morrison & Foer
755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (650) 494-075
TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 10; Conservative
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||||||||||
16 RASENIYSYL 25
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                              STREET: 752 CITY: Palo Alto
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                                                                                                     USA
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US-08-881-037-33
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                 Query Match 100.0%; Score 57; DB 4; Length 107; Best Local Similarity 100.0%; Pred. No. 0.0017; Matches 11; Conservative 0; Mismatches 0; Indels
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5. 0.029;
0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
COMPOTER: BATCHIN BELEAGE #1.0, Version #1.30
SOGTWARE: PAECHIN Release #1.0, Version #1.30
SOGTWARE: PAPLICATION DATA:
APPLICATION NUMBER: US/08/881,037
FILING DATE: 23-401-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-MAY 1995
CLASSIFICATION: 530
CLASSIFICATION: 530
CLASSIFICATION: 530
                                                                                                                                                         Sequence 68, Application US/08881037
; Sequence 68, Application US/08881037
; Patent No. 6608588
; GENERAL INFORMATION:
; APPLICANT: Glick, Gary D.
; TITLE OF INVENTION: DNA BINDING ANTIBODIES
; NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 50; DB 3; Pred. No. 0.020; Mismatches
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Patent No. 6080588
GENERAL INFORMATION:
APPLICANT: Glick, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Konski, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442110710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 87.7%; Sco
Best Local Similarity 100.0%; P:
Matches 10; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (650) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 94 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                   1 RASENIYSYLP 11
                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 RASENIYSYL 33
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STRANDEDNESS: BIN
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US-08-881-037-68
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Pred. No. 0.031;
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      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037
FILING DATE: 23-JUN-1997
CLASSIFICATION DATA: 98/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION NUMBER: US/08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION NUMBER: US/08/443,540
ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 34,202
TELECOMMUNICATION INDER: 303442110710
TELECOMMUNICATION INFORMATION:
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0
                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Glick, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Poerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-881-037-69; Sequence 69, Application US/08881037; Sequence 69, Application US/08881037; GENERAL INFORMATION: APPLICANT: Glack, Gary D. APPLICANT: Swanson, Patrick C. TITLE OF INVENTION: DNA BINDING ANTIBODIES NUMBER OF SEQUENCES: 113; CORRESPONDENCE ADDRESS: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.7%; Scor.
100.0%; Pred. No. v.
      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               CONTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                       US-08-881-037-35
; Sequence 35, Application US/08881037
; Patent No. 6080588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Morrison & Foerster
755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
1.RNGTH: 99 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 10; Conservative
      10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                1 RASENIYSYL 10
                                                                                        16 RASENIYSYL 25
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US-08-881-037-35
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      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87.7%; Score 50; DB 3; Length 99; 100.0%; Pred. No. 0.031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037
FILING DATE: 23-UN-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/881,037
FILING DATE: 13-WAY-1995
CLASSIFICATION: 530
ATTONEY/AGENT INFORMATION:
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442110710
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (650) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 34, Application US/08881037
; Patent No. 6080588
; GENERAL INFORMATION:
    APPLICANT: Glick, Gary D.
    APPLICANT: Swanson, Patrick C.
    TITLE OF INVENTION: DNA BINDING ANTIBODIES
    NUMBER OF SEQUENCES: 113
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: MORTISON & FOETSET: 755 Page Mill Road
    CITY: Palo Alto
CLASSIFICATION: 530
ATTOKNEY/AGENT INFORMATION:
NAME: KONSKi, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442110710
TELECOMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 99 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RASENIYSYL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 RASENIYSYL 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
US-08-881-037-34
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US-08-881-037-33
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US-08-881-037-34
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                                                                                                                                                                                                                                                                                                                                  87.7%; Score 50; DB 3; Length 107; 100.0%; Pred. No. 0.034; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

SOFTWARE PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/881,037

FILING DATE: 23-JUN-1997

CLASSIFICATION 530

PRIOR APPLICATION NUMBER: US 08/443,540

FILING DATE: 18-MAY-1995

CLASSIFICATION NUMBER: US 08/443,540

FILING DATE: 18-MAY-1995

CLASSIFICATION NUMBER: 34,202

REGISTRATION NUMBER: 34,202

REGISTRATION NUMBER: 34,202

REGISTRATION NUMBER: 34,202

REGISTRATION NUMBER: 203442110710

TELECOMMULICATION INFORMATION:

TELEPHONE: (650) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Glick, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                        203442110710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Morrison & Foerster STREEF: 755 Page Mill Road CITY: Palo Alto STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 71, Application US/08881037 Patent No. 6080588
                   REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-560
TELEFAX: (650) 494-0792
                                                                                                                                      INFORMATION FOR SEQ ID NO: 70
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 10; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                    Query Match 87.7
Best Local Similarity 100.
Matches 10; Conservative
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TOPOLOGY:
US-08-881-037-71
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                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037
FLING DATE: 23-UN-1997
FLING APPLICATION DATA:
APPLICATION NUMBER: US 08/443,540
FLING APPLICATION DATA:
APPLICATION NUMBER: US 08/443,540
FLING DATE: 18-MAY-1995
CLASSIFICATION: SO 08/443,540
FLING DATE: 18-MAY-1995
CLASSIFICATION: SO 08/443,540
FLING DATE: 18-MAY-1995
CLASSIFICATION: SO 08/443,540
FLING DATE: 18-MAY-1995
TELECOMMUNICATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442110710
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037
FILING DATE: 23-JUN-1997
CLASSIFICATION 530
PRIOR APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION: S30
ATTORNEY/AGENT INFORMATION:
NAME: KORSKI, Antoinette F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 70, Application US/08881037
Patent No. 6080588
GENERAL INFORMATION:
APPLICANT: Glick, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
CORRESPONDENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDUIW TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                ZIP: 94304-1018
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RASENIYSYL 10
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Palo Alto
                                               USA
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US-08-881-037-70
                                               COUNTRY:
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Sequence 2. Application US/08397411

Patent No. 6129914

GENERAL INFORMATION:
APPLICANT: Wenner, George
APPLICANT: Gingrich, Roger
APPLICANT: Link, Brian
APPLICANT: Lower Bispecific Antibody Effective to Treat
TITLE OF INVENTION: Bispecific Antibody Effective to Treat
TITLE OF INVENTION:
STATES TOWNERS.

STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87.7%; Score 50; DB 3; Length 107; 100.0%; Pred. No. 0.034;
                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,411
FILING DATE: U1-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/859,583
                                                                                                                                                                                                                                                                                                                            CARACTER AFPLICATION NUMBER: US/08/397,411
FILING DATE: 01-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION DATE: 37-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-004901
TELEPONE: 415-326-2400
TELEPAN: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Pred. No. 0.(
;ive 0; Mismatches
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OPERATING SYSTEM: PC-DOS/MS-DOS
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
             San Francisco
California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94105
                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-397-411-2
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Sequence 1, Application US/08397411

Sequence 1, Application US/08397411

Sequence 1, Application US/08397411

Septence No. 6129914

APPLICANT: Weiner, George

APPLICANT: Gingrich, Roger

APPLICANT: Link, Brian

TITLE OF INVENTION: Bispecific Antibody Effective to Treat

TITLE OF INVENTION: B-Cell Lymphoma and Cell Line

NUMBER OF SEQUENCES: 14

CORRESPONDENCES. 14

CORRESPONDENCES. 14

ADDRESSEE: Towneend and Townsend and Crew

STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 50; DB 3; Length 107; Pred. No. 0.034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUW TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/881,037

FILING DATE: 23-JUN-1997

CLASSIFICATION: 530

PRIOR APPLICATION NUMBER: US 08/443,540

FILING APPLICATION NUMBER: 30

CLASSIFICATION NUMBER: 330

ATTORNEY/AGENT INFORMATION:

NAME: KORSKI, Antoinette F.

REGISTRATION NUMBER: 34,202

REGISTRATION NUMBER: 34,202

REGISTRATION NUMBER: 3330

ATTORNEY/AGENT INFORMATION:

NAME: GOOKET NUMBER: 203442110710

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) #13-5600
                                                                                                                                                                                      Sequence 72, Application US/08881037
Sequent No. 6080588
GENERAL INFORMATION:
APPLICANT: Swanson, Patrick C.
ITILE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSE: MORTISON & FOEISTER
STREET: 755 Page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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Best Local Similarity 100.0%; P. Matches 10; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (650) 494-0792
24 RASENIYSYL 33
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US-08-881-037-72
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US-08-881-037-72
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Gaps
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                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE OR NUCLEOSIDE PHOTOAFFINITY
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  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: United States
COUNTRY: United States
TIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/681,432
FILING DATE: 23-JUL-1996
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US 08/208,822
FILING DATE: 11-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: BURN, DOANE, SWECKER & MATHIS STREET: P.O. BOX 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    COMPOUND MODIFIED AN MANUFACTURE AND USE
                                                                                                                                                                                                                                                                                              KOHLER, Heinz
RAJAGOPALAN, Krishnan
PAVLINKOVA, Gabriela
                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NUCLEOTIDE OF TITLE OF INVENTION: COMPOUND MODITIES OF INVENTION: MANUFACTURE ATTLE OF INVENTION: THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/07958140
Patent No. 5489525
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100.0%;
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TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 227 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                         APPLICANT: HALEY, Boyd E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 10; Conservative
    10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RASENIYSYL 10
                                                                                        24 RASENIYSYL 33
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APPLICANT: Pastan, I
TITLE OF INVENTION: I
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-07-958-140-2
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    Matches
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APPLICANT: Weiner, George
APPLICANT: Gingrich, Roger
APPLICANT: Link, Brian
APPLICANT: Link, Brian
APPLICANT: Link, Brian
TITLE OF INVENTION: Bispecific Antibody Effective to Treat
TITLE OF SEQUENCES: B-Cell Lymphoma and Cell Line
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.7%; Score 50; DB 3; Length 214; 100.0%; Pred. No. 0.072;
                                                                                                                                                                                                                                                                                                                                        87.7%; Score 50; DB 3; Length 107;
100.0%; Pred. No. 0.034;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Townsend and Townsend and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 01-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/859,583
FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, william M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-004901
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REPERENCE/DOCKET NUMBER: 011823-004901
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/397,411
FILING DATE: 01-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/08397411 Patent No. 6129914
                                                                                                             TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 107 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                     Query Match 87.7
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415-326-2422 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
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: California
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RASENIYSYL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 RASENIYSYL 33
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                              US-08-397-411-2
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GENERAL INFORMATION:
APPLICANT: Lopez, Osvaldo
APPLICANT: Wylie, Dwane E.
APPLICANT: Wagner, Fred W.
TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESSS:
ADDRESSEE: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.
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                                                                                                                      87.7%; Score 50; DB 5; Length 243; 100.0%; Pred. No. 0.083; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 03-JUL-1997
CLASSIFICATION NUMBER: US/08/888,366
FILING DATE: 03-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/187,407
FILING DATE: 27-JAN-1994
PRIOR APPLICATION NUMBER: US 07/990,542
FILING DATE: 14-DEC-1992
PRIOR APPLICATION NUMBER: US 07/493,299
FILING APPLICATION NUMBER: US 07/324,392
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 07/324,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Carter, Charles G.
REGISTATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.39USC1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
REDIUM TYPE: Floppy disk
CMBUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 24, Application US/08888366
Patent No. 5972656
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Best Local Similarity 90.00
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                        10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                              TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                      157 RASENIYSYL 166
                                                                                                                                                                                                                        1 RASENIYSYL 10
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       amino acid
                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55402
                                                                           PCT-US93-09166-2
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US-08-888-366-24
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GENERAL INFORMATION:
APPLICANT: Pastan, Ira H.
TITLE OF INVENTION:
NONDERCE: 1
CORRESPONDENCE: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 87.7%; Score 50; DB 1; Length 243; Best Local Similarity 100.0%; Pred. No. 0.083; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                            COMPUTER READBLE FORM:

COMPUTER READBLE FORM:

MEDIUW TYPE: IBM PC Compatible

COMPUTER: IBM PC Compatible

APPLICATION NUMBER: US/07/958,140

FILING DATE: 19921008

CLASSIFICATION: 436

ATOMORYA AGENT INFORMATION:

REFERENCE/DOCKET NUMBER: 11,990

REFERENCE/DOCKET NUMBER: 15280-77

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION OF 2:

SEQUENCE CHRAACTERISTICS:

LENGTH: 243 amino acids
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ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/09166
FILING DATE:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: One Market Plaza, Steuart Street Tower CITY: San Francisco
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NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REPRENCE/DOCKET NUMBER: 1528
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: AMNO ACID
TOPOLOGY: 14-
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 243 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-07-958-140-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157 RASENIYSYL 166
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Gaps

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APPLICANT: Hollenbaugh, biane L.
APPLICANT: Gilliland, Lisa K.
APPLICANT: Gilliland, Lisa K.
APPLICANT: Gilliland, Lisa K.
APPLICANT: Gordon, Marcia L.
APPLICANT: Bajorath, Jurgen
APPLICANT: Aruffo, Alejandro A.
APPLICANT: Aruffo, Alejandro A.
TITLE OF INVENTION: Monoclonal Antibodies Specific For
TITLE OF INVENTION: In Diagnosis and Therapy
TITLE OF INVENTION: In Diagnosis and Therapy
CORRESPONDENCE: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company
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Pred. No. 0.43;
                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,057
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
NAME: POOT, Brian W.
REGISTRATION NUMBER: 32,928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                           Bristol-Myers Squibb Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MBER: US/08/379,057
26-JAN-1995
                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release ""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Siadak, Anthony W.
Hollenbaugh, Diane L.
Gilliland, Lisa K.
Gordon, Marcia L.
Bajorath, Jurgen
Aruffo, Alejandro A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 000.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 727-3670
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
                                                             3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3005 First Avenue
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Best Local Similarity 90.v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
FRAGMENT TYPE: internal
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                                                                                  CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-379-057-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                             APPLICANT: Gilliland, Lisa.
APPLICANT: Gilliland, Lisa.
APPLICANT: Gordon, Marcia L.
APPLICANT: Gordon, Marcia L.
APPLICANT: Bajorath, Jurgen
TITLE OF INVENTION: Monoclonal Antibodies Specific For
TITLE OF INVENTION: In Diagnosis of Human gp39 and Methods For Their Use
TITLE OF INVENTION: In Diagnosis and Therapy
CORRESPONDENCE: 57
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibodies Specific For
Spitopes of Human gp39 and Methods For Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 108;
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ZIP: 98121
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,057
FILING DATE: .26-JM-1995
CTASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: POOr. Brian W.
REGISTRATION NUMBER: 32,928
REGISTRATION NUMBER: 000133-
TELECOMMUNICATION NUMBER: ON0133-
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1727-3670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                   E: Bristol-Myers Squibb Company 3005 First Avenue
                                                                                                      Sequence 27, Application US/08379057
Patent No. 5876950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 28, Application US/08379057
Patent No. 5876950
                                                                                                                                                                    Siadak, Anthony W.
Hollenbaugh, Diane L.
Gilliland, Lisa K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hollenbaugh, Diane L. Gilliland, Lisa K.
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90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RASENIYSYL 10
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24 RASENIYGYL 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Seattle
STATE: Washington
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Best Local Similarity
Matches 9; Conserv
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APPLICANT: Siadak
APPLICANT: Hollen
                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-379-057-27
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US-08-379-057-28
                                                             RESULT 19
US-08-379-057-27
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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Pred. No. 0.65;
2; Mismatches 0; Indels
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Pred. No. 0.12;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: SATO, Koh
APPLICANT: HIRATA, Yuichi
TITLE OF INVENTION: RESHARED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,501A FILING DATE: 20-FEB-1996 CLASSIFICATION: 536 PRIOR APPLICATION NUMBER: WO PCT/JP94/00859 FILING DATE: 30-MAY-1994 PRIOR APPLICATION NUMBER: US/0859 PRIOR APPLICATION NUMBER: US/0859 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53466/177/AAOK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Foley & Lardner
3000 K Street, N.W., Suite 500
                                   SEQ ID NOS: 21
FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPER: Flappy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: JP 5-129787
FILING DATE: 31-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, HACOLD C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/1
                                                                                                                                                                                                                                                                                                                                                                                           US-08-553-501A-62; Sequence 62, Application US/08553501A; Patent No. 5856135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.9%;
90.0%;
            1998-09-28
                                                                                                                                                                                         75.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (202) 672-5300
(202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                       Query Match
Best Local Similarity 80.0
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                             24 RASENIYSFV 33
                                                                                                                               ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: si
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        PRIOR FILING DATE:
NUMBER OF SEQ ID NOS
SOFTWARE: FastSEQ fo
SEQ ID NO 4
LENGTH: 107
TYPE: PRT
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US-08-553-501A-62
                                                                                                                                                  US-09-406-532-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Connie L. Erickson-Miller
APPLICANT: Stephen D. Holmes
APPLICANT: Jemes D. Holmes
TITLE OF INVENTION: TIEZ Agonist Antibodies
FILE REFERENCE: P50843
CURRENT APPLICATION NUMBER: US/09/406,532A
CURRENT FILING DATE: 1999-09-27
PRIOR APPLICATION NUMBER: 60/102,098
PRIOR FILING DATE: 1998-09-28
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Connie L. Erickson-Miller
APPLICANT: Stephen D. Holmes
APPLICANT: Stephen D. Holmes
APPLICANT: James D. Winkler
FILE OF INVENTION: TIEZ Agonist Antibodies
FILE REFERENCE: P50843
CURRENT APPLICATION UNDBER: US/09/406,532A
PRIOR APPLICATION NUMBER: 60/102,098
                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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. OTHER INFORMATION: 15B8 light chain CDR 1
US-09-406-532-8
                                                                                                                                                                                                                                                                                                                               77.2%; Score 44; 90.0%; Pred. No. (
                         NAME: Poor, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: 000133-
TELECOMMUNICATION INFORMATION:
TELEPAX: (206) 727-3670
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-406-532-4; Sequence 4, Application US/09406532A; Patent No. 6365154; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-406-532-8; Sequence 8, Application US/09406532A; Sequence 8, Patent No. 6365154; GENERAL INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Poor, Brian W.
                                                                                                                                                                                     LENGTH: 128 amino acids TYPE: amino acid
                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 90.0°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 80.0'
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ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: SITE
                                                                                                                                                                                                                                                                                         US-08-379-057-12
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STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/205,231
FLING DATE: 20-FEB-1996
APPLICATION NUMBER: US/08/553,501
FLING DATE: 20-FEB-1996
APPLICATION NUMBER: WO PCT/JP94/00859
FILING DATE: 30-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/553,501
FILING DATE: 30-MAY-1994
RILING DATE: 30-MAY-1994
ATORNEY/AGENT INFORMATION:
NAME: WEGNER, HAROLD C.
REGISTRATION NUMBER: 25,258
REPERENTATION NUMBER: 25,258
REPERENTATION NUMBER: 25,258
REPERENTATION NUMBER: 25,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 2000 Pennsylvania Avenue, NW, suite 5500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Matsushima, Kouji
APPLICANT: Matsumoto, Yoshihiro
APPLICANT: Yamada, Yoshiki
APPLICANT: Yamada, Yoshiki
APPLICANT: Tsuchiya, Masayuki
APPLICANT: Tsuchiya, Masayuki
APPLICANT: Yamazaki, Tatsumi
APPLICANT: Reshaped Human Antibody tTITLE OF INVENTION: Interleukin-8
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Pred. No. 0.12;
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                     ., Suite 500
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; Sequence 81, Application US/09416557
; Patent No. 6245894
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 53
TELECOMMUNICATION INFORMATION:
                   STREET: 3000 K Street, N.W. CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
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Best Local Similarity 90.0
Matches 9; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
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CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON
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APPLICANT: Matsum
APPLICANT: Matsum
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STATE:
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APPLICANT: SATO, Koh
APPLICANT: SATO, Koh
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6
CORRESPONDENCE: 91
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                      ISEE: MORRISON & FOERSTER: 2000 Pennsylvania Avenue, NW, suite 5500 Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,783A
FILING DATE: 07-MAR-1997
CLASSIFICATION: 530
PRIOR PEPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                APPLICANT: Yamada, Yoshiki
APPLICANT: Sato, Koh
APPLICANT: Tsuchiya, Masayuki
APPLICANT: Yamazaki, Tatsumi
TITLE OF INVENTION: Reshaped Human Antibody
TITLE OF INVENTION: Interleukin-8
NUMBER OF SEQUENCES: 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35029-20001.20
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Pred. No. (
                                                                                            Sequence 81, Application US/08765783A
Patent No. 599424
GENERAL INFORMATION:
APPLICANT: Matsushima, Kouji
APPLICANT: Matsushima, Kouji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 62, Application US/09205231
Patent No. 6121423
GENERAL INFORMATION:
                                                                                                                                                            Matsushima, Kouji
Matsumoto, Yoshihiro
Yamada, Yoshiki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: MISSANIGE, KALE H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 3502
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-822-0168
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90.0%;
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-765-783A-81
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SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
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Best Local Similarity 90.0
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ADDRESSEE: MORRISON
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RASENIYSNL 10
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US-08-765-783A-81
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US-09-205-231-62
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RESULT 28
US-08-553-501A-87
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Best Local Similarity 90.0%;
Matches 9; Conservative
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                      FILING DATE: 30-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-1
FILING DATE: 31-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
NAME: WEGNER, Harold C. 25,258 REGISTRATION NUMBER: 25,258 REFERENCE/DOCKET NUMBER: 53-TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
                                                                                                                                                                                     APPLICATION NUMBER: UFILING DATE: 20-FEB-1CASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 7-March-199
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 202-887-1500
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 3000
CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 35029-20001.10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 12-Oc
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                                                                                                                                                                           APPLICATION NUMBER: WO PCT/JP94/00859
                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Foley & Lardner
3000 K Street, N.W., Suite 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SATO, Koh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TSUCHIYA, Masayuki
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linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESHAPED HUMAN ANTIBODY TO HUMAN INTERLEUKIN-6
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                                                                                                                          JP 5-129787
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                                     53466/177/AAOK
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Pred. No. 0.12;
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Query Match
Best Local Similarity
watches 9; Conserva
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Query Match
Best Local Similarity
Thes 9; Conserve
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                                                                         US-09-205-231-87
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 20-FEB-15
FILING DATE: 30-MAY-15
FILING DATE: 30-MAY-15
FILING DATE: 30-MAY-15
FRIOR APPLICATION DATA:
APPLICATION NUMBER: JE
APPLICATION NUMBER: JE
APPLICATION NUMBER: JE
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                            REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: JP 5-129787
FILING DATE: 31-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: HIRATA, YUICHI
TITLE OF INVENTION: RESHAPED HUMAN
TITLE OF INVENTION: INTERLEUKIN-6
NUMBER OF SEQUENCES: 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                           TOPOLOGY:
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3000 K Street, N.W., Suite 500
                                                                                                                                                                                                   (202) 672-5399
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              Conservative
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                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                                                 20-FEB-1996
UMBER: WO PCT/JP94/00859
                                                                                                   single
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                            71.9%;
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                            Score 41; Pred. No. 1
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Pred. No. 1
               Mismatches
                                           DB 3;
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                                           Length 98;
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               Indels
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US-08-553-501A-84
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                                                                                                 Sequence 86, Appli
Patent No. 5856135
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                                                                 GENERAL INFORMATION:
APPLICANT: TSUCHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 904136
INFORMATION FOR SEQ ID NO:
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FILING DATE: 20-FEB-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/00859
FILING DATE: 30-MAY-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REFERENCE/DOCKET NUMBER: 53
TELECOMMUNICATION INFORMATION:
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APPLICANT: HIRATA, Yuichi
TITLE OF INVENTION:
                                APPLICANT:
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FILING DATE: 31-MAY-1993
ATTORNEY/AGENT INFORMATION:
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                                                                                                               Application US/08553501A
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                           SATO, Koh
HIRATA, Yuichi
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SATO, Koh
                                                                 TSUCHIYA, Masayuki
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90.0%;
RESHAPED HUMAN ANTIBODY TO HUMAN INTERLEUKIN-6
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Pred. No. 1.5;
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                                                                                                                                                                                                                                                                                              Length 106;
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US-09-205-231-84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: TSUCHIY
APPLICANT: SATO, K
APPLICANT: HIRATA,
                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 25,450
REFERENCE/DOCKET NUMBER: 5346
TELECOMMUNICATION INFORMATION:
THE COMMUNICATION OF 12-5300
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-1
FILING DATE: 31-MAY-1993
ATTORNEY/AGENT INFORMATION:
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          ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                ADDRESSEE: Foley & L
                                                                                                                                                                                                                                                APPLICANT: HIRATA, Yuichi
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6
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PRIOR APPLICATION NUMBER:
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CITY: Washington
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CITY: Washington
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER:
                                                                                                                                                 STATE: D.C
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                                                                                                                                COUNTRY:
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3000 K Street, N.W., Suite 500
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3000 K Street, N.W., Suite 500
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                                                                                                                                   USA
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SATO, Koh
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US/09/205,231
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Pred. No.
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CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
US/08/553,501

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/553,501
FILING DATE: 20-FEB-1996
APPLICATION NUMBER: WO PCT/JP94/00859
FILING DATE: 30-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: JP 5-129787
FILING DATE: 31-MAY-1993
ATTORNEY/AGENT INFORMATION:
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FILING DATE: 20-FEB-1996
APPLICATION UNMBER: WO PCT/JP94/0
FILING DATE: 30-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-129787
FILING DATE: 31-MAY-1993
ATTORNEY/AGENT INFORMATION:
ANASC LEGENT INFORMATION:
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                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPANIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/205, 231
APPLICATION NUMBER: US/09/205, 231
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LENGTH: 106 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: HIRATA, Yuichi
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6
NUMBER OF SEQUENCES: 91
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STRANDEDNESS: single
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/177/AAOK
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SATO, Koh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (202) 672-5300
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90.0%;
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25,258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3; Length 106;
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Best Local Similarity
Marches 9; Conserve
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                                                  US-08-553-501A-55
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                                                                                                   IELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 aminimum.
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 aming
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                              CLASSIFICATION: 536

PRIOR APPLICATION NUMBER: WO PCT/JP94/0
APPLICATION NUMBER: WO PCT/JP94/0
FILING DATE: 30-MAX-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-129787
FILING DATE: 31-MAX-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                    MOLECULE TYPE:
                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 53466/177/AAOK TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/553,501A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: HIRATA, Yuichi
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6
NUMBER OF SEQUENCES: 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 53466/177/AAOK TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                 TOPOLOGY:
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TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington
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                                                                                               amino acids
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                                                                protein
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71.9%;
90.0%;
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Score 41;
Pred. No.
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 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3;
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US-09-205-231-55
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Patent No.
                                                                                                        Patent No. 6121
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                                                 GENERAL INFORMATION:
APPLICANT: TSUCHI
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/
APPLICATION NUMBER: US/08/
FILING DATE: 20-FEB-1996
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: WO PCT
APPLICATION NUMBER: WO PCT
FILING DATE: 30-WAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-1
AP
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TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 53
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                             Application US/09205231
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     HIRATA, Yuichi
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                                                                                                                                                                                                                                                                                                                                                          Conservative
                               TSUCHIYA, Masayuki
SATO, Koh
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90.0%;
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Pred. No. 1.8;
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                                                                                                                                                                                                                                                                                                                                                        Patent No. 6121423
GENERAL INFORMATION:
APPLICANT: TSUCHIX
APPLICANT: SATO, K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 57,
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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LENGTH: 125 amino acic
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NAME: WEGNER, Harold C.
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity hes 9; Conserv
                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: CLASSIFICATION:
                                                                              ZIP: 20007-5109
                                                                                                                                                                              STREET:
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                                                                                                   COUNTRY:
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                                                                                                                                                    CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43 RASENIYSNL 52
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   amino acid

GY: linear
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                                                                                                                             D.C
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                                                                                                        USA
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APPLICANT: SATO, Koh
APPLICANT: HIRATA, Yuichi
TITLE OF INVENTION: RESHAPED HUMAN
TITLE OF INVENTION: INTERLEUKIN-6
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 53
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPHAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 30-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION UNMEER: JP 5-129787
FILING DATE: 31-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/553,501 FILING DATE: 20-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 25,258
                                                                                                                                                                                                                                 Application US/09205231
E: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Foley & Lardner
3000 K Street, N.W., Suite 500
                                                                                                                                                                    TSUCHIYA, Masayuki
                                                                                                           RESHAPED HUMAN ANTIBODY TO HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO PCT/JP94/00859
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 125
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 71.9%;
Best Local Similarity 90.0%;
           FILING DATE: 20-FBB-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/00859
FILING DATE: 30-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-129787
FILING DATE: 31-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,501A
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TOPOLOGY: linear
MOLECULE TYPE: protein
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LENGTH: 125 amino acid
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 534
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-129787
FILING DATE: 31-MAY-1993
ATTORNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: HIRATA, Yuichi
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6
                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
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APPLICATION NUMBER: WO PCT/JP94/00859
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(202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SATO, Koh
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Pred. No. 1
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1.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 5994524
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 73
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                                                                                                                                              FILING DATE: 07-MAR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MUTASHIGE, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 3502
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20006-1888

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatik
                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Reshaped Human Antibody to TITLE OF INVENTION: Interleukin-8
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MOLECULE TYPE:
FRAGMENT TYPE:
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nes 9; Conserv
                                                                                                                      TELEPHONE: 202-0168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
                            TOPOLOGY:
                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                        ENGTH:
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                                                        amino acid
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                                                                     126 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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Yamazaki, Tatsumi
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Matsumoto, Yoshihiro
Yamada, Yoshiki
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              protein
                                         single
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Pred. No.
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RESULT 40
US-08-765-783A-77
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                                                                       US-08-765-7,83A-77
                                                                                                                                                                                                                       TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
Query Match 71.9%;
Best Local Similarity 90.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 71.9%;
Best Local Similarity 90.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 77, Application US/08765783A Patent No. 5994524
                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIÚM TYPE: Diskette
COMPUTER: LIBM COMPATIBLE
OPERÁTING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,783A
FILING DATE: 07-WAR-1997
CLASSIFICATION ETABA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/765,783A
FILING DATE: 07-WAR-1997
RIOR ÀPPLICATION DATA:
APPLICATION NUMBER: 290
REFERENCE/DOCKET NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 35029-20001.20
TELLEPHONE: 202-887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                     TYPE: amino acids
STRANDEDNESS: simm'
TOPOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Tsuchiya, Masayuki
APPLICANT: Yamazaki, Tatsumi
TITLE OF INVENTION: Reshaped Human Antibody to
TITLE OF INVENTION: Interleukin-8
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW, suite 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 2000 Peni
CITY: Washington
STATE: DC
                                                                                    LOCATION: 1...19
OTHER INFORMATION:
                                                                                                        NAME/KEY: Signal Sequence LOCATION: 1...19
                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-822-0168
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Sato, Koh
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Matsumoto, Yoshihiro
Yamada, Yoshiki
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1...19
Score 41; DB 2;
Pred. No. 1.8;
0; Mismatches
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Pred. No. 1.8;
0; Mismatches
 1; Indels
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 Gaps
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Search completed: July 18, 2003, 15:11:50 Job time : 13.76 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database :
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Run on:
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               /cgn2_6/ptodata/1/pubpaa/US07_FUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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sequence 12, Appi	Sequence 936, App	Sequence 50, Appl	Sequence 41, Appl	Sequence 33, Appl	Sequence 27, Appl	Sequence 77, Appl	Sequence 73, Appl	Sequence 81, Appl	Sequence 16, Appl	Sequence 13, Appl	Sequence 19, Appl	Sequence 32, Appl	Sequence 15, Appl	Sequence 18, Appl	Sequence 7, Appli	Description

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## ALIGNMENTS

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Query Match
Best Local Similarity
Thes 10; Conserve
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TITLE OF INVENTION: CDR-H1-DERIVED PETIDE CB11, PHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: MADE THEREFROM AND METHODS OF TREATING DISORDERS IN
TITLE OF INVENTION: MAMMALS
FILE REFERENCE: 1129-R-02
CURRENT APPLICATION NUMBER: US/10/322,142
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: 60/341,349
PRIOR FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 60/374,754
PRIOR FILING DATE: 2001-12-18
PRIOR FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 7
SEQ ID NO 7
SEQ ID NO 7
SECONDO 12
SECONDO 10
SECONDO 12
SECONDO 
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                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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DEVAUX, CHRISTIAN
GRANIER, CLAUDE
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OLIVE, DANIEL
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                                                87.7%; Score 50; DB 15; Length 12; ilarity 100.0%; Pred. No. 0.0052; Conservative 0; Mismatches 0; Indels
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RESULT 4
US-10-322-142-32
Sequence 32, Application US/10322142
Publication No. US20030113322A1
GENERAL INFORMATION:
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US-10-096-246-15
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APPLICANT: Fulton, R E
APPLICANT: Nayata, Leslie
TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functiona
TITLE OF INVENTION: SCPV Antibody Against Venzuelan Equine Enceph
FILE REFERENCE: NEL-0007
FULE REFERENCE: NEL-0007
CURRENT APPLICATION NUMBER: US/10/096,246
CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin version 3.1
SOFTWARE: Patentin version 3.1
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Publication No. US20030100060A1
GENERAL INFORMATION:
APPLICANT: The Minister of National Defence, Government of Canada
APPLICANT: Fulton, R E
APPLICANT: Alvi, Azhar E
APPLICANT: Nagata, Leslie
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                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                           Query Match
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Publication No. US20030100060A1
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TITLE OF INVENTION: Cloning, Expression, Sequencing,
TITLE OF INVENTION: CFC Antibody Against Venzuelan
FILE REFERENCE: NEL-0007
CURRENT APPLICATION NUMBER: US/10/096,246
CURRENT APPLILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 37
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TYPE: PRT
ORGANISM: Mouse hybridoma cell line 1A4A1
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; SEQ ID NO 19
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-096-246-19
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                                                                                              Query Match
Best Local
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Publication No. US20030100060A1
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Best Local Similarity
                                                                             Matches
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APPLICANT: Fulton, R E
APPLICANT: Alvi, Azhar E
APPLICANT: Nagata, Leslie
TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mor
TITLE OF INVENTION: ScFv Antibody Against Venzuelan Equine Encephalitis Virus (Vee)
FILE REFERENCE: NEL-0007
CURRENT APPLICATION NUMBER: US/10/096,246
CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
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24 KASENTYSYL 33
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                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.7%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33
                                                                                              78.9%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAURENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 50;
Pred. No.
                                                                                              Score 45; DB 1
Pred. No. 0.48;
                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 15;
                                                                                                                DB 15;
                                                                                                                Length 108
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                                                                         Gaps
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RESULT 6 US-10-207-655-13

Interleukin-8

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US-09-730-857-81
; Sequence 81, Application U; Patent No. US20020082396A1; GENERAL INFORMATION:
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                                                                                                                                                                                                RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                              ) ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-096-246-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16, Application US/10096246
Publication No. US20030100060A1
GENERAL INFORMATION:
APPLICANT: The Minister of National Defence, Government of Canada
APPLICANT: Fulton, R E
APPLICANT: Alvi, Azhar E
APPLICANT: Nagata, Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069.401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
SEQ ID NO 13
LENGTH: 259
TYPE: PRT
                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 16
LENGTH: 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13, Application US/10207655 Publication No. US20030118592A1
                                                                                                                                                                                                                                                                                                                                              Best
                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/096,246
CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Nagata, Leslie
TITLE OF INVENTION: Cloning, Expression, Sequencing,
TITLE OF INVENTION: SCFV Antibody Against Venzuelan
FILE REFERENCE: NEL-0007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: SITE
LOCATION: (1)..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: MOUSE ANTI-HUMAN CD37 SCFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                        Local Similarity tes 9; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 8; Conserv
   TITLE OF
                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                   24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 RTSENVÝSÝL 53
                                                                                                                                                                                                                                                                                     1 RASENIYSYL 10
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                                                                                                                                                                                                                                                   RASVNIYSYL 33
                                                                                                                                                             Application US/09730857
                                                                                                                                                                                                                                                                                                                          Conservative
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Tsuchiya, Masayuki
Yamazaki, Tatsumi
INVENTION: Reshaped Human Antibody to
                                                                                      Matsumoto, Yoshihiro
                                                         Sato,
                                                                        Yamada,
                                                                                                                                                                                                                                                                                                                                       75.4%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.9%;
                                                                        Yoshiki
                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 45; DB 15; Length 259; Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                          Score 43; |
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                          DB 15;
1.2;
                                                                                                                                                                                                                                                                                                                                                         Length 110;
                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Equine Encephalitis Virus (Vee)
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                                                                                                                                                                                                                                                                                                                        0
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                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 73,
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US-09-730-857-73
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GENERAL INFORMATION:
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Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 81:
                                                          COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEFAX: 202-822-0168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 09/416,557
FILING DATE: 1999-10-12
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/730,857
FILING DATE: 07-Dec-2000
CLASSIFICATION: Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE DESCRIPTION: SEQ ID NO: 81:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 105
                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Reshaped Human Antibody to
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RASENIYSYL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                  3, Application US/09730857
US20020082396A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RASEIIYSYL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 35
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                       STATE: DC
                                                                                                                                                     CITY: Washington
                                                                                                                                                                           STREET: 2000 Pennsylvania Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                  Tsuchiya, Masayuk
Yamazaki, Tatsumi
                                                                                                                                                                                                                                                                                                                                                                       Matsushima, Kouji
Matsumoto, Yoshihiro
                                                                                                                                                                                                                                                                                                                                     Sato, Koh
                                                                                                                                                                                                                                                                                                                                                       Yamada,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000 Pennsylvania Avenue, NW, suite 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71.9%;
90.0%;
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                                                                                                                                                                                                                                                                                                                                                       Yoshiki
                                                                                                                                                                                                                                                      Interleukin-8
                                                                                                                                                                                                                                                                                                                  Masayuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41; DB 1
Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35029-20001.10
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                                                                                                                                                                           NW, suite 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 11;
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RESULT 10
US-09-730-857-77
IS-09-730-857-77
Sequence 77, Application US/09730857
Patent No. US20020082396A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-730-857-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/730,857
FILING DATE: 07-Dec-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                         ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                   Tsuchiya, Masayuki
Yamazaki, Tatsumi
TITLE OF INVENTION: Reshaped Human Antibody to
Interleukin-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 350
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 09/416,557
FILING DATE: 1999-10-12
ATTORNEY/AGENT INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/416,557
FILING DATE: 1999-10-12
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Matsushima, Kouji
Matsumoto, Yoshihiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RASENIYSYL 10
                                                                                                                                                                                                                                                                                                  CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Signal Sequence LOCATION: 1...19
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 126 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                          STATE: DC
                                                                                                                                                                                                                                                                                                                          STREET: 2000 Pennsylvania Avenue, NW, suite 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                     COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-822-0168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 202-887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sato,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamada,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yoshiki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41; DB Pred. No. 3.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35029-20001.10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 27, Application US/09730857
Patent No. US20020082396A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 77:
INFORMATION FOR SEQ ID NO: 27:
                                                 APPLICATION NUMBER: 09/416,557
FILING DATE: 1999-10-12
ATTORNEY/AGENT INFORMATION:
NAME: MUTAShige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 35029-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Veri
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/730,857
FILING DATE: 07-Dec-2000
CLASSIFICATION: -Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tsuchiya, Masayuki
Yamazaki, Tatsumi
TITLE OF INVENTION: Reshaped Human Antibody to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Matsushima, Kouji
Matsumoto, Yoshihiro
Yamada, Yoshiki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein FRAGMENT TYPE: internal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RASENIYSYL 10
                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20006-1888
                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 1...19
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
                                   TELEFAX: 202-822-0168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 202-822-0168
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                     <Unknown>
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Pred. No.
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. 3.1;
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US-09-848-798-41
; Sequence 41, Application US/09848798
; Publication US20030040605A1
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                                                                                                                                                                                                                             RESULT 13
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GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/848,798
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/905,243
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/300,970
PRIOR FILING DATE: 1999-04-28
NUMBER OF SECID NOS: 97
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 33, Application US/0990
Patent No. US20020062009A1
GENERAL INFORMATION:
APPLICANT: Taylor, Alexander H
                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: DOMAIN
LOCATION: (24)...(34)
OTHER INFORMATION: CDRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: CDRII
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: DOMAIN
LOCATION: (50)...(66)
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les 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                  24 RASQGIYNYL 33
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
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90.0%;
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70.0%;
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                                                                                                                                                                                                                                                                                                                                                    core 38; DB 10;
red. No. 7.6;
Mismatches 1;
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3.2;
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Query Match
Best Local Similarity
Tatches 8; Conserve
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                                                         US-08-779-457-50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 50, Appropriate Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 41
              Query Match
Best Local (
   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550 PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11 NUMBER OF SEQ ID NOS: 224
                                                                                                                                    TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585
FILING DATE: 01/08/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,37
REFERENCE/DOCKET NUMBER: F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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                                                                                                     SEQUENCE CHARACTERISTICS LENGTH: 241 amino acid
                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 415/225-1994
                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: WinPatin (Ge
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: 3.5 inch, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 460 Point San Bruno Blvd CITY: South San Francisco
                                                                            TOPOLOGY:
                                                                                                                                                                 TELEFAX:
                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 01
FILING DATE: 06/20/96
                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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Similarity 7; Conserv
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                                                                                       1: 241 amino acids
Amino Acid
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Chiang, Nancy Y.
Kyung, Jin Kim
Matthews, William
Rodrigues, Maria L.
NVENTION: WSX RECEPTOR AGONIST ANTIBODIES
                                                                                                                                                                415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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              66.7%;
70.0%;
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                                                                                                                                                                                                                         40,378
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Score 38; DB Pred. No. 23; 2; Mismatches
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                 DB 8;
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                            Length 241;
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PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-25
PRIOR FILING DATE: 2001-03-25
PRIOR FILING DATE: 2001-03-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver.
EQ ID NO 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
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SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION UNBER: US/08/844,215 FILING DATE: 17-APR-1997 CLASSIFICATION: 435 PRIOR APPLICATION UNBER: US 08/635,109 FILING DATE: 19-APR-1996
                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: PERSSON, MATS AXEL
APPLICANT: ALLANDER, TOBIAS ERIK
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR
TITLE OF INVENTION: HEPATITIS C VIRUS (HCV) E2 ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH:
                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS &
                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                COUNTRY: U
                                                                                                                                                                                                                                                                                                    STREET: 90 MIDDLE CITY: MENLO PARK
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90 MIDDLEFIELD ROAD, SUITE
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5. US20030059937A1
                                                                                                                                                                                                                                                                   USA
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70.0%;
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US-09-829-482-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LENGTH: 110'
; TYPE: PRT
; ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-096-246-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/096,246
CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin version 3.1
SEQ ID NO 14
                                                                                                                                                                                                                                               Sequence 3, Application US/09829482
Patent No. US20020001843A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/10096246 Publication No. US20030100060A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Matches 8; Conserv
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: The Minister of National Defence, Government of Canada APPLICANT: Fulton, R E APPLICANT: Alvi, Azhar E APPLICANT: Nagata, Leslie TITLE OF INVENTION: Cloning, Expression, Sequencing, and Function: TITLE OF INVENTION: ScFv Antibody Against Venzuelan Equine Encepl FILE REFERENCE: NEL-0007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 80
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 325-7812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity hes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: SIRTOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
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ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
                                                                                                                                                                                                           APPLICANT: LIGHTNER, JONATHAN EDWARD
TITLE OF INVENTION: STARCH BIOSYNTHETIC ENZYMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23
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                                                                                            CITY: WILMINGTON STATE: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                     RASENIYRNL 33
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                                                                         COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Pred. No. 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No.
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Equine Encephalitis Virus (Vee)
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RESULT 20
US-09-815-242-5565
J Sequence 5565, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
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Best Local Similarity
Thes 7; Conserve
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US-10-236-433-14
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                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: 60/317,890
PRIOR FILING DATE: 2001-09-07
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: O'CONNOY, Michael B.
APPLICANT: Gilbert, Lawrence I.
APPLICANT: Warren, James T.
TITLE OF INVENTION: Insecticide Targets
FILE REFERENCE: 09531-070001
CURRENT APPLICATION NUMBER: US/10/236,433
CURRENT FILING DATE: 2002-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/318,006
                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
                                                                                                                                                                                                                                                                                                                                                      LENGTH: 468
                                                                                                                                                                                                                                        Local Similarity
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FILING DATE: 10-Apr-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/852615
FILING DATE: MAY 7, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 SSISIYSYLP 199
                                                                                                                                               28 RGMGNLYNYLP 38
                                                                                                                                                                                  1 RASENIYSYLP 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: MAJARIAN, WILLIAM R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1083-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 302-773-0164
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                                                                                                                                                                                                                                      Score 36; DB 15;
Pred. No. 1.1e+02;
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Query Match
Best Local Similarity
Thehes 6; Conserve
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                                                                          PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2006-10-26
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5565
LENGTH: 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                   APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L. APPLICANT: Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
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CURRENT FILING DATE: 2001-03-21
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APPLICATION NUMBER: 60/257,931
                      FILING DATE: 2000-10-23
APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
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Zyskind, Judith W.
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Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                               Trawick, John D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yamamoto, Robert T
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Pred. No. 1.3e+02;
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RESULT 23
US-09-815-242-13228
; Sequence 13228, Application US/09815242
; Patent No. US2002061569A1
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                                                                                                                                                                                                                                                                                                            ; ORGANISM: Staphylococcus aureus
US-09-815-242-12952
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; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12320
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PELICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 12320
                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 12952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12952, Application US/09815242 Patent No. US20020061569A1
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Best Local (
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Best Local :
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TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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                                                                                                                                                                                                                     63.2%;
Local Similarity 54.5%;
les 6; Conservaring
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Local Similarity 54.5%;
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                                                                                                                                                                                    1 RASENIYSYLP 11
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                                                                                                                                          OSTSGIYSYLP
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                                                                                                                                            44
                                                                                                                                                                                                                                                Score 36; DB 10;
Pred. No. 1.4e+02;
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Pred. No. 1.4e+02;
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SOFTWARE: WORDERFECT 8
SEQ ID NO 57
LENGTH: 11
TYPE: PRT
                                                                                                         ; ORGANISM: Human US-10-091-300-57
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                                                                                                                                                                                                                                                                                                                                                   Sequence 57, Application US/100 Publication No. US20030108545A1 GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13228
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                                       Matches
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                           APPLICANT: Rockwell, Patricia
APPLICANT: Goldstein, Neil I.
TITLE OF INVENTION: Combination Methods of Inhibiting
TITLE OF INVENTION: Endothelial Growth Factor Recepto
FILE REFERENCE: 11245/46211
                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/091,300 CURRENT FILING DATE: 2002-03-04
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITAA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Haselbeck, APPLICANT: Ohlsen, K
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nes 6; Conserv
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                                     Similarity 7; Conserv
   RASENIYSYL 10
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Zyskind, Judith W.
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                                   Conservative
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54.5%;
                                                       61.4%;
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                                   Score 35; DB 1
Pred. No. 2.9;
2; Mismatches
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Pred. No.
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1.5e+02;
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                                                                                                                                                                                                                                                                                ibiting Tumor Growth With a Vascular Receptor Antagonist
                                                                       Length 11;
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US-09-956-206A-9
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Best Local Similarity 70.0
Conservative
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Patent No. US20020164339A1
GENERAL INFORMATION:
APPLICANT: DO COUTO, FERNANDO J.R.
CERIANI, ROBERTO L.
PETERSON, JERRY A.
TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
                                                                             Sequence 47508, Application US/09864761 Patent No. US20020048763A1 GENERAL INFORMATION:
                 APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R. APPLICANT: Hanzel, David K.
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INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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FILING DATE: 14-SEP-1995
APPLICATION NUMBER: PCT/US95/11683
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: 08/487,598
FILING DATE: 7-UNE-1995
APPLICATION NUMBER: 08/307,868
FILING DATE: 16-SEPT-1994
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 44,408
REFERENCE/DOCKET NUMBER: 276332000101
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/956,206A
FILING DATE: 19-Apr-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 9:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                            10 RASGNIHNYL 19
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TYPE: amino acid
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OPERATING SYSTEM: PC-DOS/MS-DOS
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Chen, Wensheng
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70.0%;
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                                                                                                                                                                                                                                                                                                                              Score 35; DB 11; Length 30; Pred. No. 8.6;
                                                                                                                                                                                                                                                                                                            Mismatches
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; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.8
; OTHER INFORMATION: SWISSPROT HIT: P44596, EVALUE 1.20e+00
; OTHER INFORMATION: EST_HUMAN HIT: A1286316.1, EVALUE 1.00e-09
US-09-864-761-47508
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                                                                                                                                                                    US-09-977-283A-75
Sequence 75, Application US/09977283A
Publication No. US20030031664A1
GENERAL INFORMATION:
APPLICANT: Reed, Guy L.
TITLE OF INVENTION: Composition and Method for Enhancing Fibrinolysis
FILE REFERENCE: 0609.4320003
CURRENT APPLICATION NUMBER: US/09/977,283A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence |
SEQ ID NO 47508
LENGTH: 59
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Best Local
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CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
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PRIOR FILING DATE: 2000-09-27
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APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
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Pred. No. 18;
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NT FILING DATE: 2001-10-16
APPLICATION NUMBER: 08/934,000

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US-09-977-283A-76
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                                                                                                                                                             SEQ ID NO 76
LENGTH: 107
TYPE: PRT
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Matches
   Query Match
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LENGTH: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 08/934,000
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/026,356
PRIOR FILING DATE: 1996-09-20
NUMBER OF SEQ ID NOS: 81
                                                                                                                                                                                                                                                                                                                                                EMERAL INFORMATION:
APPLICANT: Reed, Guy L.
TITLE OF INVENTION: Composition and Method for Enhancing Fibrinolysis
FILE REFERENCE: 0609.4320003
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PRIOR APPLICATION NUMBER: 60/026,356
PRIOR FILING DATE: 1996-09-20
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.1
                                                  OTHER INFORMATION: Alpha-2 Antiplasmin Antibody NAME/KEY: MISC_FEATURE LOCATION: (74)...(74)
OTHER INFORMATION: May be any Amino Acid
                                                                                                                                       ORGANISM: Artificial Sequence
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NAME/KEY: MISC FEATURE
LOCATION: (86) ''''
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LOCATION: (21)..(21)
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Pred. No. 3
   Score 35;
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 DB 12;
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                                             IOCATION: (56)...(56)
OTHER INFORMATION: May be at NAME/KEY: MISC FEATURE
LOCATION: (70)...(70)
OTHER INFORMATION: May be at NAME/KEY: MISC FEATURE
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FITLE OF INVENTION: Composition and Method for Enhancing Fibrinolysis
                                                                                                                                                                                                                                                                                                                                               LOCATION: (76)..(76)
OTHER INFORMATION: MAY
NAME/KEY: MISC_FEATURE
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OTHER INFORMATION: May
NAME/KEY: MISC_FEATURE
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OTHER INFORMATION: May
NAME/KEY: MISC FEATURE
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OTHER INFORMATION: May be
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OTHER INFORMATION: May be
OTHER INFORMATION: May be
NAME/KEY: MISC_FEATURE
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LOCATION: (9)...(9)
OTHER INFORMATION: May be any Amino Acid
NAME/KEY: MISC_FEATURE
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ORGANISM: Artificial Sequence
OTHER INFORMATION: May be any Amino Acid
           NAME/KEY: MISC_FEATURE
LOCATION: (94)..(94)
                                         COCATION: (93) . (93)
OTHER INFORMATION: May
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OTHER INFORMATION: May be
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2; Mismatches
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RESULT 32
US-10-096-246-17
Sequence 17, Application US/10096246
Publication No. US20030100060A1
GENERAL INFORMATION:
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US-10-194-975-94
; Sequence 94, Application US/10194975
; Publication No. US20030039649A1
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US-10-194-975-94
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LENGTH: 108
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Matches 7; Conserv
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CURRENT FILING DATE: 2002-10-10
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CURRENT APPLICATION NUMBER: US/10/091,300
CURRENT FILING DATE: 2002-03-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rockwell, Patricia
APPLICANT: Goldstein, Neil I.
TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth With a Vascular
TITLE OF INVENTION: Endothelial Growth Factor Receptor Antagonist
                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 122
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Foote, Jefferson
TITLE OF INVENTION: Super Humanized Antibodies
FILE REFERENCE: 501231.01
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SOFTWARE: WordPerfect
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TYPE: PRT
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8.0 for Windows
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70.0%;
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Pred. No.
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Pred. No. 34;
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US-09-977-283A-5
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Sequence 7, Application US/09977283A
Publication No. US20030031664A1
GENERAL INFORMATION:
APPLICANT: Reed, Guy L.
TITLE OF INVENTION: Composition and Method for Enhancing Fibrinolysis
FILE REFERENCE: 0609.4320003
CURRENT APPLICATION NUMBER: US/09/977,283A
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 08/934,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1996-09-20
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Reed, Guy L.
TITLE OF INVENTION: Composition and Method for Enhancing Fibrinolysis
FILE REFERENCE: 0609.4320003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/09977283A Publication No. US20030031664A1
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TITLE OF INVENTION: Cloning, Expression, Sequencing,
TITLE OF INVENTION: Scbr Antibody Against Venzuelan
FILE REFERENCE: NEL-0007
CURRENT APPLICATION NUMBER: US/10/096,246
CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 37
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/977,283A CURRENT FILING DATE: 2001-10-16 PRIOR APPLICATION NUMBER: 08/934,000 PRIOR FILING DATE: 1997-09-19 PRIOR APPLICATION NUMBER: 60/026,356 PRIOR PRIOR APPLICATION NUMBER: 60/026,356
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APPLICANT: Fulton, R.E
APPLICANT: Alvi, Azhar E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Mouse hybridoma cell line 1A4A1
                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Alpha-2 Antiplasmin Antibody NAME/KEY: MISC FEATURE LOCATION: (-12)...(-12) OTHER INFORMATION: May be either Gly or Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Pred. No.
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Pred. No.
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Equine Encephalitis Virus (Vee)
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US-09-977-283A-7
                                                                                                                                                                                                                   Sequence 17, Application US/09977283A
Publication No. US20030031664A1
GENERAL INFORMATION:
APPLICANT: Reed, Guy L.
TITLE OF INVENTION: Composition and Method for Enhancing Fibrinolysis
                   NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn version 3.1
SEQ ID NO 17
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SEQ ID NO 9
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Best Local Similarity
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                                                                          FILE REFERENCE: 0609.4320003
CURRENT APPLICATION NUMBER: US/09/977,283A
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 08/934,000
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/026,356
PRIOR APPLICATION NUMBER: 60/026,356
PRIOR FILING DATE: 1996-09-20
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PRIOR FILING DATE: 1996-09-20
NUMBER OF SEQ ID NOS: 81
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CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 08/934,000
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
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TITLE OF INVENTION: Composition and Method
FILE REFERENCE: 0609.4320003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/026,356
PRIOR FILING DATE: 1996-09-20
NUMBER OF SEQ ID NOS: 81
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TYPE: PRT
ORGANISM: Artificial Sequence
LENGTH: 127
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Similarity 70.0%;
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70.0%;
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Pred. No. 41;
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Pred. No. 41;
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Watches 7; Conserve
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Alpha-2 Antiplasmin Antibody
US-09-977-283A-17
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 109
LENGTH: 237
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TITLE OF INVENTION: Super Humanized Antibodies
FILE REFERENCE: 501231.01
CURRENT APPLICATION NUMBER: US/10/194,975
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial sequence
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            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb flo
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/863,693
                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                  TITLE OF INVENTION: METHOD FOR MAKING MULTIS HAVING HETEROMULTIMERIC
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                                                                                                                                                              CITY: South San Francisco
STATE: California
                                                                                                                                                COUNTRY: USA
FILING DATE: 23-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                     Application US/09863693
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o. US20030039649A1
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                                                                                                                                                                                                                                                                                                                MERCHANT, A.M.
                                                                                                                                                                                                                                                                                               PRESTA, L.G.
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70.0%;
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Pred. No.
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CLASSIFICATION: <Unknown>

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Query Match
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Publication No. US2003
GENERAL INFORMATION:
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                              INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ARATHOON, R. CARTER, P.J. MERCHANT, A.M. PRESTA, L.G. PRESTA, L.G. HAVING H
                                                                                                                                                                               APPLICATION NUMBER: US/09/863,693
FILING DATE: 23-May-2001
APPLICATION NUMBER: 09/070,166
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Conley, Deirdre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P1099R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-2066
TELEFAX: 650/92-9881
                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/10/143,437
PILING DATE: 10-May-2002
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 09/070,166
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION:
                                                                                                         REFERENCE/DOCKET NUMBER: P1099R1 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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                                                                                                                                            NAME: Conley, Deirdre L. REGISTRATION NUMBER: 36,487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1 DNA Way
LENGTH: 107 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                       TELEFAX: 650/952-9881
                                                                                          TELEPHONE: 650/225-2066
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No. US20030078385A1
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Pred. No. 52;
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                                                                                                                                                 Sequence 45718, Application US/09864761 Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 09/632,366 PRIOR FILING DATE: 2000-08-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Penn,
FEATURE:
OTHER INFORMATION: MAP TO AC009487.3
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.48
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.66
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.79
                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                            RIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                               RIOR APPLICATION NUMBER: PCT/US01/00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIOR APPLICATION NUMBER: GB 24263.6
                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/234,687
                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US01/00661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US01/00664
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Pred. No.
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Perfect score:
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Query Match Best Local Matches 1	PH1069 Ig light chain V region (clone 185-cl) - mous C; Species: Mus musculus (house mouse) C; Date: 30-Sep-1993 #sequence_revision 30-Sep C; Accession: PH1069 R; Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marid J. Exp. Med. 176, 761-779, 1992 A; Title: Both IgM and IgG anti-DNA antibodies A; Reference number: PH0971; MUID:92381444; PM A; Accession: PH1069 A; Status: nucleic acid sequence not shown A; Molecule type: mRNA A; Residues: 1-98 < TIL- A; Experimental source: B cell, strain [NZB x C; Superfamily: immunoglobulin V region; immur C; Keywords: immunoglobulin homology < IMM; F; 16-90/Domain: immunoglobulin homology < IMM;	Query Match Best Local Matches 1 Qy 1 Db 23	PH1068 Ig light chain V region (clone s17.166) - mouse (fraggeries: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #to C;Accession: PH1068 R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N. J. Exp. Med. 176, 761-779, 1992 A;Title: Both IgM and IgG anti-DNA antibodies are the A;Reference number: PH0971; MUID:92381444; PMID:15125- A;Accession: PH1068 A;Status: nucleic acid sequence not shown A;Molecule type: mRNA A;Residues: 1-97 <til- <imm="" [nzb="" a;experimental="" b="" c;keywords:="" c;superfamily:="" cell,="" homology="" immunoglobulin="" nzw]f1="" region;="" source:="" strain="" v="" x=""></til->		6 C C C C C C C C C C C C C C C C C C C
ch 1 Simi 10;	Mus mus per les per le	10; 10; 1 RAS 1 RAS         23 RAS	ht chain V ies: Mus mu ies: Mus im man, D.M.; man, D.M.; med. 176 e: Both Igh rence numbe ssion: PHIL us: nuclei: cule type: dues: 1-97 rimental se rfamily: in ords: immur 9/Domain: i		
h Similarity 10; Conser	regior regior 30 #se 93 #se 96 97 90, 76, 7 96, 7 96, 7 97 97 97 97 97 97 97 97 97 97 97 97 97	Similarity ); Conserv RASENIYSYL	in V region (c)  lus musculus (h)  lep-1993 #seque;  PH168 PH168 IG, 761-779,  h IgM and IgG;  number: PH0971  PH168  PH168  PH168  IgM and IgG;  number: PH0971  RH168  IgH acid seque;  ye: mRNA  1-97 <til- al="" b="" c;="" immunoglobulin;="" immunoglobulin;<="" source:="" td="" y:=""><td></td><td>66666666666666666666666666666666666666</td></til->		66666666666666666666666666666666666666
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Scc; Pr	185-cl) mouse) revision : cevision : fl, R.J.; fl, R.J.; fl) pDNA antil pDNA antil pDNA antil pDNA antil pD = 238144 p not show strain [] fregion; homology	Scc Pr 0;	region (clone s17.166) usculus (house mouse) 93 #sequence_revision 068 Jou, N.T.; Hill, R.J.; 761-779, 1992 M and IgG anti-DNA anti er: PH0971; MVID:923814 c acid sequence not sho mRNA c acid sequence not sho mRNA c TIL> ource: B cell, strain [ mmunoglobulin V region; noglobulin	ALI	AB0719 D64588 J645094 J645090 B89900 F97184 A82358 A92331 C97902 F90257
701	- mouse (fragmus 30-Sep-1993 #to; Marion, T.N.; ibodies are the 444; PMID:15125.own [NZB x NZW]F1; immunoglobuli; y <imm></imm>	50; . No. smatch	; marion, ; marion, ; bodies a ; ibodies a ; 444; PMID ; immunog ; immunog	ALIGNMENTS	
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C; Superfamily: C; Keywords: hete F; 9-83/Domain:
Ig kappa chain V region (JS34/32) - mouse C;Species: Mus musculus (house mouse) C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 C;Accession: S24290 R;Moncharmont, B. Bubmitted to the EMBL Data Library, September 1991 A;Description: Cloning and sequencing of the cDNA coal,Reference number: S24287
                                                                                                                                                                                                                         RESULT 5
S24290
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A;Note: sequence modified after extraction from NCBI backbone
A;Note: sequence extracted from NCBI backbone (NCBIN:122874)
A;Note: sequence extracted from NCBI backbone (NCBIN:122874)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
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C;Accession: £47329

R;Brinkmann, U.; Gallo, M.; Brinkmann, E.; Kunwar, S.; Pastan, I.

Proc. Natl. Acad. Sci. U.S.A. 90, 547-551, 1993

A;Title: A recombinant immunotoxin that is active on prostate cancer cells and that A;Reference number: A47329; MUID:93133825; PMID:8421689

A;Accession: B47329

A;Status: preliminary

A;Molecule type: mRNA; protein

A;Residues: 1-106 <BRI>
A;Residues: 1-106 <BRI>
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A; Residues: 1-101 < HO
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Pred. No. 0.029;
                                          September 1991
ng of the cDNA coding for the variable regions
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A;Experimental source: strain BALB/c
A;Note: this chain was isolated from a myeloma protein
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap; hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lance (Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                           Ig kappa chain precursor V region (F11) - mouse (fragment)
c;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S31488
R;Bespalov, I.A.; Shiyanov, P.A.; Lukashevich, L.V.; Lunev, V.E.; Tribush, submitted to the EMBL Data Library, December 1992
A;Reference number: S31488
                                                                                     #;Cross-references: EMBL:X69859; NID:g50929; PIDN:CAA49493.1; PID:g50930
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
E;36-110/Domain: immunoglobulin homology < IMM>
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Mol. Inmunol. 17, 1507-1513, 1980

A;Title: Amino acid sequence of the variable region of M149

A;Reference number: A01919; MUID:82057806; PMID:6795447

A;Accession: A01919
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A; Residues: 1-128 <BES>
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A; Residues: 1-107 < MON>
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0.03;
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A;Introns: 65/3; 72/3
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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A;Reference number: S22023
A;Accession: S22024
A;Status: preliminary
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C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
C;Accession: $22024
R;Caulfield, M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         k;Cross-references: EMBL:X53484
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
E;37-111/Domain: immunoglobulin homology <IMM>
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Nucleic Acids Res. 18, 5281, 1990
A;Title: Sequences of the Lym-1 antibody heavy and light
A;Reference number: S11244; MUID:90384832; PMID:2119497
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C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
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A; Residues: 1-134 <WEL>
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A; Residues: 1-81 < CAU>
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                  A;Experimental source:
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Residues: 1-107 <MEE>
;Residues: 1-107 <MEE>
;Cross-references: GB:X58596; GB:Y00794; NID:g51574; PIDN:CAA41471.1;
;Experimental source: strain BALB/c
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90.0%;
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90.0%;
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Pred. No. 0.8;
0; Mismatches
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Pred. No.
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Ig kappa chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 21-Jan-2000
C;Accession: S01320
R;Accession: Feys, V:; van de Voorde, A.; Molemans, F.; Fiers, W.
Bur. J. Biochem. 176, 287-295, 1988
Bur. J. Expression in non-lymphoid cells of mouse recombinant immunoglobul: A;Reference number: S01320; MUID:88329081; PMID:3138116
A;Accession: S01320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Note: 106-Leu is translated from the codon CUN
A;Note: the sequence shown here is from the V kappa region of an antiidiotypic monoclonal
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                      A;Gene: cpdB
C;Superfamily: 2',3'-cyclic-nucleotide 2'-phosphodiesterase; 2',3'
C;Keywords: phosphoric diester hydrolase
                                                                                                                                                                                                                                                                                                                                            R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B., deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Eil, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, ENALURE 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 11-Jan-2002
C;Accession: AC0429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X13187; NID:g51784; PIDN:CAA31579.1; PID:g51785 A;Note: this sequence was determined from the differentiated gene C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;1-20/Domain: signal sequence #status predicted <NGS-F;21-234/Product: Ig kappa chain #status predicted <MAT>
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S01320
                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-656 < KUR>
                                                                                                                                                                                                                                                                                                    A,Title: Genome sequence of Yersinia pestis, the causative agent of plague A,Reference number: AB0001; MUID:21470413; PMID:11586360
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A; Residues: 1-234 <DE1>
                                                                                                                                                                                      A; Cross-references:
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Matches
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Best Local
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                                             Query Match
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Similarity 7; Conserv
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  Conservative
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Pred. No. 1.5;
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Pred. No. 3.5;
0; Mismatches
                       Score 41;
Pred. No.
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RASENIYSYL

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N;Alternate names: myeloma protein
(Species: Homo sapiens (man)
(;Species: Homo sapiens (man)
(;Cactesion: PHO880
C;Accession: PHO880
R,Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991
A;Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype
A;Reference number: PHO862; MUID:92078875; PMID:1660528
A;Accession: PHO880
A;Molecule type: protein
A;Residues: 1-65 (MAN)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: complementarity-determining 1
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A;Recession: A01951
A;Molecule type: protein
A;Residues: 1-108 <JAT>
A;Molecule type: protein
A;Residues: 19-139 of the constant region are identical with the corresponding C;Comment: This chain was obtained from antibody to type III pneumococci and was isol C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light ( hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>
F;16-90/Domain: immunoglobulin homology <IMM>
C.Species: Homo sapiens (man)
C.Date: 19:May-1995 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000
C.Accession: S52793
R.Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougenot, B.; Ronco, P.; Denoro, submitted to the EMBL Data Library, March 1995
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                                                                                                    Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
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7;35-49/Region: 0
7;50-56/Region: 0
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Best Local
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cuniculus (domestic rabbit)
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Pred. No. 2.
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Pred. No. 2.4;
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           Matches
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R;Wu, L.C.; Mak, C.H.; Dear, N.; Boehm, T.; Foroni, L.; Rabbitts, T.H. Nucleic Acids Res. 21, 5067-5073, 1993
A;Title: Molecular cloning of a zinc finger protein which binds to the heptamer A;Reference number: S41479; MUID:94077706; PMID:8255760
A;Accession: S41479
                                                                                                                                                                                                                                                                                                                                                                                  RESULT 17
S41479
                                                                                                                                                                                                                                                                                           C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Sep-1999
C;Accession: S41479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: 2',3'-cyclic-nucleotide 2'-phosphodiesterase; 2',3'-cyclic-nucleotide 2 C;Keywords: multifunctional enzyme; periplasmic space; phosphoric diester hydrolase F;1-24/Domain: signal sequence #status predicted <SIG> F;25-652/Product: 2',3'-cyclic-nucleotide 2'-phosphodiesterase #status predicted <MAT> F;27-600/Domain: 2',3'-cyclic-nucleotide 2'-phosphodiesterase homology <CPDB> F;30-123/Domain: phosphoesterase core homology <PEC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X85742; NID:g747912; PIDN:CAA59745.1; PID:g747913 C;Comment: In E. coli the enzyme is bifunctional, catalyzing two consecutive netically distinguishable active sites for two corresponding substrates can be necessarily distinguishable active sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2',3'-cyclic-nucleotide 2'-phosphodiesterase (EC 3.1.4.16) precursor - Yers C;Species: Yersinia enterocolitica C;Species: 19-May-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000 C;Date: 19-May-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
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                                                                                  A;Cross-references: EME
C;Superfamily: HIV-EP2
                                                                                                                                                                                                                                                                                                                                                        DNA-binding
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A; Reference number: $52789
                                                                                                                              A;Residues: 1-767 <WUL>
                                                                                                                                               A; Molecule type: mRNA
                                                                                                                                                                     A;Status: preliminary
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6; Conserv
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                   Score 39;
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30;
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25;
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A; Molecule type: mRNA
A; Residues: 1-2282 <WUL>
A; Cross-references: EMBL:L46815; NID:g1377885; PID:g1377886; PIDN:AAB40884.1
A; Experimental source: strain BALB/c; clone T1; thymocyte, brain
C; Genetics:
A; Gene: Rc
C; Function:
C; Function:
A; Description: binds V(D) J recombination signal sequence and kappa B motif
C; Superfamily: HIV-EP2 enhancer-binding protein
C; Keywords: DNA recombination; transcription factor
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C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000
C;Accession: T42717
R;Wu, L.C.; Liu, Y.; Strandtmann, J.; Mak, C.H.; Lee, B.; Li, Z.; Yu, C.Y.
Genomics 35, 415-424, 1996
A;Title: The mouse DNA binding protein Rc for the kappa B motif of transcription and for ew family of large transcriptional proteins.
A;Reference number: Z22238; MUID:97001141; PMID:8812474
A;Accession: T42717
RESULT 20
A64079
2',3'.cyclic-nucleotide 2'-phosphodiesterase (EC 3.C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995
                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-2310 <MUR>
A;Cross-references: EMBL:Z98978; PIDN:CAB11683.1;
A;Experimental source: strain 972h-; cosmid c27E2
C;Genetics:
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N;Alternate names: Ig kappa chain gene enhancer Recognition component
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000
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A; Accession: T38457
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Pred. No. 97;
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                                             (EC 3.1.4.16) precursor -
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  #text_change 21-Jan-2000
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                                                                    RESULT 22
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R; Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, ; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, , D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: A64079
A.;Cression: A64079
                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 111-123 <AKI>
A; Residues: 111-123 <AKI>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Superfamily: immunoglobulin U region; immunoglobulin Logion; immunoglobulin Logion; immunoglobulin Logion; heterotetramer; immunoglobulin Logion; 
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C;Comment: In E. coli the enzyme is bifunctional, catalyzing two consecutive reactions contentially distinguishable active sites for two corresponding substrates can be identified c;Superfamily: 2',3'-cyclic-nucleotide 2'-phosphodiesterase; 2',3'-cyclic-nucleotide 2'-prosphodiesterase; 2',3'-cyclic-nucleotide 2'-prosphodiesterase; 2',3'-cyclic-nucleotide 2'-prosphodiesterase; 2',3'-cyclic-nucleotide 2'-prosphodiesterase #status predicted 4SIG>
F;12-657/product: 2',3'-cyclic-nucleotide 2'-prosphodiesterase #status predicted <MAT>
F;32-657/Domain: 2',3'-cyclic-nucleotide 2'-prosphodiesterase homology <CPDB>
F;35-128/Domain: phosphoesterase core homology <PEC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig kappa chain precursor V-J-C regions - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 03-Aug-1990 #sequence_revision 03-Aug-1990 #text_change
                                                                                                                                                                                                                                                                                                                                                                   C;Keywords: heterotetramer; immunoglobulir F;143-212/Domain: immunoglobulin homology
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A; Residues: 1-657 <TIGR>
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Best Local
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                                                                                       1 RASENIYSYL
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                                                                                                                                                                               Similarity
8; Conserv
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QASENIYSSL
                                                                                                                                                                                    Conservative
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47
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Pred. No. 40;
4; Mismatches
                                                                                                                                                                                                                          Score 37;
Pred. No.
                                                                                                                                                                                    Mismatches
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C;Species: Escherichia coli
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 08-Oct-1999
C;Accession: C32058
C;Accession: C32058
R;Genilloud, O: Moreno, F:; Kolter, R.
J. Bactericl. 171, 1126-1135, 1989
J. Bactericl. 171, 1126-1135, and transcriptional pattern of the genes i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Paillard, M.; Sederoff, R.R.; Levi
EMBO J. 4, 1125-1128, 1985
A;Title: Nucleotide sequence of the
A;Reference number: S07183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001 C;Accession: D97750
C;Accession: D97750
C;Accession: D97750
R;Cacession: D97750
R;Cacession: D97750
#text_change 30-Sep-2001
#text_change 30-Sep-
                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-272 <GEN>
                                                                                                                                                                                                                                                       A;Title: DNA sequence, products, and transcriptional pattern A;Reference number: A32058; MUID:89123111; PMID:2644225 A;Accession: C32058
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A;Molecule type: DNA
A;Residues: 1-252 <PAI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein 4 - maize mitochondrion plasmid S-1
C;Species: mitochondrion Zea mays (maize)
C;Datc: 30-5ep-1991 #sequence_revision 30-Sep-1991 #text_change 02-Jun-2000
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A;Molecule type: DNA
A;Residues: 1-230 <KUR>
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C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 24
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Matches
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Best Local 9
                                                                                                                                                       Genetics:
                                                                                                                                                                               Cross-references: GB:M24253; NID:g341145; PIDN:AAA72743.1; PID:g522292
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                             Conservative
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                                               Score 37; DB
Pred. No. 24;
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Pred. No. 22;
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                          Mismatches
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                                                                       DB 2;
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A; Note: F14P22.15
C; Superfamily: Ar
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A;Experimental source: cultivar Co
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A; Residues: 1-597 < DAN>
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A;Gene: MIPS:YMR010w
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                                                                                                     261 ASSDIYSYCP 270
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                                                                                                                                                                                                                               Similarity
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                                                                                                                                                     ASENIYSYLP
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                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Columbia; BAC clone
                                                                                                                                                                                                                               Score 37; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                       DB 7
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37;
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R;D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Lemcke, submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein F14P22.150 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change C;Accession: T45676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable membrane protein YMR010w - yeast (Saccharomyces cerevisiae) N_rAlternate names: hypothetical protein YM8270.13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Residues: 1-405 <DEV>
;Cross-references: EMBL:Z48613; NID:g728645; PID:g728658; GSPDB:GN00013; MIPS:YMR010w
;Experimental source: strain AB972
                                                                                                                                                                   299/3; 328/3; 351/3; 380/3; 409/3; 427/3; 458/2; 496/3; 546/1
                                                                                                              protein F14P22.170
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                                                       Length 597
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R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Cha Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig kappa chain V-J region (34-2B) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000
C;Accession: S09968
R;Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
Eur. J. Immunol. 20, 771-77, 1990
A;Title: Variable region sequences of pathogenic anti-mouse red blood cell a;Reference number: S09955; MUID:90269328; PMID:2347362
A;Accession: S09968
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A;Tille: Characterization of major surface glycoprotein genes of human Pneumocystis car: A;Reference number: Z17905; MUID:98380374; PMID:9712777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          major surface glycoprotein - Pneumocystis carinii (fragment)
C;Species: Pneumocystis carinii
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 15-Jun-2001
C;Accession: T30544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Cross-references: EMBL:X51856;.NID:g55403; PIDN:CAA36149.1; PID:g930233
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                           C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C;Accession: H90386
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A; Residues: 1-107 < REI>
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C; Superfamily:
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A;Cross-references: EMBL:AF033212; NID:g3560520; PID:g3560521; PIDN:AAC34975.1
                                                           A;Cross-references: GB:AE006641; NID:g13815473; PIDN:AAK42351.1; C;Genetics:
                                                                                                            A; Molecule type: DNA
A; Residues: 1-184 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein SSO2176 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
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                                                                                                                                                               A;Status: preliminary
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Best Local S
Matches 7
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RASENIYSYL 10
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70.0%;
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54.5%;
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Pred. No. 14;
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A45094
glycogenin glucosyltransferase (EC 2.4.1.186) -
N;Alternate names: glycogen synthase 38K chain;
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                                                                                  RESULT 32
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C;Accession: D64588
C;Accession: D64588
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKen Peterson, S.; Loftus, B.; Richardson, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable pertussis-like toxin chain (EC 2.4.2.-) [imported] - Salmonella enterica C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001 C;Accession: AB0719
                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-274 < TOM>
                                                                                                                                                                                                                                 Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; A;Title: The complete genome sequence of the gastric pathogen Hel A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: D64588
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D64588
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C;Keywords: glycosyltransferase;
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Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A;Title: Complete genome sequence of a multiple drug resistant
A;Reference number: AB0502; PMID:11677608
A;Accession: AB0719
                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Helicobacter pylori
C;Date: 30-Jan-1998 #sequence_revision 30-Jan-1998 #text_change
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C; Genetics:
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A; Residues: 1-242 < PAR >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Chth. T.; Connecton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.;
                                                                                                                                                        A;Cross-references:
                                                                                                                                                                                                            A;Status: preliminary; nucleic acid sequence not
                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable DNA
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Best Local
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72
                                   4 ENIYSYLP 11
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                                                                          Similarity 5; Conserv
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ENLYKYIP 79
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                                                                                                                                                    GB:AE000511; TIGR:HP0548
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                                                                                          63.2%;
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77.8%;
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Pred. No.
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Pred. No.
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Salmonella enterica s
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                                                                                                                                                                                                                                                                                               Smith, H.O.;
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rabbitglycogenin

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C; Species: O
C; Date: 21-M
C; Accession:
R; Viskupic,
submitted to the EMBL Data Library, July 1995
A;Reference number: G08914
A;Accession: G01948
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mkNA
A;Residues: 1-333 <ROD>
A;Cross-references: EMBL:U31525; NID:g976399; PIDN:AAB09752.1; PID:g976400
R;Leffers, H.; Wiemann, S.; Ansorge, W.
                                                                                                                                                                                                                                                                                                                                                                                                       glycogenin glucosyltransferase (EC 2.4.1.186) - human
N;Alternate names: glycogenin
N;Contains: glycogenis (synthase, glycogenin subunit
C;Species: Homo sapiens (man)
C;Date: 21-May-1999 #sequence revision 21-May-1999 #text_change 11-Jun-1999
C;Accession: JC4695; G01948; S45141
R;Barbetti, F:;Rocchi, M:;Bossolasco, M:;Cordera, R.;Sbraccia, P.;Finelli, P.;Cons
Biochem. Biophys. Res. Commun. 220, 72-77, 1996
A;Title: The human skeletal muscle glycogenin gene: cDNA, tissue expression, and chromos
A;Reference number: JC4695; MUID:96176958; pMID:8602861
A;Accession: JC4695; MUID:96176958; pMID:8602861
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A;Note: sequence is inconsistent with the nucleotide translation A;Note: sequence extracted from NCBI backbone (NCBIP:120846)
R;Campbell, D.G.; Cohen, P.
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A;Residues: 1-87, 'S', 89-96, 'L', 98-332 <CAM>
A;Residues: 1-87, 'S', 89-96, 'L', 98-332 <CAM>
R;Pitcher, J.; Smythe, C.; Campbell, D.G.; Cohen, P.
Eur. J. Biochem. 169, 497-502, 1987
A;Title: Identification of the 38-kDa subunit of rabbit skeletal muscle glycogen synthas
A;Reference number: S02470; MUID:88082782; PMID:3121316
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R; Rodriguez,
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C;Keywords: acetylated amino end; glycogen/starch biosynthesis; glycoprotein; glycosylt: F;1/Modified site: acetylated amino end (Thr) #status experimental
F;194/Binding site: carbohydrate (Tyr) (covalent) #status experimental
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A;Title: Rabbit skeletal muscle glycogenin. Molecular cloning and production of fully
A;Reference number: A45094; MUID:93100288; PMID:1281472
A;Accession: A45094
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A; Residues: 1-333 <BAR>
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A;Residues: 9-19;38-44,'M';90-94;204-207,'F',209-210,'KH',213-219
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                                                                                                                                                                                                                                                                                      Cross-references: GB:U44131; NID:g1174166; PIDN:AAB00114.1; PID:g1174167
Experimental source: skeletal muscle
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Best Local
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J. Biochem. 185,
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Pred. No. 46;
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DNA modification methyltransferase [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C;Date: 14-Sep-2001 #sequence consistency consistency
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C;Keywords: acetylated amino end; glycogen/starch biosynthesis; glycog
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A;Note: required to initiate the synthesis of glycogen
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A;Residues: 1-203,'KMSQEPYHICPLGRSQLWHSRLYPRKNGR','NDGNRARLIIWEQIPLTTSRGNLTLTSSR','NTAFF(
A;Cross-references: EMBL:X79537; NID:g496894; PIDN:CAA56073.1; PID:g496895
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A;Description: Cloning and sequencing of a cDNA encoding human glycogenin
A;Reference number: S45140
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A;Experimental source: strain N315
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A; Map position: 3q24-3q25
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4-3q25.1
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54.5%;
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Pred. No.
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-581 <KUR>
A;Cross-references: GB:AE001437; PIDN:AAK80265.1; PID:g15025315; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-611 <HEI>
A;Cross-references: GB:AE004105; GB:AE003852; NID:g9654551; PIDN:AAF93332.1; GSPDB:GN001
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A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: A82358
                                                                                                 A; Nolecule type: DNA
A; Molecule type: DNA
A; Residues: 1-617 < KUR>
A; Cross-references: GB: AE005672; PIDN: AAK74442.1;
A; Cross-reference: strain TIGR4
                                                                                                                                                                                                                                                            R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Pet on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D nson, T.; Hickey, E.K.; Holt, I.E. Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, A;Authors: Complete Genome Sequence of a virulent isolate of Streptococcus
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A95031
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C;Superfamily: vitamin B12 receptor; tonB-dependent receptor amino-terminal homology; to
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                                             A;Gene: SP0264
C;Superfamily:
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                                                                                                                                                                                                A; Status: preliminary
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                                                                                                                                                                                                                                            A; Reference number: A95000; MUID: 21357209; PMID: 11463916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vitamin B12 receptor VC0156 [imported] - Vibrio cholerae (strain N16961 serogroup
                                                                                                                                                                                                                                                                                                                                                                                             Species: Streptococcus pneumoniae;Date: 03-Aug-2001 #text_change 24-Aug-2001;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001;Accession: A95031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Species: Vibrio cholerae;Date: 18-Aug-2000 #text_change 02-Feb-2001;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
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                                             proline-tRNA ligase
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  Score 36;
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Radune, D.; Holtzapple,
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                                           RESULT
A32935
protein P1 - Entamoeba histolytica (fragment)
C;Species: Entamoeba histolytica
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R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B. e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, Y. P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: C97902
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-617 <KUR>
A;Cross-references: GB:AE007317; PIDN:AAK99047.1; PID:g15457791; GSPDB:GN00174
C;Genetics:
                                                                                                                                                                                                                                                                                                                   R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-V Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P. arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
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C;Superfamily: proline-tRNA ligase
C;Keywords: ligase
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A; Residues: 1-637 < KUR>
A; Cross-references: GB:
C; Genetics:
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A; Accession: F90257
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                                                                                                                                                          A;Gene:
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C;Accession: F90257
                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein SSO1053 [imported] - Sulfolobus solfataricus C_iSpecies: Sulfolobus solfataricus
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C;Species: Streptococcus pneumoniae
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Copyright (c) 1993 - 2003 Compugen Ltd
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P20301 entamoeba h

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P26265 salmonella

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P50270 drosophila

P01606 homo sapier

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P22168 foxtail moi

P03932 drosophila

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STRAIN=ATCC 51871 / WA-314 / Serotype 0:8;

Truelzsch K.S.;

Truelzsch K.S.;

Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: THIS BIFUNCTIONAL ENZYME CATALYZES TWO CONSECUTIVE REACTIONS CONVERTING 2', 3'-CYCLIC-NUCLEOTIDE TO 3'-NUCLEOTIDE TO NUCLEOTIDE TO NUCLEOTIDE TO NUCLEOTIDE TO NUCLEIC ACID AND PHOSPHATE.

-i- CATALYTIC ACTIVITY: Nucleoside 2',3'-cyclic phosphate + H(2) O nucleoside 3', phosphate.

-i- SUBCELLULAR LOCATION: Periplasmic.

-i- SIMILARITY: BELONGS TO THE 5'-NUCLEOTIDASE FAMILY.
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SEQUENCE
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eukamania, Eutheria, Lagomorpha, Leporidae, Oryctolagus
               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
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2',3'-cyclic
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MEDLINE=95350630; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Merrick J
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
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or send a
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InterPro; IPR004843; M-ppestrase.
InterPro; IPR004844; S/T_phosphtse.
Pfam; PF00149; Metallophos; 1.
Pfam; PF02872; 5_nucleotidaseC; 1.
PROSITE; P800785; 5_NUCLEOTIDASE_1; 1.
PROSITE; P800786; 5_NUCLEOTIDASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                          Venter J.C
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P44764;
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                                                                                                                 This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                 -!- SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haemophilus
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-NOV-1995 (Rel. 32, Last sequence update)
-OCT-2001 (Rel. 40, Last annotation update)
,3'-cyclic-nucleotide 2'-phosphodiesterase
                                                                                                                                                                                     SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                le-genome random sequencing
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THE 5'-NUCLEOTIDASE FAMILY.
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InterPro; IPR004843; M-ppestrase.
InterPro; IPR004844; S/T_phosphtse.
InterPro; IPR004844; S/T_phosphtse.
Pfam; PF00149; Metallophos; 1.
Pfam; PF02872; 5_nucleotidaseC; 1.
PROSITE; PS00785; 5_NUCLEOTIDASE_1; 1.
PROSITE; PS00786; 5_NUCLEOTIDASE_2; 1.
PROSITE; PS00786; 5_NUCLEOTIDASE_2; 1.
Hydrolase; Multifunctional enzyme; Periplasmic; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Paillard M., Sederoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1989 (Rel. 11, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation updat Hypothetical 29 kDa protein in mitochondria Zea mays (Maize).
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256 AA; 29338 MW; B1D6DE
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Pred. No. 12;
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Pred. No. 22;
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Best Local :
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P23185;
01-NOV-1991
01-NOV-1991
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "DNA sequence, | involved in pro B17.";
                                                                                                                                                  Q03687;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 46.9 kDa protein in PLB1-HXT2 intergenic YMR010W OR YM8270.13.
                   SEQUENCE FROM N.A.
STRAIR=S288c / AB972;
Devlin K., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genilloud O., Moreno F., Kolter R.; "DNA sequence, products, and transcriptional pattern of involved in production of the DNA replication inhibitor
                                                                                                Saccharomyces cerevisiae (Baker's yeast)
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacch
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli
Plasmid IncFII ph
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinf
the European Bioinformatics Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Bacteriol.
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MEDLINE=89123111; PubMed=2644225;
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SUBCELLULAR LOCATION: Cycoplasmic (Potential)
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PROCESSING OF TRIFOLITOXIN.
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(Rel. 20, Last sequence update)
(Rel. 37, Last annotation update)
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TISSUE-Skeletal muscle;
MEDLINE-20011289; PubMed=10542328;
van Maanen M.-H., Fournier P.A., Palmer T.N., Abr.
"Characterization of mouse glycogenin-1 cDNA and
Biochim. Biphys. Acta 1447:284-290(1999).
-!- FUNCTION: SELF-GLUCOSYLAFES, VIA AN INTER-SUE
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Q9R062;
16-OCT-2001
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                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial
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Mammalia; Eutheria;
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  EMBL; AF114031;
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GOFACTOR: SELF-GLUCOSYLATION IS DEPENDE
DIVALENT METAL IONS OF WHICH MANGANESE
DIVALENT METAL IONS OF WHICH MANGANESE
PATHWAY: Glycogen biosynthesis.
SUBUNIT: HOMODIMER, TIGHTLY COMPLEXED 1
TISSUE SPECIFICITY: SKELETAL MUSCLE, HE
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by non-profit institutions as long as its content
ified and this statement is not removed. Usage by ar
ities requires a license agreement (See http://www.isb-
send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                     PTM: SELF-GLYCOSYLATED BY THE TRANSFER OF UDP-GLUCOSE TO ITSELF, FORMING AN ALPHA-1, RESIDUES ATTACHED TO TYR-194.
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CATALYTIC ACTIVITY: UDP-glucose + glycogenin = UDP
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                                                                                                                                                 MEDLINE=94192798;
Alonso M.D., Lomak
                                                                                                                                                                                                                                                                                                              "The occurrence of serine phosphate in regulatory site.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smythe C., Villar-Palasi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=New Zealand white; TISSUE=Skeletal muscle; MEDLINE=90032666; PubMed=2806254; Campbell D.G., Cohen P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Rabbit skeletal muscle glycogenin. Molecular cloning of fully functional protein in Escherichia coli."; J. Biol. Chem. 267:25759-25763(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93100288; Puk
Viskupic_E., Cao Y.,
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TISSUE=Skeletal muscle;
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Mammalia; Eutheria;
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Pfam; PF01501; Glyco_transf_8; 1.
Transferase; Glycogen biosynthesis; Acetylation;
   CHARACTER I ZATION
                                                                                        "Tyrosine-194 of glycogenin undergoes autocatalytic glucosylation is not essential for catalytic function and activity.";
                                                                                                                                                                                                                                                                                                                                                              MEDLINE=89374676; PubMed=3151442; Lomako J., Whelan W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 34-47,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eur. J. Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=89325337; PubMed=2526735;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The amino acid sequence of rabbit skeletal muscle glycogenin.";
Eur. J. Biochem. 185:119-125(1989).
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Thang W., Cheng
                                                                                                                                                    PubMed=8143846;
ko J., Lomako W.M., Whelan W.J.;
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Lagomorpha;
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a; Leporidae; Oryctolagus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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"Self-glucosylation of glycogenin, the initiator of glycogen
biosynthesis, involves an inter-subunit reaction.";
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Cao Y., Steinrauf L.K., Roach P.J.;
"Mechanism of glycogenin self-glucosylation.";
Arch. Biochem. Biophys. 319:293-298(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002495; GT_8.
Pfam; PF01501; Glyco_transf_8; 1.
Transferase; Glycogen biosynthesis; Acetylation; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHARACTERIZATION, AND MUTAGENESIS MEDLINE=99160387; PubMed=10049511
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                           Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L01791; AAA31404.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLYCOGEN SYNTHASE.
CATALYTIC ACTIVITY: UDP-glucose + glycogenin = UDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glucosylglycogenin.
COFACTOR: SELF-GLUCOSYLATION
                                                                 OR GYG1.
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A45094; A45094.
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PHOSPHORYLATION (BY PKA)

O-LINKED (GLC. . .).

K->Q: LOSS OF ACTIVITY.

T -> L (IN REF. 4).
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Pred. No. 25;
Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -> L (IN REF. 4)
-> S (IN REF. 2)
-> L (IN REF. 2)
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MANGANESE ION
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N IS THE MOST EFFECTIVE.
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RESULT 11
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Best Local
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Pak B.J., Sangaralingham S.J., Pang S.C.;
"Molecular cloning and developmental exprecardiac tissue.";
           SEQUENCE FROM N.A. (ISOFORM GN-1)
TISSUE=Skeletal muscle;
MEDLINE=96176958; PubMed=8602861;
                                                     Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                               Eukaryota;
                                                                                                                                                                                           HUMAN
                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: SELF-GLUCOSYLATES, VIA AN INTER-SUBUNIT MECHANISM, FORM AN OLIGOSACCHARIDE PRIMER THAT SERVES AS SUBSTRATE FOR GLYCOGEN SYNTHASE (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF021343; AAB81219.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                              nterPro;
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SUBUNIT: HOMODIMER TICHTLY COMPLEXED TO THE 86 KDA CATALYTIC SUBUNIT OF GLYCOGEN SYNTHASE (BY SIMILARITY).
PTM: SELF-GLYCOSYLATED BY THE TRANSFER OF GLUCOSE RESIDUES FR UDP-GLUCOSE TO ITSELF, FORMING AN ALPHA-1,4-GLYCAN OF AROUND RESIDUES ATTACHED TO TYR-194 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glucosylglycogenin.
COPACTOR: SELF-GLUCOSYLATION IS DEPENDENT ON THE PRESENCE OF DIVALENT METAL DONS OF WHICH MANGANESE ION IS THE MOST EFFECTIVE
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IPR002495; GT_8.
1501; Glyco_trans
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                                                                                  Metazoa;
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70.0%;
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Bossolasco M.,
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Pred. No.
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BY SIMILARITY.
                                                                     Catarrhini; Hominidae; Homo
                                                                                  Craniata; Vertebrata; Euteleostomi;
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Cordera R., Sbraccia P.,
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EMBL; U31525; AAB09752
EMBL; X79537; CAAS6073
                                                                                                                                                                                                                                                                               This $WISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Rodriguez I.R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM GN-1S).
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MEDLINE=96299648; PubMed=8661012;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUN-1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Skin;
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GLYCATOR: SELF-GLUCOSYLATION IS DEPENDENT ON THE PRESENCE OF COFACTOR: SELF-GLUCOSYLATION IS DEPENDENT ON THE PRESENCE OF DYVALENT METAL IONS OF WHICH MANGANESE ION IS THE MOST EFFECTIVE PATHWAY: GLYCOGEN DIOSYNTHASE.

SUBUNIT: HOMODIMER, TICHTLY COMPLEXED TO GLYCOGEN SYNTHASE.

ALTERNATIVE PRODUCTS: 3 ISOFORMS; GN-11 (SHOWN HERE), GN-1 AND CLIP ALTERNATIVE SPLICING.

15; ARE PRODUCED BY ALTERNATIVE SPLICING.

15; ARE PRODUCED BY THE TRANSFER OF GLUCOSE RESIDUES FROM UDP-GLUCOSE TO ITSELF, FORMING AN ALPHA-1, 4-GLYCAN OF AROUND 10 RESIDUES ATTACHED TO TYR-194.

SIMILARITY: BELONGS TO THE GLYCOGENIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
FUNCTION: SELF-GLUCOSYLATES, VIA AN INTER-SUBUNIT MECHANISM,
FORM AN OLIGOSACCHARIDE PRIMER THAT SERVES AS SUBSTRATE FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: UDP-glucose + glycogenin =
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ucture and chromosomal
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                        AF065480;
AF087942;
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JUN-1994) to the EMBI
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                                                                                                                                                                                     1; ALT_FRAME
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1. 220:72-77(1996).
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P20302;
P20302;
O1-FEB-1991 (Rel. 17, Last sequence update)
O1-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Antigenic protein P1 (Pathogenic protein 1) (Fragment).
Entamoeba histolytica.
Entamoeba.
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13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
SEQUENCE
                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                 KV1V_HUMAN
                                                                                                                                                                                                                                                                                                                                                                    HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Entamoeba histolytica.";
Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=89296955; PubMed=2544890;
Tannich E., Horstmann R.D., Knobloch
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                                                  NCBI_TaxID=9606;
                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tannich E., Horstmann R.D., Knobloch J., Arr
"Genomic DNA differences between pathogenic
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                                                                                                                                                                           kappa chain
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                                                                                         Primates;
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                                                                                                               Chordata;
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Pred. No. 49;
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                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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RESULT 14

KV5C MOUSE

ID "KV5C MOUSE

ID "CV5C AC P0163

DT 21-JU

DT 15-JU

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Matches S
                       Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
SIGNAL 1 20
CHAIN 21 ...
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P01635;
21-JUL-1986
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                       or send a
                                                                                                                                                                                                                                                        EMBL; V00778; CAA24155.1; -. PIR; A01918; KVMSK2. HSSP; P01607; 1REI.
                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Organization and complete sequence of identical embryonic and plasmacytoma kappa V-region genes.";
J. Biol. Chem. 255:3691-3694 (1980).
-i- MISCELLANEOUS: THE GENE WAS ISOLATED AND SEQUENCED SEPARATELY E TWO DIFFERENT SOURCES, EMBRYOS AND CULTURED PLASMACYTOMA CELLS THAT SECRETE THE SIMILAR KAPPA CHAIN MOPC 149.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-V region K2 precursor (Fragment).
Mus musculus (Mouse).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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SMART; SM00406; IGv; 1.
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InterPro; IPR003596; Ig_v.
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Wol. Immunol. 23:73-78(1986)
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COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
   IG KAPPA CHAIN V-V REGION FRAMEWORK-1.
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PRINTS; PRO0765; P_GLUCOSE_ISOMERASE.2; 1.

PROSITE; PS00174; P_GLUCOSE_ISOMERASE.2; 1.

Isomerase; Gluconeogenesis; Glycolysis; Complete ACT_SITE 386 BY SIMILARITY.

ACT_SITE 514 514 BY SIMILARITY.
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16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Glucose-6.phosphate isomerase (EC 5.3.1.9) (G
                                                                                                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See
                                                                                                                                                      InterPro; IPR001672; G6P_Isomerase.
Pfam; PF00342; PGI; 1.
                                                                                                                                                                                     EMBL; AP001119; BAB13263.1; -.
                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                            "Genome sequence of the endocellular bacterial symbiont of Buchnera sp. APS.";
Nature 407:81-86(2000).
-i- CATALYTIC ACTIVITY: D-glucose 6-phosphate = D-fructose
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                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Tokyo 1998;
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PATHWAY: Involved in glycolysis and in gluconeogenesis.

PATHWAY: Involved in glycolysis and in gluconeogenesis.
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16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR004154; HGTP anticodon.
InterPro; IPR004500; ProS_fam_II.
InterPro; IPR002314; tRNA-synt_2b.
InterPro; IPR002316; tRNA-synt_pro.
Pfam; PP00587; tRNA-synt_pro.
Pfam; PF00587; tRNA-synt_codon; I.
Pfam; PF03129; HGTP anticodon; I.
Pfam; PF03149; TRNASYNTHPRO.
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-!- SUBURNIT: HOMODIMER (BY SIMILARITY).
-!- SÜBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
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MEDLINE=20150255; PubMed=10684935;
Read T.D. Brunham R.C., Shen C., Gill S.R., Heidelberg
Read T.D. Brunham R.C., Shen C., Utterback T., Berry
White O., Hickey E.K., Peterson J., Utterback T., Berry
Linher K., Weidman J., Khouri H., Craven B., Bowman C.,
Linher K., Weidman W., Deboy R., Kolonay J., McClarty G.,
Gwinn M., Nelson W., Deboy R., Kolonay J., McClarty G.,
Eisen J., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGREAMS; TIGR00409; pros_fam_II; 1.
PROSITE; PS50862; AA_TRNA_LIGASE_II; 1.
Aminoacyl-trNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
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pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
-!- CATALYTIC ACTIVITY: ATP + L-proline + t
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
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PROS OR TC0672
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l (Rel. 40, Last s
synthetase (EC 6
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(Rel. 29, Created)
(Rel. 39, Last sequence update)
(Rel. 40, Last annotation update)
synthetase (EC 6.1.1.15) (Proline--tRNA ligase) (ProRS).
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6.1.1.15) (Proline--tRNA ligase) (ProRS).
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Salzberg
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P20301;
01-FEB-1991 (Rel. 17, Created)
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STRAIN=D/UW-3/Cx;
MEDLINE=99000809; PubMed=9784136;
Stephens R.S., Kalman S., Lammel C.
Mitchell W.P., Olinger L., Tatusov
                                                                                                                                                                                                                                                                                                            InterPro; IPR004500; ProS_fam_II.
InterPro; IPR002314; tRNA-synt_2b.
InterPro; IPR002316; tRNA-synt_pro.
Pfam; PF00587; tRNA-synt_2b; 1.
Pfam; PF03129; HGTP_anticodon; 1.
PFRINTS; PR01046; TRNASYNTHPRO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
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                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                         TIGRFAMs; TIGR00409;
PROSITE; PS50862; AA_
                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002106; AAtRNA ligaseII
InterPro; IPR004154; HGTP anticodon.
InterPro; IPR004500; ProS_fam_II.
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EMBL; AE001312; AAC67990.1;
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    -!- SUBCELLULAR LOCATION: Cycoplasmic.
    -!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.

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-i- SUBRUTI: HOMOINER (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 282:754-759(1998)
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MEDLINE=94320787; PubMed=8045424;
Schmiel D.H., Wyrick P.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chlamydia trachomatis.
Bacteria; Chlamydiales;
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                                                                                                                                                                                                                                                                              Aminoacyl-tRNA synthetase;
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_TRNA_LIGASE_II;
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16-OCT-2001 (Rel. 40, I
Antigenic protein NP1 (
Entamoeba histolytica.
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CN16 ECOLI
P08331;
01-AUG-1988
01-FEB-1995
16-OCT-2001
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Blattner F.R.;
"Analysis of the Escherichia coli genome
region from 92.8 through 100 minutes.";
region Acids Res. 23:2105-2119(1995).
SEQUENCE: 5EQUENCE: STRAIN=KIZ / EMGZ;
STRAIN=KIZ / EMGZ;
MEDLINE=97443975; PubMed=9298646;
MEDLINE=97443975; PubMed=9298646;
MEDLINE=97443975; PubMed=9298646;
                                                                                                                                                                                      "Transcription and regulation of the cpdB gene in Escherichia K12 and Salmonella typhimurium LT2: evidence for modulation of constitutive promoters by cyclic AMP-CRP complex."; Mol. Gen. Genet. 222:161-165(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE :... SEQUENCE :... STRAIN-KIZ / MG1655;
MEDLINE-95334362; PubMed=7610040;
MEDLINE-95334362; PubMedt G. III, Sofia H.J., Daniels D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Isolation and sequence analysis of the gene (cpdB) encoding periplasmic 2',3'-cyclic phosphodiesterase.";
J. Bacteriol. 165:1002-1010(1986).
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MEDLINE=86139859; PubMed=3005231;
Liu J., Burns D.M., Beacham I.R.;
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Proc. Natl. Acad. Sci. U.S.A. 86:5118-5122(1989).
-!- SIMILARITY: 88% IDENTITY WITH PROTEIN FROM PATHOGENIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=SAW 1734;
MEDLINE=89296955; PubMed=2544890
                                                                                    SEQUENCE OF :
STRAIN=K12 /
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640 AA; 72352 MW;
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(Rel. 31, Last sequence up
(Rel. 40, Last annotation
                                                                                                                          20-31
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(Non-pathogenic prote
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tween pathogenic and
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Best Local S
Matches 5
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EcoGene; EG10160; cpdB.

InterPro; IPR002224; 5 nucleotidase.

InterPro; IPR004843; M-ppestrase.

InterPro; IPR004844; S/T phosphtse.

Pfam; PF00149; Metallophos; 1.

Pfam; PF00149; Metallophos; 1.

PFAM; PF02872; 5 nucleotidaseC; 1.

PROSITE; PS00786; 5 NUCLEOTIDASE 1; 1.

PROSITE; PS00786; 5 NUCLEOTIDASE 2; 1.

Hydrolase; Multifunctional enzyme; Periplasmic; Signature; Signature 2 nucleotidase 2 nucleotidase 3 
                                                                                                                                                                                                                                       CN16_SALTY STANDARD; PRT; 647 AA. P26265; 01-MAY-1992 (Rel. 22, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 2',3'-cyclic-nucleotide 2'-phosphodiesterase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Comparing the predicted and observed properties of proteins encoded in the genome of Escherichia coli K-12."; Electrophoresis 18:1239-1313 (1997).

-i- FUNCTION: THIS SIFUNCTIONAL ENZYME CATALYZES TWO CONSECUTIVE REACTIONS CONVERTING 2',3'-CYCLIC-NUCLEOTIDE TO 3'-NUCLEOTIDE AND THEN 3'-NUCLEOTIDE TO NUCLEIC ACID AND PHOSPHATE.

-i- CATALYTIC ACTIVITY: Nucleoside 2',3'-cyclic phosphate + H(2)O =
SEQUENCE FROM N.A.
STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
McClelland M., Sanderson K.E., Spietl
Courtney L., Porwollik S., Ali J., D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE000492; AAC77170.1; -.
EMBL; X54008; CAA37954.1; -.
PIR; A26398; ESECPC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                            Bacteria; Proteobacteria;
                                                                                                                                                                                                      Salmonella
                                                                                                                                                                                                                             CPDB OR STM4403
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                                                                                                                                  NCBI_TaxID=602;
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SUBGELLULAR LOCATION: Periphasmic.
MISCELLANBOUS: TWO KINETICALLY DISTINGUISHABLE ACTIVE
MISCELLANDOUS: TWO KINETRATES CAN BE IDENTIFIED.
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K.E., Spieth J., ., Ali J., Dante
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Pred.
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A -> G (IN REF. 1)
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  Clifton S.W.,
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S., Layman
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Q19673;
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Pfam; PF02872; 5 nucleotidaseC; 1.

PROSITE; PS00785; 5 NUCLEOTIDASE 1; 1.

PROSITE; PS00786; 5 NUCLEOTIDASE 2; 1.

PROSITE; PS00786; 5 NUCLEOTIDASE 2; 1.
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EMBL; X54009; CAA379
PIR; S11915; S11915.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                   F21C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            StyGene; SG10065; cpdB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (S or serid an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                        Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MISCELLANBOUS: TWO KINETICALLY DISTINGUISHABLE ACTIVE TWO CORRESPONDING SUBSTRATES CAN BE IDENTIFIED. SIMILARITY: BELONGS TO THE 5'-NUCLEOTIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: THIS BIFUNCTIONAL ENZYME CATALYZES TWO CONSECUTIVE REACTIONS CONVERTING 2',3'-CYCLIC-NUCLEOTIDE TO 3'-NUCLEOTIDE AND THEN 3'-NUCLEOTIDE TO NUCLEIC ACID AND PHOSPHATE.

CATALYTIC ACTIVITY: Nucleoside 2',3'-cyclic phosphate + H(2)O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleoside 3'-phosphate.
SUBCELLULAR LOCATION: Periplasmic.
                                                                                                                                                                                          CAEEL
                                                                                                                                                                                                                                                                                                                358 KSADNMYSYL 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AE008906; AAL23223.1; -. X54009; CAA37956.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 5; Conserv
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Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
n R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51
84
96
133
174
647
                                                                                        (Rel. 36, Created)
(Rel. 38, Last seq
(Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                       tyrosinase-like
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                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=2172762;
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50.0%;
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                                                                  sequence update)
annotation update)
ke protein F21C3.2
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2', 3'-CYCLLC-NUCLEOTIDE
2', PHOSPHODIESTERASE.
G -> A (IN REF. 2).
GDYMAA -> RLYGG (IN REF. 2)
DVH -> GIQ (IN REF. 2).
A -> G (IN REF. 2).
I -> N (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                             Score 35;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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76;
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                                                                       chromosome
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                                                                                                                                                                        P50270; Q9ME70;
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
ATP synthase protein 8 (EC 3.6.3.14) (ATPASE
MTATPB OR ATPASE8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS;
SMART; S
                                                                                                                                                                                                                                                                                                                                                                                                                      METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genet.
                                unusually high level of polymorphism Genet. Res. 61:195-204(1993).
                                                  MEDLINE=93374296; PubMed=8365657;
Kaneko M., Satta Y., Matsuura E.T., Chi
"Evolution of the mitochondrial ATPase
                                                                                     SEQUENCE FROM N.A.
                                                                                                                   Eukaryota; Metazoa; Arthropóda; Mandibulata; Pancrustacea;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Braci
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                 Drosophila simulans (Fruit
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical
METAL :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McMurray A.;
Submitted (APR-1996)
STRAIN=NC48, TT00,
           SEQUENCE FROM N.A.
                                                                                                        NCBI_TaxID=7240;
                                                                                                                                                       Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                             METAL
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InterPro; IPR002227; Tyrosinase
Pfam; PF00264; tyrosinase; 1.
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                              Res.
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291 291
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813 AA; 9
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HW00, HW09, and
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Pred. No.
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base 6 gen
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A (BY SIMILARITY).
B (BY SIMILARITY).
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B (BY SIMILARITY).
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(ATPase:
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                                           melanogaster.";
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(By similarity)
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                                                                                                                                 Brachycera;
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RESULT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P01606;
21-JUL-1986 (Re
21-JUL-1986 (Re
15-JUL-1999 (Re
Ig kappa chain
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Submitted
                                                                                             InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                     PIR;
                                                                                                                                                                                                                                                                                                                                                             Science 169:56-59(1970).
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chains."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=70201507; PubMed=5447531;
Kohler H., Shimizu A., Paul C., P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Macroglobulin structure: variable sequence of light and heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                     DOMAIN
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FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.
CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate + H(+)(Out).
                                                                                                                                                                                                                                                                                                                                     MACROGLOBULIN
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; P01607; 1REI.
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gen ion transport; CF(0); Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25
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region.
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dsim\mt:ATPase8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M -> I (IN REF. 1).
IPN -> MPD (IN REF. 1)
45D2C68EE47491E3 CRC64
FRAMEWORK-2.
                           FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Putnam F.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Usage
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RESULT 24
CY21_RHOCE
ID CY21
AC P811=
AC P811=
DT 15-J1
DT 30-M
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OC Rhoc
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RESULT 25
CARA_NEIGO
ID CARA_NEIGO
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InterPro; lrave.
InterPro; IPR002327; cyc__
InterPro; IPR002327; cyc__
InterPro; IPR002327; cyc__
Pfam; PF00034; cytochrome_c; 1.

R PRINTS; PR00604; CYTOCHRMECIAB.

PRODITE; PS0013075; Cyt_CIAB; 1.

PROSITE; PS00130; CYTOCHROME_C; 1.
                                                                                                                                                                                                        Query Match
Best Local S
Matches 6
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Best Local S
Matches 7
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98323574; PubMed=9659396;
Samyn B., Fitch J., Meyer T.E., Cusanovich M.A.,
"Purification and primary structure analysis of t
isozymes from the purple phototrophic bacterium R
centenum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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DOMAIN
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- I:- FUNCTION: CYTOCHROME C2 IS FOUND MAINLY IN PURPLE, NONSULFUR, PHOTOSYNTHETIC BACTERIA WHERE IT FUNCTIONS AS THE ELECTRON DONOR TO THE OXIDIZED BACTERIOCHLOROPHYLL IN THE PHOTOPHOSPHORYLATION PATHWAY. HOWEVER, IT WAY ALSO HAVE A ROLE IN THE RESPIRATORY CHAIN AND IS FOUND IN SOME NONPHOTOSYNTHETIC BACTERIA. THE REDOX POTENTIAL OF THIS CYTOCHROME IS 316 MV.
                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P00083; 1CRY.
InterPro; IPR003045; CytC heme_bind.
InterPro; IPR003088; Cyt_CI.
InterPro; IPR002327; Cyt_CIAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
30-NAY-2000 (Rel. 39, Last annotation update)
Cytochrome C2, iso-1 (C552).
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                                                                                                                                                                                                                                                                                                                          METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; alpha subdivision; Rhodospirillaceae;
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15-JUL-1998
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                                                                                                                                                              3 SENIYSYLP
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                                                                                                                                                                                                        Similarity 6; Conserv
                                                                                                                    AENIMAYLP
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                                                                                                                                                                                                                                                                                                12818 MW;
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66.7%;
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Pred. No.
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COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPLEMENTARITY-DETERMINING-2.
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                                                                                                                                                                                                                                                                                           RON (HEME AXIAL LIGAND).
RON (HEME AXIAL LIGAND).
BBE05414A003E6BF CRC64;
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Rhodospirillum
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                                                                                                                                                                                                        Indels
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STANDARD;

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Query Match
Best Local Similarity
                                                        DOMAIN
ACT SITE
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               also present in other Neisseria species.";

Microbiology 141:1183-1191(1995).

-!- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP phosphate + L-glutamate + carbamoyl phosphate.
-!- PATHWAY: Arginine biosynthesis.
-!- PATHWAY: Pyrimidine biosynthesis; first step.
-!- SUBUNIT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used being large (or ammonia) chain to synthesize carbamoyl phosphate.
-!- SIMILARITY: BELONGS TO THE CARA FAMILY.
-!- SIMILARITY: CONTAINS 1 TYPE-1 GLUTAMINE AMIDOTRANSFERASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted [2]
                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the EMropean Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsenid an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lawson F.S., Billowes F.M., Dillon J.A.; "Organization of carbamoyl-phosphate synthase genes gonorrhoeae includes a large, variable intergenic se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase small chain (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rudel T., Boxberger H.J., Pandit J., Meyer T.F.; "The Neisseria gonorrhoae carA gene: Generation of mutant implication of pyrimidine biosynthesis for the infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q50983; Q59598;
15-JUN-2002 (Rel. 41, Creat
15-JUN-2002 (Rel. 41, Last
15-JUN-2002 (Rel. 41, Last
                                            SEQUENCE
                                                                                                                                                                                                                              PROSITE; PS00442; GATASE_TYPE_I; 1.
Arginine biosynthesis; Pyrimidine biosynthesis; Ligase;
                                                                                                                                                                                                                                                           PRINTS; PRO0099; CPSGATASE..
PRINTS; PR00096; GATASE.
                                                                                                                                                                                                                                                                                       Pfam; PF00988; CPSase sm chain; 1. Pfam; PF00117; GATase; 1.
                                                                                                                                                                                                                                                                                                                  InterPro; IPR002474; CPSase_sm_chain.
InterPro; IPR001317; CPS_GATase.
InterPro; IPR000991; GATase_1.
                                                                                                                                                                                                                                                                                                                                                           EMBL; U11295; AAA74995.1;
HSSP; P00907; 1A9X.
                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z54242; CAA91011.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=MS11;
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phosphate synthetase
                                                                                                                                                                                                                    Glutamine amidotransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95291461; PubMed=7773412;
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X
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                                                      MLAS -> ISP (IN REF. NG -> QR (IN REF. 2) G -> A (IN REF. 2) S -> F (IN REF. 2) S -> F (IN REF. 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ databases
 Score
Pred.
                                                                                                                                                         GLUTAMINE AMIDOTRANSFERASE
GATASE (BY SIMILARITY).
T -> A (IN REF. 2).
                                                                                               SVYA -> TVLP (IN REF. 2)
MISSING (IN REF. 2).
MLAS -> ISP (IN REF. 2).
NG -> QR (IN REF. 2).
                                                      -> A (IN REF. 2).
-> F (IN REF. 2).
-> F (IN REF. 2).
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                                           BD54FAF60506BCA2 CRC64;
34;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.
 DB
66;
             <u>بر</u>
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             Length 377,
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                      Query Match
Best Local :
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Q9JVZ6;
15-JUN-2002
15-JUN-2002
                                                                                     ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              meningitidis Z2491.";

Nature 404:502-506(2000).

-I- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2).

-phosphate + L-glutamate + carbamoyl phosphate.

-I- PATHWAY: Arginine biosynthesis.

-I- PATHWAY: Pyrimidine biosynthesis; first step.

-I- SUBUNIT: Composed of two chains; the small (or g. promotes the hydrolysis of glutamine to ammonia, the large (or ammonia) chain to synthesize carban
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher Klee S.R., Morelli G., Basham D., Chillingworth T Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Hi Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Ratherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.; Minghill R., Gusteria Whitehead S., Spratt B.G., Barrell B.G.; Minghill R., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.; Minghill R., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.; Minghill R., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.; Minghill R., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.; Minghill R., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.; Minghill R., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.; Minghill R., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.; Minghill R., Whitehead S., Spratt B.G., Barrell B.G., Whitehead S., Spratt B.G., Whitehead S., Whitehead S., Spratt B.G., Whitehead S., Spratt B.G., Whitehead S., Spratt B.G., Whitehead S., Spratt B.G., Whitehead S.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUN 2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence updat
15-JUN-2002 (Rel. 41, Last annotation upd
Carbamoyl-phosphate synthase small chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEIMA
                                                                                                                                                                          Glutamine amidotransferase;
                                                                                                                                                                                            PROSITE; PS00442; GATASE_TYPE I; 1.
Arginine biosynthesis; Pyrimidine biosynthesis; Ligase;
                                                                                                                                                                                                                                                                             Pfam; PF00988; CPSase sm chain; Pfam; PF00117; GATase; 1
                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002474; CPSase_sm_chain
InterPro; IPR001317; CPS_GATase.
                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AL162753;
HSSP; P00907; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Z2491 / Serogroup A / Serotype 4A;
MEDLINE=20222556; PubMed=10761919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria meningitidis (serogroup
Bacteria; Proteobacteria; beta sul
                                                                                                                               DOMAIN
                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                    PRINTS; PR00096; CPSGATASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=65699;
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                                                                                                                                                                                                                                                                                                                            InterPro; IPR001317; CPS_GA!
InterPro; IPR000991; GATase_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity).
SIMILARITY: BELONGS TO THE CARA FAMILY.
SIMILARITY: CONTAINS 1 TYPE-1 GLUTAMINE AMIDOTRANSFERASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93
Similarity 6; Conserv
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  Conservative
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                    Score 34;
Pred. No.
                                                                                                           GATASE
                                                                                                                               GLUTAMINE AMIDOTRANSFERASE
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subdivision;
                                                                                     TASE (BY SIMILARITY)
    Mismatches
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ain (EC
                        66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (or glutamine) chain
monia, which is used |
  carbamoyl phosphate
                                          Length 377;
                                                                                       CRC64;
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Query Match
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ACT SITE
SEQUENCE
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-!- CAPALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP phosphate + L-glutamate + carbamoyl phosphate.
-!- PATHWAY: Arginine biosynthesis.
-!- PATHWAY: Pyrimidine biosynthesis; first step.
-!- SUBUNIT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used the large (or ammonia) chain to synthesize carbamoyl phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon B.R., Rappuoli R., Venter J.C.; Complete genome sequence of Neisseria meningitidis serogroup B strain Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase small chain (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=MC58 / Serogroup B;
MEDLINE=20175755; PubMed=10710307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phosphate synthetase glutamine CARA OR NMB1849.
                                                                                                                                         Glutamine
                                                                                                                                                    PROSITE; PS00442; GATASE TYPE I; 1.
Arginine biosynthesis; Pyrimidine biosynthesis; Ligase;
                                                                                                                                                                                                                        Pfam; PF00988; CPSase sm chain; 1.
Pfam; PF00117; GATase; 1.
                                                                                                                                                                                                                                                          InterPro; IPR002474; CPSase sm_chain.
InterPro; IPR001317; CPS_GATase.
InterPro; IPR000991; GATase_1.
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                                                                                                                                                                                        PRINTS; PR00099; CPSGATASE.
PRINTS; PR00096; GATASE.
                                                                                                                                                                                                                                                                                                                 TIGR; NMB1849; -.
                                                                                                                                                                                                                                                                                                                                                                                            s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE CARA FAMILY. SIMILARITY: CONTAINS 1 TYPE-1 GLUTAMINE AMIDOTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity).
SIMILARITY:
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P00907; 1CS0.
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                                                                                                                                                                                                                                                                                                                                                                                   an email to license@isb-sib.ch).
Similarity 6; Conserv
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                                                                                                                                       amidotransferase;
   Conservative
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                                                                                                        186
377
                                                                      40587 MW;
              59.6%;
                                                                                                                       Complete proteome.
Score 34; DB Pred. No. 66; 3; Mismatches
                                                                  GLUTAMINE AMIDOTRANSFERASE GATASE (BY SIMILARITY).; 36733FC0806B1670 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chain)
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                                Length 377;
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RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bortier P.,
RA Bortis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Gelbos B., Dicher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Gelbos B., Dicher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Golec C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Howland T.J., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Liang Y., Lin X., Match B., McIntosh T.C., McLeod M.P., McPherson D.L.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Liang Y., Marson D.R., Nurphy B., Murphy L., Murny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Harris A.L., Ranger G. J., Non Sheel M.,
Ranger S., Yao Q.A.,
RA Shue B.C., Scheeler S., Wang S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Cytochrome P450 302a1, mitochondrial precursor
(Disembodied protein).
DIB OR CYP302A1 OR CG12028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DROME
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16-OCT-2001 (Re
                                    and codes for a cytochrome ecdysone levels."; Submitted (FEB-2000) to the
                                                                                   Chavez V.M., Marques G., Kob
Natzle J.E., O'Connor M.B.;
"The Drosophila disembodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brach
                                                                                                                                                                                   "The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Berkeley;
                                                                                                                                                SEQUENCE FROM N.A.
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 -!- FUNCTION: REGULATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DROME
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                 B-2000) to
REGULATES
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 EMBRYONIC ECDYSONE LEVELS RH + reduced flavoprotein
                                    the EMBL/GenBank/DDBJ databases
                                                                                                                               Kobayashi K.,
                                                                           d gene
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                                                                           enzyme
                                                                                          controls late
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 flavoprotein + O(2)
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                                                                                                                               J.P.,
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                                                                                                                               Burr J.,
                                                                                            morphogenesis
   ROH
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Best Local
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P52453;
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CONFLICT
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                                                                                                                                                                                                                     "Nucleotide sequence analysis of a 21-kbp region of the genome of human herpesvirus-6 containing homologues of human cytomegalovirus major immediate-early and replication genes.";
Virology 704.778 = 75.11.07.
                                                                                                                                                                                                                                                                                                                                                                                         numan nerpesvirus (type 6 / strain Uganda-1102) (HHV6).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Roseolovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        virion protein U76.
U76 OR HDLF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSV6U
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HSSP; P14779; 1JPZ.
FlyBage; FBgn0000449; dib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=95027704; PubMed=7941342;
                     Virology 209:29-51(1995)
                                                                                                   Gompels U.A., Nicholas J., Lawrence Martin M.E., Efstathiou S., Craxton
                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                            Nicholas J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996
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                                                          "The DNA sequence of human and genome evolution.";
                                                                                                                                            MEDLINE=95266321; PubMed=7747482;
                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
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                                                                                                                                                                                                          Virology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001
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SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oxidized
    PACKAGING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide.
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(Rel. 34, Last seq
(Rel. 40, Last ann
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186
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327
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LAR LOCATION: Mitochondrial (Potential)
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71.4%;
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                     VIRION
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                                                                           , Lawrence G., Jo
., Craxton M., Ma
n herpesvirus-6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence update)
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HEME (BY SIMILARITY).
C -> S (IN REF. 2).
R -> S (IN REF. 2).
S -> G (IN REF. 2).
L -> M (IN REF. 2).
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Pred. No. 86;
2; Mismatches
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                     PROTEIN;
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86;
                     POSSIBLE
                                                                                                   Jones M.,
Macaulay F
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                                                                                  structure,
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                     ROLE
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                                                                                                 H.A.;
                                                                                                                        Thomson B.J.,
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                     Ä
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  Matches
              Query Match
Best Local
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                                                 InterPro; IPR002660; Herpes UL6.
Pfam; PF01763; Herpes UL6; 1.
ProDom; PD003210; Herpes UL6; 1.
SEQUENCE 662 AA; 77199 MW; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the Buropean Bioinformatics Institute. There are no restrue by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                          "Restriction endonuclease mapping herpesvirus 6 variant B strain 220 Arch. Virol. 141:367-379 (1996).
                                                                                                        EMBL; AF157706; AAB06359.1;
                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                          Stamey F.R., Dambaugh T.R Frenkel N., Pellett P.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                     Betaherpesvirinae; Roseolovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                 Human herpesvirus (type 6 / strain Z29) (HHV6).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Virion protein U76. U76 OR CB3L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996
01-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96195263; PubMed=8634027;
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=36351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001
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Pfam; PF01763; Herpes_UL6; 1.
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                                                                                                                                                                                                                                     EHV-1 56, EBV BBRF1,
                                                                                                                                                                                                                                                                  PACKAGING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSV6Z
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m; PD003210; Herpes_UL6; 1.
NCE 662 AA; 77234 MW; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X83413;
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6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 6; Conserv
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(Rel. 34, Last sequence update)
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  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
             59.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.6%;
                                                                                                                                                                                                                                     HCMV UL104, AND VZV 54.
                                                                                                                                                                                                                                                   FAMILY
 Mismatches
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              Score 34;
Pred. No.
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                                                    5126392A37C67B90 CRC64;
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                                                                                                                                                                                                                                                   THAT GROUPS
                                                                                                                                                                                                                                                                                                                 and molecular cloning
                                                                                                                                                                                                                                                                                                   genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        662
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                                                                                                                                                                                                                                                                            POSSIBLE ROLE
                           DB 1;
                                                                                                                                                                                                                                                                                                                                         Castelli J.W.,
., Danovich R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A
              2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2e+02;
                                                                                                                                                                                                                                                   TOGETHER HSV-1 UL6
                         Length 662
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  Indels
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SENIYSYLP

SKNLLSYLP

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RESULT 32
ATP8 DROME
ID ATP8 DI
AC P03932
DT 21-JUL
DT 21-JUL
DT 15-JUN
DE ATP 89
GN MTATP8
OS Drosop
OG Mitoch
OC Eukary
OC Insect
OC Muscom
OX NCBI_T
RN [1]
RP SEQUEN
RX MEDLIN
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Best Local S
Matches 5
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01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
RNA replication protein (152 kDa protein) (ORF 1) [Contains: RNA-directed RNA polymerase (EC 2.7.7.48); Probable helicase).
                                                                                                                                                                                                               ATP8 DROME P03932;
                                                                                                                                                                                                                                                                                                                                                                                                                                NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                          Eukaryota; Metazoa; Arthropoda; Mandibulata;
Insecta; Pterygota; Neoptera; Endopterygota;
Muscomorpha; Ephydroidea; Drosophilidae; Dros
                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ATP synthase protein 8 (EC 3.6.3.14) (ATPass
MTATP8 OR ATP8 OR ATPASE8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M62730; AAA43826.1; -. PIR; JQ1258; JQ1258.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Gen. Virol. 72:2173-2181(1991).
-- FUNCTION: RNA-replication. Function possibly functions as an ATP-binding helicase.
-- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bancroft J.B., Rouleau M., Johnston R., Prins L., "The entire nucleotide sequence of foxtail mosaic J. Gen. Virol. 72:2173-2181(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Foxtail mosaic virus.
Viruses; ssRNA positi
                                                                                                       Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro, IPRO01788; RNA dep_RNApol2.
InterPro; IPRO00606; Viral_helicase1.
Pfam; PF00978; RNA dep_RNApol2; 1.
Pfam; PF01443; Viral_helicase1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91374015; PubMed=1840610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RRPO
   MEDLINE=83245048;
              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP-binding; Helicase; RNA replication; RNA-directed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                            NCBI_TaxID=7227,
                                                                                                                     Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=12179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (RNA) (N).
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                                                                                                                                                                                                                                                                                                           131
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                                                                                                                                                                                                                                                                                                                                                                    Similarity 5; Conserv
                                                                                                                                                                                                                                                                                                        DTVYSYLP 138
                                                                                                                                                                                                                                                                                                                                                                                                                                1335
                                                                                                                                                                                                                                                                                                                                                                                                                                                603
                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              positive-strand viruses, no DNA stage; Potexvirus
                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
   PubMed=6408489
                                                                                                                                                                                                                                                                                                                                                                                                                                                610
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MW;
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                                                                                                                                                                                                                                                                                                                                                                                                 Score 34;
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                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
D2ECBBA932F49DB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                    No. 2
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                                                                                                                                                    n update)
(ATPase:
                                                                                                                                                                                                                               53
                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                          ata; Pancrustacea; Hexapoda;
ota; Diptera; Brachycera;
Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                    .4e+02;
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virus R
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RNA.";
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ATP8_DROYA
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ATP synthase protein 8 (EC 3.6.3.14) (ATPase subunit MTATP8 OR ATP9 OR ATPASE8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            de Bruijn M.H.L.;
"Drosophila melanogaster mitochondrial DNA, a novel organization and genetic code.";
Nature 304:234-241(1983).
-i- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.
-i- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
             and ATPase subunit 6.";
Nucleic Acids Res. 11:4211-4227(1983).

-!- FUNCTION: THIS IS ONE OF THE CHAINS OF THE
-(CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASI
-!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In)
H(+)(Out).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement incorremoved. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                    Clary D.O., Wolstenholme D.R.;
"Nucleotide sequence of a segment of Dithat contains the genes for cytochrome
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=2317.6 IVORY COAST;
MEDLINE=86089137; PubMed=3001325;
Clary D.O., Wolstenholme D.R.;
                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brach Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. NCBI_TaxID=7245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001421; ATPase8_mit.
Pfam; PF0095; ATP-synt 8; 1.
Hydrogen ion transport; CF(0); Mitochondrion;
SEQUENCE 53 AA; 6364 MW; 45D2C68AA437FC23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=83246544; PubMed=6306579;
                                                                                                                                                                                                      "The mitochondrial DNA molecular of Drosophila yakuba: nucleotide sequence, gene organization, and genetic code.";
J. Mol. Evol. 22:252-271(1985).
                                                                                                                                                                                                                                                                                                                                                                                                  Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                              MTATP8 OR ATP8 OR ATPASE8
Drosophila yakuba (Fruit :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A93307; PWFF8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; J01404; AAB59241.1; -. EMBL; U37541; AAC47814.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FlyBase; FBgn0013673; mt:ATPase8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: N
SIMILARITY: BELONGS TO
SUBCELLULAR LOCATION: Membrane-bound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DROYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SENIYSYLP 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                 fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Membrane-bound.
O THE ATPASE PROTEIN 8 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33; DB
Pred. No. 13;
1; Mismatches
                                            THE CHAINS OF THE NONENZYMATIC COMPONENT ITOCHONDRIAL ATPASE COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                           of Drosophila r
hrome c oxidase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane
                               II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 53
                                                                                                           mitochondrial DNA e subunits II and
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                                                                                                                                                                                                                                                                                                                                                                                  Hexapoda;
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RESULT
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Best Local S
Matches 6
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EMBL; X00924; CAA25441.1; -.
PIR; A93477; PWF68Y.
PIR; D25797; D25797.
P19ase; FBgn0013178; Dyak\mt:ATPase8.
InterPro; IPR001421; ATPase8 mit.
Pfam; PPF00895; ATP-synt_8; 1.
Pfam; PPF00895; ATP-synt_8; 1.
Hydrogen ion transport; CF(0); Mitochondrion; Tr.
SEQUENCE 53 AA; 6337 MW; 6741C69A7E57EF9B CR
                                                                                                                                                                                                                                                                                                                                                                                                      P01596;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
                                                                                                 CARBOHYD
NON TER
SEQUENCE
                                                                                                                                                                                                                     PIR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                           MEDLINE=75075135; PubMed=4216454; Milstein C.P., Deverson E.V.;
                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                   nterPro; 1:..., ig; 1.
Viam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Glycoprotein.
Immunoglobulin 28 28 N-LINKED
                                                                                                                                                                                                                                                                                  protein.
                                                                                                                                                                                                                                                                                                         Milstein C.P.,
                                                                                                                                                                                                                                                                                                                                     SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                         HSSP;
                                                                                                                                                                                                                              -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN
                                                                                                                                                                                                                                                          -!- MISCELLANEOUS:
                                                                                                                                                                                                                                                                                              "Primary structure
                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
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                                                                                                                                                                        A01864; KIHUAR.
; P80362; IWTL.
;rPro; IPR003006; Ig_MHC.
;rPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMAN
24
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                                                  Similarity 7; Conserv
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ص
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RASQNISSWL 33
                      RASENIYSYL 10
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                                                                                                 28
107
107 AA;
                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                         THE
                                                                                                                                                                                                                                                                                             of kappa light chain from a human myeloma
                                                                                                                                                                                                                                                                                                                                                                          Chordata;
Primates;
                                                            57.9%;
70.0%;
                                                                                                   11703 MW;
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66.7%;
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Pred. No.
                                                             Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                   E1BF0DF9844C3346 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                  Mismatches
                                                                                                                                                                                                                                                         THIS CHAIN HAS THE INV (1,2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107
                                                                                                                           (GLCNAC. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                           update)
                                                                         DВ
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                                                                         Length 107;
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                                                 Indels
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RESULT 35 KV1H\_HUMAN

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SEQUENCE
SEQUENCE, AND BLOCKAGE OF N-TERMINUS.
Ambler R.P., Meyer T.E., Murray S.;
Submitted (DEC-1974) to the PIR data bank.
-!- FUNCTION: CYTOCHROME C2 IS FOUND MAINLY IN
PHOTOSYNTHETIC BACTERIA WHERE IT FUNCTIONS
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DOMAIN
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"The primary structure of a monoclonal kappa-type immunoglobulin l chain of subgroup I (Bence-Jones Protein Hau): subdivision within subgroups.";
                                                                                                                                                                                                                                                                                Rhodopseudomonas palustris (strain ATCC 17001 Bacteria; Proteobacteria; alpha subdivision; R Bradyrhizobium group; Rhodopseudomonas. NCBI_TaxID=1076;
                                                                                                                                                                                                                                                                                                                                                                                     P00090;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seq
15-JUN-2002 (Rel. 41, Last ann
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
                                                                                                                     "Cytochrome c2 sequence variation among the purple nonsulphur photosynthetic bacteria."; Nature 278:659-660(1979).
                                                                                                                                                                                  Ambler R.P.,
Kamen M.D.;
                                                                                                                                                                                                                          MEDLINE=79199667;
                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                    Cytochrome C2.
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SMART; SM00406; IGv;
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HSSP; P80362; 1WTL.
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-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE
-!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
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IPR003596;
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el M., Hermoso
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Primates;
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COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
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COMPLEMENTARITY-DETERMINING-2.
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                                                                                                                                                                                                       J., Meyer T.E.,
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  PURPLE, NONSULFUR, AS THE ELECTRON DONOR
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HSSP; P00094; 1C2R.

InterPro; IPR000345; Cyt_Cl.

InterPro; IPR0003088; Cyt_CI.

InterPro; IPR002327; Cyt_CIAB.

Pfam; PF00034; CytOChrome C; 1.

PRINTS; PR00604; CYTCHRMEČIAB; 1.

PROSITE; PS00190; CYTOCHROME_C; 1.
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P01641;
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                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                  MEDLINE=81064681; PubMed=6777049;
Max E.E., Seidman J.G., Miller H., Leder P.;
"Variation in the crossover point of kappa immunoglobulin recombination: evidence from a cryptic gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-V region MOPC 173B precursor
                                                                                                    Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                      HSSP; P01607; 1REI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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PIR; A01924; KVMS3B.
                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                         Cell 21:793-799(1980).
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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  DOMAIN
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                    IG KAPPA CHAIN V-V REGION MOPC FRAMEWORK.1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK.2.
COMPLEMENTARITY-DETERMINING-2.
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Pred. No.
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IRON (HEME AXIAL LIGAND).
IRON (HEME AXIAL LIGAND).
IRON (HEME AXIAL LIGAND).;
13657331CCOD4464 CRC64;
 COMPLEMENTARITY-DETERMINING-3
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InterPro; IPR000348; Cyt_CI.
InterPro; IPR003388; Cyt_CI.
InterPro; IPR002327; Cyt_CIAB.
Pfam; PF00034; cytochrome_c; 1.
PRINTS; PR00604; CYTCHRMECIAB; 1.
PRODOM; PD000375; Cyt_CIAB; 1.
PROSITE; PS00190; CYTOCHROME_C; 1.
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BINDING 15
BINDING 18
METAL 19
METAL 98
SEQUENCE 121 AA; 1
            P22347;
01-AUG-1991
16-OCT-2001
16-OCT-2001
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15-JUL-1998 (
15-JUL-1998 (
30-MAY-2000 (
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
30-WAY-2000 (Rel. 39, Last annotation update)
Cytochrome C2, iso-2 (C552).
Rhodospirillum centenum (Rhodocista centenaria)
                                                                                                                                                                                                                                                                                                                                                                                                                             Biochim. Biophys. Acta 1384:345-355(1998).

- I- FUNCTION: CYTOCHROME C2 IS FOUND MAINLY IN PURPLE, NONSULFUR,
- PHOTOSYNTHETIC BACTERIA WHERE IT FUNCTIONS AS THE ELECTRON DONOR
TO THE OXIDIZED BACTERIOCHLOROPHYLL IN THE PHOTOPHOSPHORYLATION
                                                          YVDE_LACLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=ATCC 43720;
MEDLINE=98323574; PubMed=9659396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; alpha subdivision; Rhodospirillaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=34018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhodospirillum
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                                                                                                                                                                                                                                                                                                                                                                                           PATHWAY. HOWEVER, IT MAY ALSO HAVE A ROLE IN THE RESPIRATORY CHAIN AND IS FOUND IN SOME NONPHOTOSYNTHETIC BACTERIA. THE REDOX POTENTIAL OF THIS CYTOCHROME IS 293 MV.
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88939C3C6022430A CRC64;
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P57326;
16-OCT-2001 (Rel. 40, C
16-OCT-2001 (Rel. 40, L
16-OCT-2001 (Rel. 40, L
Elongation factor Te (E
TSF OR BUZ32
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

STRAIN=TOkyo 1998;

MEDLINE=20445173; PubMed=10993077;

MEDLINE=20445173; PubMed=10993077;

Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;

"Genome sequence of the endocellular bacterial symbiont of aphids

Buchnera sp. APS.";

Nature 407:81-86 (2000).

-i- FÜNCTION: ASSOCIATES WITH THE EF-TU.GDP COMPLEX AND INDUCES THE

EXCHANGE OF GDP TO GTP, IT REMAINS BOUND TO THE AMINOACYL-TRNA.

EF-TU.GTP COMPLEX UP TO THE GTP HYDROLYSIS STAGE ON THE RIBOSOME.

-i- SÜBCELLULAR LOCATION: CYCLOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BUCAI
                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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"Cloning and DNA sequence analysis of an X-prolyl dipeptidyl
aminopeptidase gene from Lactococcus lactis subsp. lactis NCI
Appl. Environ. Microbiol. 57:45-50(1991).
-!- SIMILARITY: TO E.COLI YCIL.
-!- CAUTION: Ref.1 sequence differs from that shown due to a
frameshift in position 165.
                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
  EMBL;
                                                                                                     use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 symbiotic bacterium)
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MEDLINE=91241789; PubMed=1674656;
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae, Lactococcus.
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                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE EF-TS FAMILY.
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AP001118;
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66.7%;
                                                                          license agreement (See http://www.isb-sib.ch/announce/
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(EF-Ts).
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문 5

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HSSP; P0299; LL.-

R InterPro; IPR001816; EFTS.

R InterPro; IPR001449; UBA domain.

R Pfam; PF00627; UBA; 1.

DR Pfam; PF00689; EFTS; 1.

DR Pfam; PF00889; EFTS; 1.

DR PROSITE; PS01126; EFTS_1; 1.

DR PROSITE; PS01127; EFTS_2; 1.

DR PROSITE; PS01126; EFTS_2; 1.

DR PGMILLRITY; Complete proteome.

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85.7%;
2003, 15:07:18
                                                                                                                        Score 33;
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Search completed: July 18, Job time: 7.82 secs

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Title:
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      SPTREMBL_21:*
1: sp_archea:*
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6: sp_mammal:*
7: sp_mhc:*
8: sp_organe11:
9: sp_phage:*
10: sp_plant:*
11: sp_virus:*
13: sp_verteb:
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57
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sp_organelle:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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37	37	37	37	37	37	37	37	38	38	39	39	40	40	41	50	Score
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## ALIGNMENTS

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01-MAR-2002 (TrEMBLrel. 2
01-JUN 2002 (TrEMBLrel. 2
2',3'-cyclic-nucleotide 2
CPDB OR YPO3530.
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Q8ZB89;
Q1-MAR-2002
Q1-MAR-2002
Q1-JUN-2002
                                                                               SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDILINE=20450683; PubMed=10997877;

Nagase T., Kikuno R., Nakayama M., Hirosawa M., Ohara O.;

"Prediction of the coding sequences of unidentified human avail. The complete sequences of 100 new cDNA clones from code for large proteins in vitro.";

DNA Res. 7:273-281(2000)

EMBL; AB046775; BAB13381.1; -.

EMBL; AB046775; BAB13381.1; -.
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MEDLINE=21470413; PubMed=11586360;

Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,

Prentice M.B., Sebathia M., James K.D., Churcher C., Mungall K.L.,

Prentice M.B., Sebathia M., James K.D., Brooks K., Cerdeno-Tarraga A.M.,

Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

Peltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,

Leather S., Moule S., Oyston P.C.F., Whitehead S., Barrell B.G.;

"Genome sequence of Yersinia pestis, the causative agent of plague."
Interpro; IPR000822; Znf (
Pfam; PF00096; Zf-C2H2; Z
SMART; SM00355; ZnF_C2H2;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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PROSITE; PS00785; 5_NUCLEOTIDASE_1;
PROSITE; PS00786; 5_NUCLEOTIDASE_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02872; 5_nucleotidaseC; 1.
Pfam; PF00149; Metallophos; 1.
PRINTS; PR01607.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KIAA1555 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KIAA1555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002224; 5_nucleotidase.
InterPro; IPR004843; M-ppestrase.
InterPro; IPR004844; S/T_phosphtse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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Primates;
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                                   Znf_C2H2.
H2; 2.
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20, Last sequence update)
21, Last annotation update)
2'-phosphodiesterase (EC 3.1.4.16)
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Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; I Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEF21AF90E9DF13F CRC64;
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brain which
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RESULT RESULT Q61479
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Best Local
                                                                                                                                                                                         Q61479;
Q1-NOV-1996 (TrEMBLrel. (
Q1-NOV-1996 (TrEMBLrel. (
Q1-MAR-2002 (TrEMBLrel. 2
DNA binding protein Rc.
KRC OR RC.
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TISSUE=BRAIN, AND THYMOCYTES;
MEDLINE=21100880; PubMed=11161801;
Hicar M.D., Liu Y., Allen C.E., Wu L.C.;
Hicar M.D., Liu Y., Allen Cinc Finger Protein HIVEP3: Molecular Cloning,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SMOUDED; ALTER HOMOCIT SYNTH 1;
PROSITE; PS00815; ALTER HOMOCIT SYNTH 1;
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 5.
DNA-binding; Metal-binding; Zinc-finger.
DNA-binding; Metal-binding; Zinc-finger.
SEQUENCE 2406 AA; 259381 MW; 7F498F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hicar M.D., Liu Y., Allen C.E., Wu "Structure of the Human Zinc Finger Expression, Exon-Intron Structure, Genes HIVEP1 and HIVEP2.";
Genomics 71:89-100(2001).
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InterPro; IPRO002034; AIPM/Hcit_synth.
InterPro; IPR000202; Znf_C2H2.
Pfam; PF00096; Zf-C2H2; 5.
SMART; SM00355; ZnF_C2H2; 5.
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01-JUN-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
Kappa B and V(D)J recomb
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NON_TER 1 1
SEQUENCE 1628 AA; 174427
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                                         NCBI_TaxID=10090;
[1]
                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                    Q61479
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Mammalia; Eutheria;
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   SEQUENCE FROM N.A.
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Rodentia;
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MW; 7F498F2BBF3AE93F CRC64;
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Pred. No.
                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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Best Local S
Matches 6
                    InterPro; IPR001789; Response_reg.
Pfam; PF01590; GAF; 1.
Pfam; PF002518; HATPase_c; 1.
Pfam; PF00069; pkinase; 1.
Pfam; PF00072; response_reg; 1.
Pfam; PF00072; signal; 1.
Pfam; PF00314; BCTRLSENSOR.
ProDom; PD00001; Euk_Dkinase; 1.
ProDom; PD000039; Response_reg; 1.
SWART; SM00065; GAF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O14002 PRELIMINARY; FAL, CO14002; O1-JUN-1998 (TrEMBLrel. 06, Created)
O1-JUN-1998 (TrEMBLrel. 06, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97001141; PubMed=8812474;
Wu L.C., Liu Y., Strandtmann J., Mak C.H., Lee B., Li Z., Yu C.Y.;
Wu L.C., Liu Y., Strandtmann J., Mak C.H., Lee B., Li Z., Yu C.Y.;
"The mouse DNA binding protein Rc for the kappa B motif of
transcription and for the V(D)J recombination signal sequences
contains composite DNA-protein interaction domains and belongs to
contains composite transcriptional proteins.";
Genomics 35:415-424(1996).
Genomics 35:415-424(1996).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL; L46815; AAB40884.1; -.
EMBL; L46815; AAB40884.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murphy L., Harris D., Barrell B.G., Rajandream M.A., Wood V.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL):
-!- SIMILARITY: TO PROKARYOTIC SENSORY TRANSDUCTION HISTIDINE KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Schizosaccharomyceteese; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Putative sensor-like histidine kinase C27E; SPAC27E2.09. Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:106589; Krc.
InterPro; IPR000822; Znf_C2H2.
Pfam; PF00096; zf-C2H2; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z98978; CAB11683.1; -. HSSP; P06657; 2CHF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=972;
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                                                                                                                                                                                                                                                                          InterPro;
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InterPro; IPR004358; Bact_sens_pr_C
                                                                                                                                                                                                                                                                                                                          InterPro;
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     SM00065;
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                                                                                                                                                                                                                                                                     IPR002114; | IPR001610; | IPR000014;
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                                                                                                                                                                                                                                                                                                                                                                   IPR003661;
                                                                                                                                                                                                                                                                                                                                                                                                IPR000719;
IPR003018;
                                                                                                                                                                                                                                                                                                                                                 IPR004359;
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HATPase_c; 1.
                                                                                                                                                                                                                                                                                                   ; His_kinA.
; HIS_KIN_sig.
; HPr_SerP_site.
; PAC.
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54.5%;
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Euk pkinase
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; Mismatches
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Best Local S
Matches 6
     HSSP; P06982; 1AJ6.
InterPro; IPR003594; ATPbind ATPase.
InterPro; IPR003595; DNAprim toprim.
InterPro; IPR001241; DNA topoisoII.
Pfam; PF00204; DNA gyraseB; 1.
Pfam; PF002518; HANTBase_c; 1.
Pfam; PF01751; Toprim; 1.
PRINTS; PR00418; TPI2FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00448; KEC; 1.
TIGREPAMS; TIGR00229; Sensory box; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00589; PTS_HPR_SER; UNKNOWN_1.
PROSITE; PS00589; PTS_HPR_SER; UNKNOWN_1.
                                                                                         SEQUENCE FROM N.A.

STRAIN=IFO14945;

SUZUKİ M., Nakagawa Y., Harayama S., Yamamoto S.;

SUZUKİ M., Nakagawa Y., Harayama S., Yamamoto S.;

SUZUKİ M., Nakagawa Y., Harayama S., Yamamoto S.;

"Phylogenetic analysis and taxonomic study of marine Cytophaga like bacteria. Proposal of Haerentibaculum gen. nov. with Haerentibaculum maritinum comb. nov. and Haerentibaculum ovolyticus comb. nov., and two new species ";

SUBMITTED (OCT-1999) to the EMBL/GenBank/DDBJ databases.

-!- CATALYTIC ACTULTY: ATP-DEPENDENT BREAKAGE, PASSAGE AND REJOINING OF DOUBLE-STRAINED DNA.

-!- SIMILARITY: BELONGS TO THE TYPE II TOPOISOMERASE FAMILY.

EMBL; AB034239; BAB12497.1; -.
                                                                                                                                                                                                                                                                           Q9FAU3 PRELIMINARY; PRT; 474 AA. Q9FAU3; 01-MAR-2001 (TrEMBLrel. 16, Created) 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) DNA gyrase B subunit (Fragment).
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DOMAIN
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SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 1.
SMART; SM00448; REC; 1.
                                                                                                                                                                                                                              Sauceria; CFB group;
NCBI_TaxID=256;
                                                                                                                                                                                                                                              Myroides odoratus.
Bacteria; CFB grou
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SM00433; TOP2c;
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                                                                                                                        databases.
E, PASSAGE AND REJOINING
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Best Local S
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Best Local S
Matches 7
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ATP-binding;
NON_TER
NON_TER 4
SEQUENCE 47
                                                                                                                                                             Q9XEV5;
Q9XEV5;
01-NOV-1999
         Llaca V., Lou A., Young S., Messing J.;
"Microsynteny in a gene-dense region in maize,
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ c
EMBL; AF119222; AAD27682.1; -.
                                                                                  Hypothetical 23.5 kDa protein.
Oryza sativa (Rice).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Spermatroideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-LIVER;
Arai Y., Kim B., Nishikawa T., Shiraishi H.;
"vitellogenin I cDNA in Oryzias latipes.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ
EMBL; AB064220; BAB79696.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adianichthyidae; Oryziinae; Oryzias.
NCBI_TaxID=8090;
                                                                                                                                          01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002
01-JUN-2002
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01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01347; Vitellogenin_N; Pfam; PF00094; vwd; 1.
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Hypothetical protein
                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryzias latipes (Medaka fish).
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                                                                        NCBI_TaxID=4530;
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InterPro; IPR001846; VWF_D.
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5; Conserv
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474 AA;
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53012 MW;
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45.5%;
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Pred. No. 2.1e+02;
4; Mismatches 2
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Pred. No. 53;
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annotation update)
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Q921L6;
01-DEC-2001
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01-OCT-2000
01-OCT-2000
01-OCT-2000
EMBL; X02451; CAB57810.1; Mitochondrion. . . NON TER 1 1
                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Spermatophyta; Magnoliophyta; Liliopsid Panicoideae; Andropogoneae; Zea.
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                            of maize.";
EMBO J. 4:1125-1128(1985).
                                                Paillard M., Sederoff
"Nucleotide sequence of
                                                                      SEQUENCE
                                                                                                 Spermatophyta; Magnoliophyta; Panicoideae; Andropogoneae;
                                                                                                                                   Mitochondrion.
                                                                                                                                          Zea mays (Maize).
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Hypothetical protein; Complete proteome.
SEQUENCE 230 AA; 26825 MW; F7547039385EA374 CRC64;
                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002725; DUF45.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF01863; DUF45; 1.
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EMBL; AE008604; AAL02942.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21442074; PubMed=11557893;
Ogata H., Audic S., Renesto-Audiffren P., Fo
Samson D., Roux V., Cossart P., Weissenbach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=MALISH 7;
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                                                                                       NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=781;
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S-1 mitochondrial
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Pred. No.
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38;
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Q9M2G0;
01-OCT-2000
01-OCT-2000
01-JUN-2002
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Q9FAU4;
01-MAR-2001
01-MAR-2001
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Suzuki M., Nakagawa Y., Harayama S., Yamamoto S.;
"Phylogenetic analysis and taxonomic study of marine Cytophaga like bacteria. Proposal of Haerentibaculum gen. nov. with Haerentibaculum marithmum comb. nov. and Haerentibaculum ovolyticus comb. nov., and two new species.";
                                  Hypothetical F14P22.150.
                                                                                                                                                                                                                                                                                                                                                                          NON TER
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pfam; pF02518; HATFBASE_C; 1.
pfam; pF01751; Toprin; 1.
pRINTS; PR00418; TP12FAMILY.
SMART; SM00433; TOP2C; 1.
PROSITE; PS00154; ATPASE_E1_E2; UNKNOWN_1.
PROSITE; PS00177; TOPOISOMERASE_II; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P06982; lAJ6.
InterPro; IPR001757; ATPase E1-E2.
InterPro; IPR003594; ATPbind ATPase.
InterPro; IPR002936; DNAprim toprim.
InterPro; IPR001241; DNA_topoisoII.
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-!- SIMILARITY: BELONGS TO THE TYPE II EMBL; AB034238; BAB12496.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; CFB group; NCBI_TaxID=1027;
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   Eukaryota;
                   Arabidopsis thaliana (Mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
subunit (Fragment).
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                                                                                                                        Conservative
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Streptophyta; Embryophyta; Tracheophyta;
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597 AA; 6
                   PRELIMINARY;
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Cheuk R., Chen H., Kim C.J., Meyers M.C., Banh J., Bowser L.,
Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
A Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
A Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,
A Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
"Arabidopsis cDNA clones.";
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, Ap468845; AALS932.1;
InterPro; IPR002106; AAtRNA ligaseII.
InterPro; IPR002106; AAtRNA ligaseII.
InterPro; IPR002106; AATRNA LIGASE II 1; UNKNOWN 1.
PROSITE; PS00179; AA TRNA LIGASE II 1; UNKNOWN 1.
SEQUENCE 602 AA; 66761 MW; 233754749BCE74DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O8W0Z9;
Q8W0Z9;
O1-MAR-2002 (TrEMBLrel. 2
O1-MAR-2002 (TrEMBLrel. 2
O1-JUN-2002 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111
SEQUENCE FROM N.A.
D'Angelo M., Vezzi A., Modesto D., Pigazzi M.,
Lemcke K., Mayer K.F.X., Quetier F., Salanouba
Lemcke K., Mayer K.F.X. (Duetier F.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AT3958560/F14P22_150.
Arabidopsis thaliana (Mouse-ear cress).
Eukarydota; Viridiplantae; Streptophyta; Embryophyta;
Espermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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InterPro; IPR005135; Exo endo phos.
Pfam; PF03372; Exo endo phos; 1.
PROSITE; PS00179; AA TRNA LIGASE II 1;
Hypothetical protein.
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Submitted (JAN-2000) to the EMBL/GenBank/DDBJ
EMBL; AL137082; CAB68194.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-NOV-1996
01-DEC-2001
Helicase
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MEDLINE-98380374; PubMed=9712777;
MEDLINE-98380374; Sorial V., Klivington D.,
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MEDLINB=94314421; PubMed=7518806;
Garbe T.R., Stringer J.R.;
Garbe T.R., Stringer J.R.;
"Molecular characterization of clustered variants of major surface antigens of human Pneumocystis carinii. Infect. Immun. 62:3092-3101(1994).
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EMBL; L20708; AAA50986.1; -.
InterPro; IPR003840; Herpes_helicase.
Pfam; PF02689; Herpes Helicase; 1.
SEQUENCE 833 AA; 9\overline{5}016 MW; 8DFFC7
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01-NOV-1998
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MEDLINE=94303212; PubMed=8030256;
Dean H.J., Cheung A.K.;
"Identification of the pseudorabi
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Alphaherpesvirinae; Varicellovirus.
NCBI_TaxID=10345;
                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                               Infect. Immun. 66:4268-4273(1998).
EMBL; AF033212; AAC34975.1; -.
InterPro; IPR003330; MSG.
                                                                                                                                                                                                                                                                                                                                                                                                                                  "Characterization of major surface glycoprotein genes of human Pneumocystis carinii and high-level expression of a conserved
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                                                                                                               Similarity 6; Conserv
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(TIEMBLrel. 08, Last sequence up
(TIEMBLrel. 17, Last annotation
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Pred. No. 1.5e+02;
                                                                                                                                          Score 37; DB 3;
Pred. No. 1.9e+02;
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SEQUENCE
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84 AA; 21050
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                           163
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rel. 18, L
rel. 18, L
1 SSO2176.
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12,
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SEQUENCE FROM N.A.

STRAIN-ATCC 35092 / DSM 1617 / P2;

MEDLINE=2132296; PubMed=11427726;

MEDLINE=2132296; PubMed=11427726;

She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

De Moors A., Erauso G., Fletcher C., Gordon P.M.C.,

Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.

Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

"The complete genome of the crenarchaeon Sulfolobus solfataricus

Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=ATCC 43504;
MEDLINE=99214098; PubMed=10198012;
MCGee D.J., May C.A., Garner R.M., Himps
"Isolation of Helicobacter pylori genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteriol. 181:2477-2484(1999).
BL; AF125214; AAD27694.1; -.
QUENCE 88 AA; 10190 MW; 6C30
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teria; epsilon subdivision; Helicobacter group;
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21050 MW;
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Last sequence update)
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Pred. No.
Pred. No. 47;
); Mismatches
                                        Score 36;
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555DF2EEED2172D7
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                DB
47;
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                                      Length 184;
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RESULT 20
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ID Q826A
AC Q826A
DT 01-MA
DT 01-MA
DT 01-JU
DE Putat
GN STY18
OS Salmo
OC Bacte
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojbbori T., Bono H., Kasukawa T., Saito R.,
RA Saito T., Okazaki Y., Gojbbori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Garriboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                            Q8Z6A4 PRELIMINAL,
Q8Z6A4;
Q1-MAR-2002 (TrEMBLrel. 20, Created)
Q1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Q9DAA4;
01-JUN-2001
01-JUN-2001
01-JUN-2002
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STRAIN=C57BL/6J; TISSUE=TESTIS;
MEDLINE=21085660; PubMed=11217851;
 Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
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NCBI_TaxID=10090;
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                   Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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InterPro; IPR001254; Ser_protease_Try.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Functional annotation of a full-length mouse cDNA collection.";
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1700016G05RIK.
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S; PR00722; CHYMOTRYPSIN.
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                                                                                                                                                                                                                                                                                           Similarity 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                             Serine protease.
                                                                                                                                                                                                                                                                                                                                                               237 AA;
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                                                                                                                                                                                                                                                                                           Conservative
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85.7%;
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21,
 gamma subdivision; Enterobacteriaceae;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                               Pred.
                                                                                                                                                                                                                                                                                                                             Score 36;
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                                                                                                                                                                                                                                                                                                                                                             EF91396566B0394A CRC64;
                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                           Length 237;
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Matches
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01-MAR-2002
01-MAR-2002
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                                                                                                                                                                     Shchelkunov S.N., Totmenin A.V., Safronov P.F., Gutorov Ryazankina O.I., Petrov N.A., Babkin I.V., Uvarova B.A., Esposito J.J., Moss B., Sisler J.R., Jahrling P.B., Sand Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases EMBL; AF380138; AAL40532.1; --
                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=ZAIRE-96-I-16;
MEDLINE=21592287; PubMed=11734207;
Shchelkunov S.N., Totmennin A.V., Babkin I.V., Safron Shchelkunov S.N., Totmennin A.V., Bubkin I.V., Uvarova Ryazankina O.I., Petrov N.A., Gutorov V.V., Uvarova Mikheev M.V., Sisler J.R., Esposito J.J., Jahrling F Sandakhchiev L.S.;
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Pfam; PF02917; Pertussis_S1; 1.
Transferase; Glycosyltransferase; Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
Nature 413:848-852 (2001).
EMBL; AL627271; CAD02123.1; -.
                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                              STRAIN=ZAIRE-96-I-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                      FEBS Lett.
                                                                                                                                                                                                                                                                                                                                                                                                "Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monkeypox virus
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5; Conser
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     ENIYSYLP 11
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MEDLINE=99156950; PubMed=10037760;
Guillen E., Abeijon C., Hirschberg C.B.;
"The genes for the Golgi apparatus N-acetylglucosaminyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9Y761 PRELIMINARY; PRT; 460 AA. Q9Y761; 01-NOV-1999 (TrEMBLrel. 12, Created) 01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) AlphaN-acetylglucosamine transferase.
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J. Biol. Chem. 274:6641-664
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Best Local
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InterPro; IPR005110; MoeA_C.
InterPro; IPR005110; MoeA_N.
IfterPro; IPR005110; MoeA_N.
IfterPro; IPR005110; MocF biosynth; 1.
Pfam; PP00994; MCCF biosynth; 1.
Pfam; PP00453; MoeA_N; 1.
ProDom; PD002460; MCCF biosynth; 1.
TIGRPAMS; TIGR00177; molyb syn; 1.
PROSITE; PS01079; MCCF BIOSYNTHESIS_2; UNKNOWN_1.
Hypothetical protein; Complete proteome.
                                                                                                                                                                                                                                                                                                                   Q99UK9;
01-JUN-2001
01-JUN-2001
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nawarawayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A., Oshima T., Kikuchi H.;
                                                 SPECIES-S.aureus (strain Mu50), and S.aureus (strain N315);
MEDLINB-21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Puruya K., Yoshino C., Shib,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
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01-DEC-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
Putative molybdopterin
                         "Whole genome sequencing of meticillin-resistant aureus.";
                                                                                                                                                                         SPECIES=S.aureus (
                                                                                                                                                                                                                                              Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                            Staphylococcus aureus
Staphylococcus aureus
                                                                                                                                                                                                                                                                                        Proline-tRNA ligase.
PROS OR SAV1263 OR SA1106.
                                                                                                                                                                                                                                                                                                                                                                              Q99UK9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein; SEQUENCE 545 AA; 6
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EMBL; AP000982; BAB65499.1; -.
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Archaea; Crenarchaeota;
             Lancet 357:1225-1240(2001)
                                                                                                                                                                                                                NCBI_TaxID=158878,
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CATALYTIC
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54.5%;
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biosynthesis moeA protein.
ATP
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Last annotation update)
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Pred. No. 1.5e
3; Mismatches
L-AMINO
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E21E5B8355F85C27 CRC64;
ACID +
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ches 2;
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TRNA (AMINO ACID) =
                                          Staphylococcus
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Ito T.,
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RESULT 27
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ID Q9KVI
AC Q9KVI
DT 01-0C
DT 01-0C
DT 01-DE
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Best Local S
Matches 6
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Best Local Similarity
Q9KVI9
Q9KVI9;
01-OCT-2000
01-OCT-2000
01-DEC-2001
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Pfam; PRO1046; TRNASYNTHPRO.

PRINTS; PRO1046; TRNASYNTHPRO.

TIGREAMS; TIGR00409; proS_fam_II; 1.

TIGREAMS; TIGR00409; proS_fam_II; 1.

PROSITE; PS00179; AA TRNA LIGASE II 1; 1.

PROSITE; PS00179; AA TRNA Bynthetase; Ligase; (ATP-binding; Aminoacyl-tRNA Bynthetase; Ligase; (ATP-binding; ATP-binding;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  097GQ7; PRELIMINARY;
097GQ7; PRELIMINARY;
01-OCT-2001 (TrEMBLrel. 18,
01-DCT-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
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-!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILAR -:- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRN EMBL; AP003361; BAB57425-1; -- EMBL; AP003133; BAB42358.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=ATCC 824 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clostridium acetobutylicum.
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InterPro; IPRO04154; HGTP anticodon.
InterPro; IPRO04500; ProS; fam II.
InterPro; IPRO02314; tRNA-synt_2b.
InterPro; IPRO02316; tRNA-synt_pro.
Pfam; PF00587; tRNA-synt_2b; 1.
Pfam; PF00587; tRNA-synt_2b; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1488;
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(TrEMBLrel.
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                                                                                                                               PRELIMINARY;
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54.5%;
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   15,
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3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1.66
L; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36;
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Pred. No.
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AMINOACYL-TRNA SYNTHETASE FAMILY
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RESULT 28
Q97SR1
ID Q97SR
AC Q97SR
AC Q97SR
DT 01-OC
DT 01-JU
DE Proly
GN SPIOLS
GN STREP
OC STREP
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MEDLINE-20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Brmolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                           Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L., McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K., Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.; "Complete genome sequence of a virulent isolate of Streptococcus
                                              InterPro;
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PROSITE; PS001430; TONB_DEPENDENT_REC_1; PS001156; TONB_DEPENDENT_REC_2; Receptor; Complete proteeme.

SEQUENCE 611 AA; 68609 MW; 0C6D9A9A6
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01-OCT-2001
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                                                                                                                                                           EMBL; AE007339
TIGR; SP0264;
                                                                                                                                                                                                            pneumoniae.";
Science 293:498-506(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21357209; PubMed=11463916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pneumoniae.
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
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                                nterPro;
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                                                                                                                                                                                 AE007339; AAK74442.1;
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JFR002106; AATRNA_ligaseII.
JFR004154; HGTP_anticodon.
JFR004500; ProS_fam_II.
JFR002314; tRNA-synt_2b.
JFR002316; tRNA-synt_pro.
F03129; HGTP_anticodon; 1.
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77.8%;
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Pred. No.
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PRINTS; PR01046; TRNASYNTHPRO.
TIGRPAMS; TIGR0409; pros_fam_II; 1.
TIGRPAMS; TIGR0409; pros_fam_II; 1.
PROSTTE; PS00179; AA TRNA_LIGASE II_1; 1.
PROSTTE; PS00179; AA TRNA_LIGASE II_1; 1.
PROSTTE; PS00179; AA TRNA_LIGASE II_1; 1.
PROSTTE; PS00179; AA TRNA_LIGASE II_1; 1.
PROSTTE PROST II; Length
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01-DEC-2001
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01-OCT-2001
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STRAINATCC 35092 / DSM 1617 / P2;

MEDLINE=21332296; PubMed=11427726;

MEDLINE=21332296; PubMed=11427726;

She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

She Q., Singh R.K., Confalonieri F., Clausen I.G., Curtis B.A.,

De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

Chariebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

"The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";

EMBL, AE006724; AAX41317.1;

TENED2724; AAX41317.1;

TENED2724; AAX41317.1;

TENED2724; AAX41317.1;

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TENED2724; TENED2724; AAX41317.1;
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PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
Hypothetical protein; Complete proteome.
SEQUENCE 637 AA; 74021 MW; 17EF843BB5AB13BF CRC64;
SEQUENCE FROM N.A.
STRAIN=CLIP 11262 / SEROVAR 6A;
                                                                                                              Bacteria; Firmicutes; Bacillus/Clostridium
Listeriaceae; Listeria.
                                                                                                                                                                                                   Hypothetical LIN0050.
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01-MAR-2002
                                                                                                                                                                      Listeria innocua.
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(TrEMBLrel. 18, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
protein SSO1053.
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(TrEMBLrel. 19, Last
(TrEMBLrel. 20, Last
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Pred. No. 1.8e+02;
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Pred. No. 1.7e+02;
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Baquero F., Gerche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Barnal G., Duchaud E., Durant L., Dussurget O.,
Gautier L., Goebel W., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
"Comparative genomics of Listeria species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8YAQ9;
01-MAR-2002
01-MAR-2002
01-MAR-2002
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Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Fishi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Depez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
"Comparative genomics of Listeria species.";
                                                                                                                                                                                                                                                                                         Science 294:849-852(2001).
EMBL; AL591973; CAC98272.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=EGD-E
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Listeriaceae; Listeria.
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Racteria: Firmicutes; Bacillus/Clostridium group; Bacillales;
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SEQUENCE 1067 AA; 119192 MW; B5DA562BAD505064 CRC64;
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EMBL; AL596163; CAC95283.1; -.
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                                                                                                                                                                                                                                    Hypothetical
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RQNENLYSFL
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119645 MW; 4341B4
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Last annotation update)
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Pred. No. 3.1e
3; Mismatches
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3; Mismatches
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3.1e+02;
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RESULT 33
Q920E
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AC Q920E
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Best Local Similarity
Matches 5; Conserv
  Q9HLG1;
Q9HLG1;
01-MAR-2001
01-MAR-2001
01-JUN-2002
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Q920E6
01-DEC-2001
01-DEC-2001
01-MAR-2002
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NON_TER
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J. EXP. Med. 172:879-888 (1990).

EMBL; X55028; CAA38847.1; -.

Interpro; IPR000130; Zn MTDeptdse.

PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1.

SEQUENCE 1114 AA; 125570 MW; 0445F99609313E1D CRC64;
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Q05352;
Q05352;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Tmmuno-dominant variable surface antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Atkin J.D., Iape A., Jenning "Definition of the Idiotope in Mammalian Cells.";
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Pterin-mimicking anti-idiotope kappa chain variable
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MEDLINE=90354789; PubMed=1696956;
Edman U., Meraz M.A., Rausser S., Agabian N., Meza I.;
"Characterization of an immuno-dominant variable surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ευκαγγοτα; Entamoebidae; Entamoeba.
NCBI TaxID=5759;
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Entamoeba histolytica.
Eukaryota; Entamoebida
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    (TrEMBLrel. 16, (TrEMBLrel. 16, (TrEMBLrel. 21,
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                                                                                                                                                                                                                                                                                                                                                                                                          11943 MW;
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70.0%;
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diotope of Pterin-Mimicking
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Last sequence update)
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RESULT 35
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                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

Cheuk R., Chen H., Kim C.J., Shinn P., Banh J., Bowser L.,
Cheuk R., Chen M.K., Goldsmith A.D., Hayashizaki Y., Ishida J.,
Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y., Ishida J.,
Carninci R., Chung M.K., Goldsmith A.D., Kawai J., Lam B., Lee J.M.,
Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M.,
Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M., Seki M.,
Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K., Davis R.W.
"Arabidopsis cDNA clones.";
"Arabidopsis cDNA clones.";
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Nature 407:508-513(2000).

EMBL; AL445063; CAC11412.1; -.

InterPro; IPR005182; DUF304.

Pfam; PF03703; DUF304; 1.

Hypothetical protein; Complete proteome.

SEQUENCE 120 AA; 13907 MW; F630AB0CB5772CED CRC64;
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Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Epermatophyta, Magnoliophyta, eudicotyledons, core eudicots; Rosidae,
Epermatophyta, Brassicales, Brassicaceae, Arabidopsis.
                                                          Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF361848; AAK32860.1; -. EMBL; AY066053; AAA47420.1; -. SEQUENCE 140 AA; 15024 MW; A9B60C5B65EA2506 CRC64;
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01-MAR-2002 (TrEMBLrel.
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01-JUN-2001
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Mewes H.-W., Frishman
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MEDLINE=20479972; PubMed=11029001;
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Similarity 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thermoplasma.
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              61.4%;
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Last annotation update)
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Pred. No. 46;
3; Mismatches
            Score 35;
Pred. No.
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46;
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Query Match
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Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
1: FÜNCTION: CATALYZES THE REVERSIBLE OXIDATION OF CO2 AND
METHANOFURAN (MFR) TO N-FORMYLMETHANOFURAN (CHO-MFR). CAN
OXIDISE FORMYLMETHANOFURAN. THIS ENZYME IS OXYGEN-LABILE.
1: CATALYTIC ACTIVITY: FORMYLMETHANOFURAN + H(2)O + ACCEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shmer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics."; J. Bacteriol. 179:7135-7155 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hochheimer A., Linder D., Thauer R.K., Hedderich R.; "The molybdenum formylmethanofuran dehydrogenase operon and the tungsten formylmethanofuran dehydrogenase operon from Methanobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Molybdenum-containing formylmethanofuran dehydrogenase isoenzyme subunit E (EC 1.2.99.5).
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"The formylmethanofuran dehydrogenase isoenzymes in Methanobacterium
wolfei and Methanobacterium thermoaurotrophicum: Induction of the
molybdenum isoenzyme by molybdate and constitutive synthesis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES=M.wolfei;
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Archaea; Euryarchaeota; Methanobacteria;
Methanobacteriaceae; Methanothermobacter
MCBI_TaxID=187420, 145261;
                                              Oxidoreductase; Molybdenum; Methanogenesis; Comp
SEQUENCE 180 AA; 20454 MW; D09C57F5FCADEE2D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES=M.thermoautotrophicum; STI
MEDLINE=98037514; PubMed=9371463;
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                                                                                Pfam; PF02663; FwdE;
                                                                                                InterPro; IPR003814; FwdE.
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L; X97820; CAA66400.1;
                                                                                                                                                                                                SUBUNIT: CONSISTS
                                                                                                                                                                                                               ENZYME REGULATION: INACTIVATED BY CYANIDE PATHWAY: FIRST STEP IN METHANOGENESIS.
                                                                                                                                                                                                                                             COFACTOR: MOLYBDENUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Biochem.
                                                                                                              AE000867; AAB85415.1; -. AJ009689; CAA08786.1; -.
                                                                                                                                                                                                                                                              METHANOFURAN + REDUCED ACCEPTOR
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                                                                                                                                                              BY GROWTH ON MOLYBDENUM,
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66.7%;
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01-DEC-2001
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Rohwer F.L., Segall A.M., Steward G., Seguritan V., Bre:
Wolven F., Azam F.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AF189021; AAG02605.1; -.
SEQUENCE 200 AA; 20825 MW; 8D0FDAA312594E0C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wolven F., Azam F.:
"The complete genomic sequence of the shares homology with nonmarine phages. Limnol. Oceanog. 45:408-418(2000).
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"The sequence of 200 kb preveals a high degree of
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Rohwer F.L., Segall A.M.,
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                                                                                           Local
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; AY003872; AAF99448.1
ENCE 270 AA; 31249
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Best Local Similarity 70.0%;
Matches 7; Conservative
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OB3275;

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O1-NOV-1998 (TrEMBLrel. 08,

O1-DEC-2001 (TrEMBLrel. 19,
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InterPro; IPRO03596; Ig_v.
Pfam; PF00047; ig; 2.
SMART; SM00406; IGv; 2.
SEQUENCE 298 AA; 31867 MW;
                                                                                                                                                 "Complete genome sequence of Treponema pallidum, spirochete.", Science 281:375-388(1998).
EMBL; AE001206; AAC65234.1; -.
TIGR; TP0247; -...
                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98332770; PubMed=9665876;
Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Petterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
N-acceylmuramoy1-L-alanine amidase (AMIA).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
        Complete proteome. SEQUENCE 357 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treponema pallidum.
Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
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EMBL; AB036341; BAA88633.1; -.
HSSP; P01607; IREI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=BALB/C; TISSUE=SPLEEN; MEDLINE=20183931; PubMed=10706631;
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                                                                    Pfam; PF01520; Amidase_3; 1.
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        AA; 39810 MW;
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Pred. No.
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        C46ED7EDB3AEFB71 CRC64;
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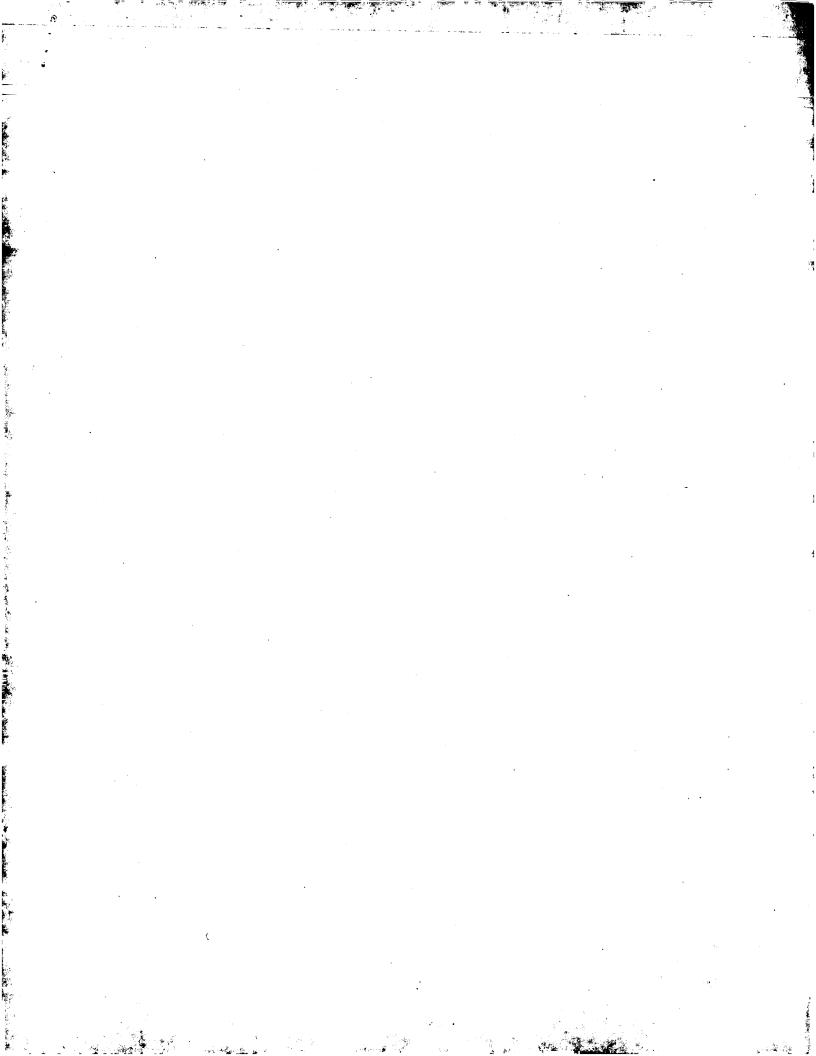
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Query Match 61.4%; Score 35; DB 16; Length 357;
Best Local Similarity 70.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps

Qy 1 RASENIYSYL 10
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Db 162 RASQNIYDLL 171
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Search completed: July 18, Job time : 30.38 secs

2003,

15:09:47



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Database :
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No. 1 2 3 4 4 5	Score 34 34 34 34	Query Match Length DB 100.0 7 21 100.0 7 23 100.0 92 23 100.0 107 23 100.0 107 23	Match Length Match 100.0 7 100.0 7 100.0 92 100.0 107 100.0 107 100.0 495	21 23 23 23 23 23	1 H
	3 2 2 3 4 4 4 4	100.0 100.0 100.0	7 7 92 107	21 23 21	AAY87661 AAE22198 AAE22190 AAY87656
	34	100.0	107	23	AAE22189
σ	34	100.0	495	23	AAE22193
7	31	91.2	149	23	ABB48303
8	31	91.2	714	23	ABB97340
9	29	85.3	99	18	AAW04596
10	29	85.3	99	18	AAW04597

	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
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	23	22	22	22	14	12	22	22	20	21	23	23	23	23	23	23	23	23	23	23	23	23	15	17	17	23	17	12	12	22	19	18	17	16	18
ALIGNMENTS	AA015140	AAB80158	AAB80118	AAG89856	AAR32800	AAR12970	AAB80159	AAB80119	AAY37571	870	ABB05982	ABB05997	ABB05996	ABB05995	ABB05994	ABB05993	ABB05992	ABB05991	ABB05990	ABB05963	ABB05962	AAU72864	AAR53148	AAW05828	AAW03725	ABP00079	AAW03721	AAR12357	AAR12235	AAB84742	AAW46483	AAW07439	AAW05822	AAR78971	AAW04598
	•	Corynebacterium gl	Ħ	$\sim$	ance F	еp	Corynebacterium gl	Corynebacterium gl	Chlamydia trachoma	Arabidopsis thalia	Monoclonal antibod	Human monoclonal a	Human monoclonal a	Human monoclonal a	Mouse and human ch	and human	æ	and human	8	lonal	oclonal	singl	of M	1D10 an	ised M	Human ORFX protein	Anti-human gp39 MA	Light (kappa) chai	Mouse MAb 2G12 L c	Variable region of	8019 VK antibody.	ω		Light chain variab	Anti-DNA antibody

## ALIGNMENT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIP3; phosphatidylinositol-3,4,5-triphosphate; variable region; CDR2; immunogen; antibody; light chain; complementarity determining region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-AUG-2000 (first entry)
                                                        Claim 11; Page 13; 15pp; Japanese.
                                                                                                                                               A monoclonal antibody recognizing phosphatidylinositol-3,4,5-triphosphate
                                                                                                                                                                                                                                                                                                   WPI; .2000-353334/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                               (FUKU/) FUKUI Y.
(IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98JP-0252921.
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Best
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The invention relates to the use of an antibody and/or chemokine construct that binds a chemokine receptor for preparing a pharmaceutical composition for eliminating cells latently infected with a primate immunodeficiency virus (e.g. human immunodeficiency virus (HIV-I). They are used in gene therapy and as vaccines. The antibody and/or chemokine construct is also used for preparing a pharmaceutical composition for treating, preventing and/or alleviating immunological disorders including autoimmune diseases (e.g. multiple sclerosis, type I diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes a novel antibody specifically recognizing phosphatidylinositol-3,4,5-triphosphate (PIP3). The antibody of the invention is used in immunogenic compositions in which a dead Salmonella genus microbe is used as an adjuvant and mixed with PIP3. The antibody can be used in an immunoassay containing a step in which the above antibody or its variable region is reacted with PIP3 present in a sample and the bond based on their immunological reaction. The method can determine PIP3 easily in a high sensitivity. This sequence represents the murine PIP3 recognizing monoclonal antibody variable region heavy chain complementarity determining region, CDR2 described in the method of
                                                                                                                                                                                                                     Use of an antibody and/or chemokine construct that binds to a chemokine receptor, for eliminating cells latently infected with primate immunodeficiency virus, or treating, preventing and alleviating immune
                                                                                                                                                                                                                                                                                                                                                                                                           08-SEE-2000; 2000EP-0119694
05-SEE-2001; 2001US-0948004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diabetes; skin inflammation; atopic dermatitis; inflammatory disease; inflammatory renal disease; HIV-1; transplant rejection; murine; CDR2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              skin disease; immunological disorder; autoimmune disease; ps
multiple sclerosis; rheumatoid arthritis; inflammatory bowel
                                                                                                                                                                 Disclosure; Page 116; 117pp; English.
                                                                                                                                                                                                                                                                                                                                     Mack M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200220615-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chemokine construct; human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibody.
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7; Conser
                                                                                                                                                                                                                                                                                                                                     Schloendorff
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Pred. No.
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7.8e+05;
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RESULT 3
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                                                                                                                                                                       The invention relates to the use of an antibody and/or chemokine construct that binds a chemokine receptor for preparing a pharmaceutical composition for eliminating cells latently infected with a primate
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05-SEP-2001; 2001US-0948004
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                                                                                                                                                                                                                                                                  Sequence
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N-PSDB; AAY87656.
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(IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO
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N-PSDB; AAD35248.
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05-SEP-2001; 2001US-0948004
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                                                AAE22193 standard;
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Pred. No. 5.5;
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AAE22193;

(first entry)

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RESULT 7
ABB48303
ID ABB4
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AC ABB4
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                                                                                                                                                                                                                                                                       The invention relates to the use of an antibody and/or chemokine construct that binds a chemokine receptor for preparing a pharmaceutical composition for eliminating cells latently infected with a primate immunodeficiency virus (e.g. human immunodeficiency virus (HIV-1). They are used in gene therapy and as vaccines. The antibody and/or chemokine construct is also used for preparing a pharmaceutical composition for treating, preventing and/or alleviating immunological disorders including autoimmune diseases (e.g. multiple sclerosis, type I diabetes and rheumatoid arthritis), allergic diseases, skin diseases (e.g. skin inflammatory diseases such as inflammatory joint diseases (e.g. multiple sclerosis, type I diabetes and inflammatory joint diseases (chronic arthritis), inflammatory renal diseases and graft versus host and transplant rejections. The present sequence is CCR5xCD3 bispecific single chain antibody construct. This antibody construct comprises of murine MC-1 antibody specific for human chemokine receptor 5 (CCR5) and VH and VL domains of an antibody specific for a CD3 antigen joined
                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                     Query Match
Best Local
                 ABB48303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of an antibody and/or chemokine construct that binds to a chemokine receptor, for eliminating cells latently infected with primate immunodeficiency virus, or treating, preventing and alleviating immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 skin disease; immunological disorder; autoimmune disease; psoriasis; multiple sclerosis; rheumatoid arthritis; inflammatory bowel disease; diabetes; skin inflammation; atopic dermatitis; inflammory disease; inflammatory renal disease; HIV-1; transplant rejection; CCR5xCD3;
                                               ABB48303 standard; Protein; 149 AA
                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 29; Page 52; 117pp;
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05-SEP-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-SEP-2001; 2001WO-EP10433
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                                                                                                                                                                                                       Similarity 7; Conserv
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                                                                                                                                    NAKTLTE 56
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                                                                                                                                                                                                                                                                       495
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                                                                                                                                                                                                                                                                                                       linker.
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2001US-0948004
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100.0%; :
1tive 0;
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                                                                                                                                                                                                   Score 34; DB
Pred. No. 31;
0; Mismatches
                                                                                                                                                                                                                                    23;
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                                                                                                                                                                                                                                   Length 495;
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RESULT 8
ABB97340
ID ABB9
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AC ABB9
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DT 27-J
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Compositions for the treatment or prevention of infections by L. monocytogenes and related organisms.

Compositions for the treatment or prevention of the printed composition, but was obtained in electronic format directly from WIPO at fife, wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomic sequence for Listeria monocytogenes, useful e.g. for and prevention of Listeria and related bacterial infections, related polypeptides -
                                      ABB97340;
                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                        ABB97340 standard; Protein; 714 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to the genome sequence of Listeria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibacterial; gene therapy; vaccine; bios vitamin B12; bacterial infection; disease.
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Pred. No.
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37;
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27-JUN-2002

(first entry)

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RESULT 9
AAW0450
ID AAW0
XX AAW0
XX AAW0
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XX L19h
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Best Local
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                                    Region
                                                                                                                                                                      Light chain; variable region; anti-DNA; monoclonal; antibody; MAb 9f11; hairpin; diagnosis; inflammatory glomerulomephritis systemic lupus erythematosus; screening; treatment; preventio; SLE; disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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N-PSDB; ABN32526.
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                                                                                                                    Mus spp
                                                                                                                                                                                                                                                                                                      Anti-DNA antibody 9f11 light chain variable region
                                                                                                                                                                                                                                                                                                                                                             12-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW04596 standard; Protein;
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Yang Y,
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NSKTLTE 112
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                                                             Location/Qualifiers
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Wehrman
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85.7%;
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Pred. No. 2.2e-
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                                                                                                                                                                                               screening; treatment; prevention
                                                                                                                                                                                                                     inflammatory glomerulonephritis;
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RT;
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                                                                                                                                                                                                                                                                                                                            Calf thymus DNA was used to immunise a MRL-lpr mouse, spleen ce from which were then fused with Sp2/0 myeloma cells to give hybridomas producing the anti-DNA MAb. 9f11 was found to react strongly with single stranded DNA and poly(dT), and weakly with poly(dG).
                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is the light chain variable region of the anti-DNA monoclonal antibody (MAb) 9f11, which has a high affinity for single stranded DNA, low or no affinity for double stranded DNA and specifically binds a DNA hairpin. The MAb can be used diagnose disorders associated with the pathological complexation of DNA, e.g. inflammatory glomerulonephritis and systemic lupus erythematosus. It can also be used to generate reagents to screen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-DNA antibody which specifically binds DNA hairpin - useful develop prods. for diagnosis and treatment of disorders, e.g. glomerulonephritis or systemic lupus erythematosus
Light chain; variable region; anti-DNA; monoclonal; antibody; MAb 15b10; hairpin; diagnosis; inflammatory glomerulonephritis; systemic lupus erythematosus; screening; treatment; prevention;
                                                    Anti-DNA antibody 15b10 light chain variable region.
                                                                              12-AUG-1997
                                                                                                        AAW04597
                                                                                                                                  AAW04597 standard; Protein; 99
                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example; Fig 8; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAT43741.
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                                                                                                                                                                                                                                                   Similarity 6; Conserv
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/label=
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42..58
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                                                                              entry)
                                                                                                                                                                                                                                                                85.3%;
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                                                                                                                                                                                                                                                   Score 29; DB
Pred. No. 65;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                 spleen cells
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RESULT 11
AAW04598
ID AAW04
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AC AAW04
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                                                                                                                                                                                   Query Match
Best Local S
Matches 6
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                                                                                                                                                                                                                                                                                  The present sequence is the light chain variable region of the anti-NNA monoclonal antibody (MAb) 15b10, which has a high affinity for single stranded DNA, low or no affinity for double stranded DNA and specifically binds a DNA hairpin. The MAb can be used diagnose disorders associated with the pathological complexation of DNA, e.g. inflammatory glomerulonephritis and systemic lupus erythematosus. It can also be used to generate reagents to screen
                                                                                                                                                                                                                                                                                                                                                                                                     Anti-DNA antibody which specifically binds DNA hairpin - useful to develop prods. for diagnosis and treatment of disorders, e.g. glomerulonephritis or systemic lupus erythematosus
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             AAW04598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-011854/01.
N-PSDB; AAT43742.
                                 AAW04598 standard; Protein;
                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                               Example; Fig 8; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glick
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                                                                                          42
                                                                                                                                      6; Conserv
                                                                                          NAKTLAE
                                                                                                              NAKTLTE 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Swanson PC;
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                                                                                                                                      85.3%; ilarity 85.7%; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'label= CDR_III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   label= framework_III
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                                  99
                                                                                                                                     Score 29; DB Pred. No. 65; 0; Mismatches
                                                                                                                                      <u>.</u>.
                                  8
                                                                                                                                                 DB
65;
                                                                                                                                                             18;
                                                                                                                                                           Length 99;
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                                                                                                                                      Gaps
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Best Local S
Matches 6
                                                                                                                                                         The present sequence is the light chain variable region of the anti-DNA monoclonal antibody (MAb) 5f3, which has a high affinity for single stranded DNA, low or no affinity for double stranded DNA and specifically binds a DNA hairpin. The MAb can be used diagnose disorders associated with the pathological complexation of DNA, e.g. inflammatory glomerulonephritis and systemic lupus erythematosus. It can also be used to generate reagents to screen for pharmaceutical agents, and treat and/or prevent an above
                                                                                                              Calf thymus DNA was used to immunise a MRL-1pr mouse, spleen cells from which were then fused with Sp2/0 myeloma cells to give hybridomas producing the anti-DNA MAb.
                                                                                                                                                                                                                                                                                        Anti-DNA antibody which specifically binds DNA hairpin - undevelop prods. for diagnosis and treatment of disorders, e glomerulonephritis or systemic lupus erythematosus
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                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAT43743
                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-011854/01.
                                                                                                                                                                                                                                                                                                                                                                          Glick GD,
                                                                                                                                                                                                                                                                                                                                                                                                                      18-MAY-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             16-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9636361-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Light chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-DNA antibody 5f3 light chain variable region
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42
                                           6; Conserv
              1 NAKTLTE
NAKTLAE
                                                                                                                                                                                                                                                                                                                                                                         Swanson PC
                                                                                         99 AA;
                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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rpin; diagnosis; inflammatory glomerulonephritis;
                                                                                                                                                                                                                                                                                                                                                                                                                       95US-0443540.
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48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= J_region
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                                                        . 79
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                                             0,
                                                       Score
Pred.
                                             Mismatches
                                                       No.
                                                      65;
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                                                                   Length 99
                                             Indels
                                                                                                                                                                                                                                                                                                                useful
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                                            Gaps
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RESULT 12

AAW05822 standard; Protein; 107

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AAR78971
ID AAR
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                                                                Query Match
Best Local S
Matches 6
                                                                                                                                                                            by Mulv reverse transcriptase. The primers used for CDNA synthesis were complementary to the 5' end of the CHI domain of the heavy Chain expressed by the hybridoma of interest, or to the 5' and of the C kappa domain. Some of the primers used for CDNA synthesis are shown in AAQ97511-Q97518. The primer used for CDNA synthesis of the C variable region of a particular antibody polypeptide was also used for PCR amplification of that variable region, in conjunction with an appropriate V-region primer. In addition, the VH primer AAQ97518 was used to amplify the mAb 2D5 and 5B6 heavy chains. The sequences of the PCR amplified nucleotides were determined. These are given in AAQ97498-Q97510 and the deduced AA sequences in AAR79241-R79250 & AAR78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45 and in the claims are different from the descriptions in the claims are different from the descriptions in the sequence listings are
                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                       5B6 and 3E8) were producing MAbs that were strongly positive against glutatione-mercuric ions but negative against glutathione without mercuric ions. RNA was isolated from hybridoma cells with guanidine isothiocyanate. First strand cDNA synthesis was catalysed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hybridoma antibodies have been produced with the spleen cells of BALB/c mouse that had received multiple injections of mercuric ions reacted with glutathione to produce a mercuric ion coordinate covalent compound which was covalently bound to keyhole limpet hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptide(s) which bind heavy metals, esp. mercury - derived from monoclonal antibodies, used for detecting, removing, adding or neutralising heavy metals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1995-275415/36
N-PSDB; AAQ97509.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 23; Page 69; 106pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lopez 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-JAN-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    light chain.
50 NAKTLAE 56
                                1 NAKTLTE 7
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                                                                                 Similarity
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                                                                 Conservative
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                                                                Score 29; DB Pred. No. 71; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for monoclonal antibody 2D5.
                                                                 <u>.</u>
                                                                                                16;
                                                                1;
                                                                                              Length 107
                                                                 Indels
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                                                              0,
                                                              Gaps
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RESULT 13 AAW05822

Sequence

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The variable region (AAW05822) of the humanised 1D10 antibody light chain (AAW05828) consists of human R3.5H5G kappa light chain variable region framework (substd. at 5 positions with mouse or consensus human amino acids) and complementarity determining regions from the murine 1D10 antibody specific for a 28/32 kDa heterodimeric antigen present on the surface of malignant B-cells. It can be coexpressed with humanised 1D10 heavy chain (see also AAW05829) in e.g. mouse myeloma NSO cells. Humanised antibody fragments can be incorporated into novel bispecific antibodies reactive with both effector cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                New bispecific antibody reactive with both T or NK cells and malignant B cells - also their humanised forms and hybridom producing them, useful for treating or preventing leukaemia,
                                                                                                                                                                                                                                                                                            Gingrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B-cell lymphoma; humanised antibody; bispecific antibody; myeloma; leukaemia; hybridoma; monoclonal antibody.
                                                                                                                                                                           Claim 14; Fig 4a; 85pp; English.
                                                                                                                                                                                                                                                                     WPI; 1996-412742/41.
                                                                                                                                                                                                                                                                                                                       (IOWA-) IOWA IMMUNOTHERAPY INVESTIGATORS (PROT-) PROTEIN DESIGN LABS INC.
                                                                                                                                                                                                                                                                                                                                                            01-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                      29-FEB-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Humanised 1D10 antibody light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-JAN-1997
                                    antigens (see also AAW05824-25, AAW05826 and AAW05830)
                                                                                                                                                                                                     lymphoma and myeloma
                                                                                                                                                                                                                                                                                              Link BK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                              95US-0397411.
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89..97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "human framework
    consensus amino
    murine residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "human framework residue 70 is substd. by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
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                                                                                                                                                                                                                                                                                            Tso JY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "human framework residue 69
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k residue"
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                                     and malignant
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RESULT 14
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XX 12-AU
DT 12-AU
XX Light
XW 9filt
XW 9filt
XW 5yste
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XX Synth
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Best Local S
Matches 6
      The present sequence is the light chain variable region of the group 9f11 putative consensus anti-DNA monoclonal antibody (MAb), which has a high affinity for single stranded DNA, low or no affinity for double stranded DNA and specifically binds a DNA hairpin. The MAb can be used diagnose disorders associated with the pathological complexation of DNA, e.g. inflammatory glomerulonephritis and systemic lupus erythematosus. It can also be used to generate reagents to screen for pharmaceutical agents, and
                                                                                                                                                  Anti-DNA antibody which specifically binds DNA hairpin - useful develop prods. for diagnosis and treatment of disorders, e.g. glomerulonephritis or systemic lupus erythematosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Light chain; variable region; anti-DNA; monoclonal; antibody; 9f11 group; hairpin; diagnosis; inflammatory glomerulonephritis; systemic lupus erythematosus; screening; treatment; prevention;
treat
                                                                                                                           Example; Fig 9; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                  Region
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                                                                                                                                                                                                                                                                                                 18-MAY-1995;
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                                                                                                                                                                                                                                                                                                                         16-MAY-1996;
                                                                                                                                                                                                                    1997-011854/01.
and/or
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prevent
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24..34
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                                                                                                                                                                                                                                                                                                                                                                                                                              label
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         label=
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an above disorder.
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85.7%;
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RESULT 15
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Best Local
                                                                  claimed are: photoaffinity compound-antibody conjugates produced this way, and immuno-conjugates comprising cytotoxic or therapeutic agent site-specifically attached to the photoaffinity compound in the conjugate. When the conjugate is labelled it is used for detection or quantitation of an antigen (Ag) by any standard immunoassay format, while immuno-conjugates are used therapeutically, e.g. in cases of tumours, infections or genetic diseases, or as imaging agents. The photoaffinity compounds are attached under mild, physiological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence was derived by aligning homologous anti-DNA MAb, whose sequences have been published, as well as several MAb of other specificities obtained from a database search.
Sequence
                                                                                                                                                                                                                  This is the amino acid sequence of 8019 VK antibody. The invention relates to the site-specific photo-attachment of a nucleic photoaffinity compound to an antibody which comprises reacting them
                                                                                                                                                                                                                                                                                                                     Conjugates formed by site-specific attachment of nucleic photo-affinity agents to antibodies - useful as immunoassay reagents for detecting antigen, also immuno-therapeutic complex also containing cytotoxin for treating cancer, infection or genetic
                              molecules
                                          conditions, particularly a single 2-5 minute photoactivation almost 100% attachment (contrast conditions usually required
                                                                                                                                                                                      under conditions that promote attachment of the photoaffinity compound to at least 1 nucleotide binding site in the antibody. Also
                                                                                                                                                                                                                                                                           Disclosure; Figure 12c; 75pp; English
                                                                                                                                                                                                                                                                                                         disease
                                                                                                                                                                                                                                                                                                                                                                                                                         Haley BE,
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 109
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Query Match Best Local Similarity

85.3%; 85.7%;

Score Pred.

29; No.

DB 19; 72;

Length 109;

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RESULT 17
AAR12235
ID AAR12
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AAB84742
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                                                                                                                                                                                                                                                                                                          monoclonal antibody. The antibodies are used to monoclonal antibody. The antibodies are useful binding activity of polyglutamine expansion. The antibodies are useful for detecting an agent capable of modulating the binding interaction between polyglutamine expansion comprising protein in a cell and a target of the protein. They are also useful in immunoassays that are
                                                                                                                                                                                                                                                         capable of providing the detection of disease associated polyglutamine expansion containing proteins. The antibodies are useful for treating a host suffering from a disease condition associated with the presence of polyglutamine expansion containing protein, such as neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                    The present chain represents the variable region of the heavy chain of murine antibody 4H7H7. This antibody recognizes a protein having a polyglutamine expansion, where number percentage of non-glutamine residues in the polyglutamine expansion does not exceed 10. The antibody binds to the protein in a manner that differs from the 1C2 monoclonal antibody. The antibodies are used to modulate intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel antibody useful for detecting the presence of polyglutamine expansion comprising protein in a sample, binds to the protein in manner that differs from the IC2 monoclonal antibody -
                AAR12235 standard; Protein; 126 AA
                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 18; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-451842/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Finkbeiner S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JAN-2000; 2000US-0478960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JAN-2001; 2001WO-US00361.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Variable region of the light chain of murine antibody 4H7H7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neurodegenerative disorder; Huntington's disease.
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                                                                                                                                                       Local Similarity
mes 6; Conserv
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                                                                                                                   1 NAKTLTE 7
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                                                                                                                                                       Conservative
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                                                                                                                                                                     Score 29; DB
Pred. No. 83;
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RESULT 18
AAR12357
ID AAR12
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DT 15-AL
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XX Chime
XX Mus m
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PN WO910
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                                                                                                                                                                                               30-MAY-1991
                                                                                                                                                                                                                                                                                                                                       Chimeric antibodies; immunoconjugates; HIV; AIDS
                                                                                                                                                                                                                                                                                                                                                                                                              Light (kappa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR12357 standard; Protein; 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 8; 108pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New chimeric mouse human antibodies - used and prophylaxis of HIV infections.
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N-PSDB; AAQ12015.
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                                                                                               13-NOV-1989;
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                         (XOMA-) XOMA CORP.
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85.7%;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Light chain; variable region; murine; mouse; anti-human; diseas glycogrotein 39; gp39; monoclonal; antibody; 39-1.106; hybridom diagnosis; inhibition; B-cell; activation; treatment; disorder; immune; autoimmune; allergic response; organ rejection; drug; graft versus host; cell imaging; tumour; targetted; delivery;
                                                                                                                                                                                                                                                                                                                                              Region
                                                      26-JAN-1995;
                                                                                                                                                                                                                WO9623071-A2
                                                                                                                                                                                                                                                                                          Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-APR-1997
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(BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                        26-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
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                                                    95US-0379057.
                                                                                                        96WO-US01119
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                                                                                                                                                                                                                                                                                                109
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                                                                                                                                                                                                                                                                                                                note= "complementarity determining
                                                                                                                                                                                                                                                                                                                                                                    note= "complementarity
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for an HIV-1
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Harris
                                                         30-MAY-2000; 2000US-206132P.
29-AUG-2000; 2000US-228716P.
                                                                                                                                                    29-MAY-2001; 2001WO-US10836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                numan; open reaging irame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; bening tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovagonlar disoase. disharan malling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human ORFX protein sequence SEQ ID NO:140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-JUN-2002
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                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                 myasthenia gravis.
                                                                                                                                                                                                                                                                                                                                                                                                            autoimmune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                mmune deficiency; immune disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                               disorder; rheumatoid
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Hollenbaugh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          frame; ORFX; gene therapy; cancer;
disorder; psoriasis; benign tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85.3%;
85.7%;
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D, Siadak AW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 29; DB Pred. No. 87; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  arthritis; autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    different epitope(s) on human activation and for the diagnosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                             infectious disease;
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87;
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Best Local :
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                                                                                                                                                                            Light chain; variable region; murine; mouse; anti-human; diseas; glycoprotein 39; gg39; monoclonal; antibody; 39-1.106; hybridom; diagnosis; inhibition; Becell; activation; treatment; disorder; immune; autoimmune; allergic response; organ rejection; drug; graft versus host; cell imaging; tumour; targetted; delivery; graft versus host; cell imaging; tumour; targetted; delivery;
                                                                                                                                                                                                                                                                                                          Humanised MAb 39-1.106 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bone degenerative disorders, or periodontal disease, and for gut
protection or regeneration and treatment of lung or liver fibrosis,
reperfusion injury in various tissues and conditions resulting from
systemic cytokine damage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes substantially purified human proteins (referred to as open reading frame, 0x877.52 encode the human OREX in the specification). ABN15762 to ABN277.52 encode the human OREX proteins given in ABP00010 to ABP11500. OREX proteins are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders -
                       Misc-difference
                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                     02-APR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW03725 standard; Protein; 171 AA
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                                                            Misc-difference
                                                                                                                                                                 targeted;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for treating burns, incisions, ulcers,
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                                                                Location/Qualifiers
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                                      'note= "corresponding
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71.4%;
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Pred. No. 1.2e+02;
2; Mismatches 0;
                                      codon TAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for treating osteoporosis
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Best Local Similarity
Thes 6; Conserv
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Harris LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease states, inhibiting B-cell activation and for treating immunological disorders, e.g. autoimmune disorders, allergic responses, organ rejection and graft versus host disease. It may also be used for imaging cells which express gp39 on their surface, e.g. tumour cells, and to target therapeutic agents to such cells. The MAD inhibits the CO40/gp39 interaction, therefore limiting both prim. and sec. responses to T-cell dependent antigens and Ab prodn. specific to these antigens. A typical compsn. for intramuscular injection pref. contains 50 mg of MAD in 1 ml of sterile buffered
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                                                                                                                                                                                                                                        B-cell lymphoma; humanised antibody; bispecific antibody; myeloma; leukaemia; hybridoma; monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is the light chain variable region of th humanised murine anti-human glycoprotein (gp) 39 monoclonal antibody (MAb) 39-1.106. The MAb may be useful for diagnosing
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                            Region
                                                                                 Domain
                                                                                                                                                               Chimeric
                                                                                                                                                                                        Chimeric
                                                                                                                                                                                                                                                                                                                                                                              27-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW05828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW05828 standard; Protein; 214 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 13; Fig 16; 167pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monoclonal antibodies specific for different epitope(s) on human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAT36018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1996-362694/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BRIM ) BRISTOL-MYERS SQUIBB CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     various disorders, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - used for inhibiting B cell activation and for the diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 NAKTLTE 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAKTLAE
                                                                                                                                                               Mus
                                                                                                                                                                                        Homo sapiens;
                                                                                                                                                                                                                                                                                                                            1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bajorath J, Gilliland LK, Hollenbaugh D, Siadak AW;
                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                            ďs
                                                                                                                                                                                                                                                                                                                            antibody light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ä,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95US-0379057.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96WO-US01119
                            /label= Variable_domain
24..33
                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "corresponding codon TAA"
     /label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "corresponding codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 29;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     psoriasis etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 17;
1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gordon ML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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AAR53148
ID AARS
XX AAR5
AC AAR5
AC AAR5
AC VH a
XX U7-E
XX U7-E
XX U7-E
XX VE PE38
XW PE38
XW PF1m
XW PC1m
XW PC1m
XW CC11
XX Synt
XX Synt
XX YFH Key
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                                                                                                                                                                                                                                                                                                                                                             S
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The humanised 1D10 antibody light chain (AAW05828) includes a variable region (see also AAW05822) consisting of human R3.5HG light chain variable region framework and complementarity determining regions from the murine 1D10 antibody specific for a 28/32 kDa antigen found on the surface of malignant B-cells. It can be coexpressed with humanised 1D10 heavy chain (see also AAW05829) in mammalian host cells. Bispecific antibodies can be constructed that include a first binding fragment comprising humanised M291 heavy and light chain variable regions (see also AAW05826, AAW05830), and a second binding fragment comprising humanised 1D10 heavy and 115ht chain variable regions. Such antibodies are reactive with both T or NK cells and malignant B cells, and have therapeutic and diagnostic
                                                        PE38KDEL; plasmid; pULI40; heavy; chain; light; variable region; VH VL; monoclonal antibody; MAb; PRI; PCR; amplify; PRI-hybridoma RNA; primer; complementarity determining regions; CDR; drug; cytotoxin; prostate cell associated antigen; radioisotope; PCAA; prostate; cells; cancer; diagnosis; benign prostate hyperplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      malignant B cells - also their humanised forms and hybridon producing them, useful for treating or preventing leukaemia, lymphoma and myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New bispecific antibody reactive with both T or NK cells and malignant B cells - also their humanised forms and hybridomas
                                Synthetic.
                                                                                                                                                                                        07-DEC-1994
                                                                                                                                                                                                                       AAR53148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; Fig 4c; 85pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gingrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                         VH and
                                                                                                                                                                                                                                                    AAR53148 standard; Protein; 243 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-412742/41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9626964-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PROT-)
                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 6; Conserv
                                                                                                                                                                                                                                                                                                                                  50
                                                                                                                                                         VL of MAD
                                                                                                                                                                                                                                                                                                                                                   1 NAKTLTE 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IOWA IMMUNOTHERAPY INVESTIGATORS PROTEIN DESIGN LABS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 AA;
                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Link BK,
                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95US-0397411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96WO-US02754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label:
89..97
 Location/Qualifiers
                                                                                                                                                         PR1.
                                                                                                                                                                                                                                                                                                                                56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Human_C-kappa_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                         85.3%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tso JY,
                                                                                                                                                                                                                                                                                                                                                                                              <u>.</u>.
                                                                                                                                                                                                                                                                                                                                                                                                          Score 29; DB 17;
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Weiner G;
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 214;
                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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RRESULT 24
AAU772864
ID AAU77287
AC AAU7
XX AU7
XX AU7
XX 26-1
DT 26-1
XX DE P4-1
XX Hums
XW Hums
XW intt
XW intt
XW sarc
XW sarc
XW harc
XW sarc
XW harc
                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                              S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence is encoded by the PEJSKDEL fragment of the plasmid CC pULI40 and represents the heavy chain and light chain variable regions (VH and VL) of the monoclonal antibody (MAD) PRI. The cDNA encoding this sequence was derived by PCR amplification of reverse transcribed PRI-hybridoma RNA using the primer sequences given in AAQ64477-81. The CVH and VL complementarity determining regions (CDRs) are used in the CC construction of the MAD of the invention which competes with PRI CC invention can be used for targetting a drug, cytotoxin or radioisotope to prostate cells of a patient suffering from prostate cancer. It can also be used for diagnosing the presence of prostate cancer in an CC individual and for the diagnosis and treatment of other conditions involving abnormal growth of prostate cells, eg. benign prostate CC invention and the prostate cancer cells but conly weakly with a few other normal human tissues. The effect of therapy on normal prostate cells does not threaten the overall health CC therapy on normal prostate cells does not threaten the overall health
                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
             Human; NKG2D; NKG2D receptor complex; cancer; infectious disease; tumour; autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary; intrahepatic bile duct; pancrease; lung; larynx; breast; uterus; cervix; prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; Fv; sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DAP10; sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DAP10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monoclonal antibody specific for prostate cells - used in the diagnosis and treatment of conditions involving abnormal growth of prostate cells, esp prostate cancer.
                                                                                                                            P4-15 single chain Fv.
                                                                                                                                                               26-FEB-2002
                                                                                                                                                                                                   AAU72864;
                                                                                                                                                                                                                                       AAU72864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Fig 1; 64pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-OCT-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (USSH ) US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9409150-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1994-151334/18
                                                                                                                                                                                                                                                                                                                               183 NAKTLAE 189
                                                                                                                                                                                                                                                                                                                                                      1 NAKTLTE 7
                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 6; Conserv
                                                                                                                                                                                                                                       standard; Protein; 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEC DEPT HEALTH
                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                               (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92US-0958140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= PR1 VH
119 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= PR1 V1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Linker
                                                                                                                                                                                                                                                                                                                                                                                                                    85.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 243
                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 29;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        1.8e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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helminth;

cytostatic;

antimicrobial;

immunomodulatory; 11B2D10; 6H7E7;

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TXAX EXEX EXXXXX
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                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                               as a receptor or ligand. The polypeptide and its associated polynucleotide are used for the preparation of a pharmaceutical composition for the treatment of cancer, infections and/or autoimmune conditions. The cancer may be a tumour of the head and neck, stomach, oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung, larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid, bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma. The infectious diseases can be caused by viruses, bacteria, fungi, protozoa or helminths. The autoimmune diseases include multiple sclerosis, Grave's disease, ankylosing spondylitis, acute anterior uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and autoimmune hepatitis. Sequences ANU72820-ANT72875 represent the NKG2D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a multifunctional polypeptide comprising a domain with a binding site that specifically recognises an extracellular group of the NKG2D receptor complex and a second domain which functions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Multifunctional polypeptides comprising binding sites that specifically recognise extracellular groups of the NKG2D receptor complex and domains which function as receptors or ligands, useful for treating cancers and infectious diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mayer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8G7C10; 6E5A7; 11B2D10x4-7; 8G7C10x4-7; 6E5A7x4-7; P4-2; P4-3; P4-14; P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; 3B10xP4-3; 3B10xP4-14; P53 tetramerisation domain; 3B10xP5-2; 3B10xP5-23.
            Synthetic
                           Mus sp
                                                            Monoclonal
                                                                                                                        09-MAY-2002
                                                                                                                                                                                  ABB05962 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-MAR-2000; 2000EP-0106467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-2001; 2001WO-EP03414.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (KUFE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                  187
                                                                                                                                                                                                                                                                                             1 NAKTLIE 7
                                                                                                                                                                                                                                                                                                                          6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KUFER P.
                                                                                                                                                                                                                                                              NAKTLAE 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Riethmueller G,
Hofmeister R;
                                                        antibody; fusion protein; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fig 16; 114pp;
                                                                                                                                                                                                                                                                                                                                                                                          256 AA;
                                                                                         antibody
                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     the polypeptides of
                                                                                                                      (first
                                                                                         related
                                                                                                                      entry)
                                                                                                                                                                                                                                                                                                                                           85.3%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lutterbuese R,
                                                                                                                                                                                    258
                                                                                                                                                                                                                                                                                                                            0
                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                         Score 29; DB 23; Length 256; Pred. No. 1.9e+02;
                                                                                                                                                                                    ₿
                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       invention.
                                                                                       sequence SEQ ID NO:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Borschert
                                                        cell surface; receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ζ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kischel
                                                                                                                                                                                                                                                                                                                            <u>.</u>
                                                                                                                                                                                                                                                                                                                            Gaps
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can transfer a gene by combining with the gene and containing a human combining site for the gene. Also described is a complex of a monoclonal antibody-fused protein which is a complex of monoclonal antibody-fused protein which is a complex of monoclonal antibody-fused protein against a receptor present on cell surface in which: (1) an mRNA extracted from a hybridoma cell having productivity of said monoclonal antibody against a receptor present on cell surface in conclusional antibody against a receptor present on cell surface is used as the template to amplify a single-stranded antibody gene of a mouse type monoclonal antibody by PCR; (2) the framework portion of the mouse type monoclonal antibody is converted to prepare a single-stranded antibody gene of a human type monoclonal antibody is converted to prepare a single-stranded the munino acid tail is added to the single-stranded antibody gene of the human type monoclonal antibody to prepare a human type single-stranded immunoporter gene; and (4) the human type single-stranded immunoporter gene; and (4) the human type single-stranded immunoporter single-stranded immunoporter single-stranded immunoporter of the human type single-stranded immunoporter single-stranded immunoporter in the above complex of monoclonal antibody-fused protein of the product a cell surface receptor. The method for the preparation
                                                                       through a cell surface receptor. The method is used for the preparation of a monoclonal antibody-fused protein against a receptor present on cesurface. The present sequence represents a specifically claimed amino
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Sequence
                                                  acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 14; Page 9; 24pp; Japanese
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  258
                                                  from the present invention.
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Matches
              Query Match
6; Conserv
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       85.3%;
0
       Score 29;
Pred. No.
 Mismatches
        1.9e+02;
              Length 258;
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                                      ABB05963;
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191

NAKTLTE NAKTLAE 197

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04-DEC-2001:
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                                                                                                                                                                                                                                                                            Monoclonal antibody related amino acid sequence SEQ ID NO:2
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29-MAY-2000; 2000JP-0158575.
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RESULT 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          which: (1) an mRNA extracted from a hybridoma cell having productivity of said monoclonal antibody against a receptor present on cell surface is used as the template to amplify a single-stranded antibody gene of a mouse type monoclonal antibody by PCR; (2) the framework portion of the mouse type monoclonal antibody is converted to prepare a single-stranded antibody gene of a human type monoclonal antibody; (3) a gene encoding the amino acid tail is added to the single-stranded antibody gene of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                combining site for the gene. Also described is a complex of a monoclonal antibody-fused protein which is a complex of monoclonal antibody-fused protein and a DNA, and a method for the preparation of a monoclonal antibody, fused protein against a receptor present on cell surface in
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                                                                                   29-MAY-2000; 2000JP-0158575
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                                                                                                                                                                                           Synthetic.
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                                                                                                                                                                                                                                                                             Mouse monoclonal antibody related protein sequence
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                (KEIO-) GH KEIO GIJUKU
                                                 29-MAY-2000; 2000JP-0158575
                                                                                                                                                                                                                                            Monoclonal antibody; fusion protein; antigen; cell surface; receptor
                                                                                                                                                                                                                                                                                                                                                    ABB05990;
                                                                                                                                                                                                                                                                                                                                                                                     ABB05990 standard; Protein; 258 AA
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mes 6; Conserv
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                                                                                                                                                                                                                                                                                                                  (first entry)
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Pred. No. 1.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 258;
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WPI; 2002-135945/18. N-PSDB; ABA94201.

29-MAY-2000; 2000JP-0158575 29-MAY-2000; 2000JP-0158575.

(KEIO-) GH KEIO GIJUKU

04-DEC-2001. JP2001333780-A. Synthetic.

Chimeric - Mus sp. Chimeric - Homo sapiens.

chimeric.

Monoclonal antibody; fusion protein; antigen; cell surface; receptor; Mouse and human chimeric monoclonal antibody related protein CvB

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85.7%;
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Pred. No. 1.9e+02;
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RESULT 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC monoclonal antibody against an antigen present on cell surface and which CC can transfer a gene by combining with the gene and containing a human CC type single-stranded monoclonal antibody and a peptide which is the CC combining site for the gene. Also described is a complex of a monoclonal antibody-fused protein which is a complex of monoclonal antibody-fused protein which is a complex of monoclonal antibody-fused protein and a method for the preparation of a monoclonal CC antibody-fused protein against a receptor present on cell surface in CC which: (1) an mRNA extracted from a hybridoma cell having productivity of CC said monoclonal antibody against a receptor present on cell surface is CC used as the template to amplify a single-stranded antibody gene of a mouse type monoclonal antibody by PCR; (2) the framework portion of the CC mouse type monoclonal antibody is converted to prepare a single-stranded antibody gene of a human type monoclonal antibody; (3) a gene encoding CC the amino acid tail is added to the single-stranded antibody gene of the LC the human type single-stranded immunoporter gene; and (4) the human type single-stranded for the muman type single-stranded is a method for CC introducing the above complex of monoclonal antibody-fused protein of the CC monoclonal antibody-fused protein of the CC monoclonal antibody-fused protein for the preparation of a monoclonal antibody-fused protein for the preparation and monoclonal antibody-fused protein for the monoclonal antibody-fused protein for the preparation of a monoclonal antibody-fused protein for the preparation of a monoclonal antibody-fused protein for the surface. The method for the preparation of a monoclonal antibody-fused protein for the surface. The method for the preparation of the contract of the protein for the preparation of the contract of the protein for the preparation of the contract of the protein for the preparation of the contract of the protein for the protein for the protein for the protein for the protein for the protein
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Best Local
A protein fused with a monoclonal antibody against an antigen present
                                         WPI; 2002-135945/18
N-PSDB; ABA94202.
                                                                                                                                                                                                                                                                                      JP2001333780-A.
                                                                                                                                                                                                                                                                                                                                                      Chimeric -
Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse and human chimeric monoclonal antibody related protein CaB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB05992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB05992 standard; Protein; 258 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   given in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A protein fused with a monoclonal antibody against an antigen present on cell surfaces - \,
                                                                                                                                                                                             29-MAY-2000; 2000JP-0158575.
                                                                                                                                                                                                                                           04-DEC-2001
                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                           chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example; Fig 10; 24pp; Japanese
                                                                                                                                                    29-MAY-2000; 2000JP-0158575
                                                                                                                                                                                                                                                                                                                                                                                                                                             Monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a protein which is fused with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191 NAKTLAE 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NAKTLTE 7
                                                                                                           ΩĤ
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                                                                                                                                                                                                                                                                                                                                                                                                                                        antibody; fusion protein; antigen; cell surface; receptor;
                                                                                                           KEIO GIJUKU
                                                                                                                                                                                                                                                                                                                                                      Homo
                                                                                                                                                                                                                                                                                                                                                                        Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            258 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                      sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.3%;
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Pred. No. 1.9e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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RESULT 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibody-fused protein against a receptor present on cell surface in which: (1) an mRNA extracted from a hybridoma cell having productivity of said monoclonal antibody against a receptor present on cell surface is used as the template to amplify a single-stranded antibody gene of a mouse type monoclonal antibody by PCR; (2) the framework portion of the mouse type monoclonal antibody by PCR; (2) the framework portained antibody gene of a human type monoclonal antibody; (3) a gene encoding the amino acid tail is added to the single-stranded antibody gene of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human type monoclonal antibody to prepare a human type single-stranded immunoporter gene; and (4) the human type single-stranded immunoporter gene is expressed in a microbe to prepare a recombinant protein of the human type single-stranded immunoporter. Also described is a method for introducing the above complex of monoclonal antibody-fused protein through a cell surface receptor. The method is used for the preparation of a monoclonal antibody-fused protein surface. The present sequence represents a protein sequence which is given in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a protein which is fused with a monoclonal antibody against an antigen present on cell surface and which can transfer a gene by combining with the gene and containing a human type single-stranded monoclonal antibody and a peptide which is the combining site for the gene. Also described is a complex of a monoclonal antibody-fused protein which is a complex of monoclonal antibody-fused protein and a DNA, and a method for the preparation of a monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                 A protein fused with a monoclonal antibody against an antigen present on cell surfaces -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric - Mus sp.
Chimeric - Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-MAY-2002
                                                                                                                             N-PSDB; ABA94203
                                                                                                                                                                                                                                                                                     29-MAY-2000; 2000JP-0158575
                                                                                                                                                                                                                                                                                                                                                29-MAY-2000; 2000JP-0158575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JP2001333780-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Monoclonal antibody; fusion protein; antigen; cell surface; receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse and human chimeric monoclonal antibody related protein DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB05993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB05993 standard; Protein; 258 AA
                                                                                                                                                                                                                      (KEIO-) GH KEIO GIJUKU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity es 6; Conserva
                                                                                                                                                       2002-135945/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NAKTLIE 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAKTLAE 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 29;
Pred. No.
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1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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Example; Fig

12;

24pp; Japanese

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CC combining site for the gene. Also described is a complex of a monoclonal contibody-fused protein which is a complex of monoclonal antibody-fused protein which is a complex of monoclonal contibody-fused protein against a receptor present on cell surface in complex of a monoclonal contibody-fused protein against a receptor present on cell surface in complex of a monoclonal antibody against a receptor present on cell surface is considered as the template to amplify a single-stranded antibody gene of a complex type monoclonal antibody by PCR; (2) the framework portion of the conset type monoclonal antibody is converted to prepare a single-stranded contibody gene of a human type monoclonal antibody is converted to prepare a single-stranded contibody gene of a human type monoclonal antibody to prepare a tranded antibody gene of the consent sype monoclonal antibody to prepare a moneyorter gene; and (4) the human type single-stranded continuon type single-stranded immunoporter gene; and (4) the human type single-stranded immunoporter controducing the above complex of monoclonal antibody-fused protein of the contradicting the above complex of monoclonal antibody-fused protein continuous antibody-fused protein continuous antibody-fused protein antibody-fused protein antibody-fused protein antibody-fused protein antibody-fused protein sequence which is cover in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                    A protein fused with a monoclonal antibody against an antigen present
                                                                                                                                      N-PSDB; ABA94204
                                                                                                                                                                                                                                                                                                     29-MAY-2000; 2000JP-0158575
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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Chimeric -
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                                                                                                                                                                                                                                                     29-MAY-2000; 2000JP-0158575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse and human chimeric monoclonal antibody related protein
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                                                                                                                                                                                                       (KEIO-) GH KEIO GIJUKU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB05994 standard; Protein; 258 AA
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                                                                                                                                                         2002-135945/18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in an example
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                                                                   surfaces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibody; fusion protein; antigen; cell surface; receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               258 AA;
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Pred. No. 1.9e+02;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention
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Example; Fig 13; 24pp; Japanese

The present invention describes a protein which is fused with a monoclonal antibody against an antigen present on cell surface a can transfer a gene by combining with the gene and containing a type single-stranded monoclonal antibody and a peptide which is

and which

can transfer a gene by combining with the type single-stranded monoclonal antibody

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RESULT 32
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Matches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibody-fused protein against a receptor present on cell surface in which: (1) an mRNA extracted from a hybridoma cell having productivity of said monoclonal antibody against a receptor present on cell surface is used as the template to amplify a single-stranded antibody gene of a mouse type monoclonal antibody by PCR; (2) the framework portion of the mouse type monoclonal antibody by PCR; (2) the framework portion of the single monoclonal antibody is converted to prepare a single-stranded antibody gene of a human type monoclonal antibody; (3) a gene encoding the amino acid tail is added to the single-stranded antibody gene of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human monoclonal antibody related protein sequence CvC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         type single-stranded monoclonal antibody and a peptide which is the combining site for the gene. Also described is a complex of a monoclona antibody-fused protein which is a complex of monoclonal antibody-fused protein and a DNA, and a method for the preparation of a monoclonal antibody-fused protein against a receptor present on cell surface in
                                                                                                                                                                                   N-PSDB; ABA94205.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monoclonal antibody; fusion protein;
                                                                                                                                              A protein fused with a monoclonal antibody against an
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                                                                                                                            cell surfaces -
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monoclonal antibody against an antigen present on cell surface and which can transfer a gene by combining with the gene and containing a human type single-stranded monoclonal antibody and a peptide which is the combining site for the gene. Also described is a complex of a monoclonal antibody-fused protein which is a complex of monoclonal antibody-fused protein which is a complex of monoclonal antibody-fused protein and a method for the preparation of a monoclonal antibody-fused protein against a receptor present on call antibody-fused protein against a receptor present on call antibody-fused
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85.7%;
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The present invention describes a protein which is fused with a monoclonal antibody against an antigen present on cell surface and which can transfer a gene by combining with the gene and containing a human type single-stranded monoclonal antibody and a peptide which is the combining site for the gene. Also described is a complex of a monoclonal antibody-fused protein which is a complex of monoclonal antibody-fused protein ada method for the preparation of a monoclonal antibody-fused protein against a receptor present on cell surface in which: (1) an mRNA extracted from a hybridoma cell having productivity of said monoclonal antibody against a receptor present on cell surface is used as the template to amplify a single-stranded antibody gene of a mouse type monoclonal antibody by PCR; (2) the framework portion of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ABA94207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example; Fig 16; 24pp; Japanese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein fused with a monoclonal antibody against an antigen present
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Pred. No.
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1.9e+02;
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RESULT 35
ABB05982
                     The present invention describes a protein which is fused with a compositional antibody against an antigen present on cell surface and which can transfer a gene by combining with the gene and containing a human type single-stranded monoclonal antibody and a peptide which is the combining site for the gene. Also described is a complex of a monoclonal antibody-fused protein which is a complex of monoclonal antibody-fused protein and a DNA, and a method for the preparation of a monoclonal antibody-fused protein against a receptor present on cell surface in which: (1) and mRNA extracted from a hybridoma cell having productivity of said monoclonal antibody against a receptor present on, cell surface is mouse type monoclonal antibody a single-stranded antibody gene of a human type monoclonal antibody is converted to prepare a single-stranded antibody gene of a human type monoclonal antibody is converted to prepare a single-stranded the minimal type monoclonal antibody to the single-stranded antibody gene of the minimal cold tail is added to the spingle-stranded antibody gene of the single-stranded antibody is converted to prepare a single-stranded but the single-stranded antibody gene of a human type monoclonal antibody servance a single-stranded antibody the prepare a single-stranded servance and servance as single-stranded antibody the prepare as single-stranded antibody the prepare as single-stranded antibody the prepare as single-stranded servances.
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Matches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monoclonal antibody related protein sequence pBH.
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        numan type monoclonal
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antibody to prepare a human type single-stranded
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Pred. No. 1.9e+02;
0; Mismatches 1
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(4) the human type single-stranded

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RESULT 36
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                                                                                                                                                                                                       16-APR 1999;
19-APR 1999;
21-APR 1999;
23-APR 1999;
23-APR 1999;
28-APR 1999;
30-APR 1999;
30-APR 1999;
04-MAY 1999;
05-MAY 1999;
06-MAY 1999;
07-MAY 1999;
07-MAY 1999;
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
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14-MAY-1999
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99US-0132484

99US-0132485

99US-0132487

99US-0132863

99US-0134218

99US-0134218

99US-0134219

99US-0134219

99US-013470

99US-013470

99US-0134768

99US-0134941

99US-013533

99US-013553
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99US-0132048.
99US-0132407.
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99US-0130510
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99US-0129845
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99US-0126264
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17-DEC-1997;
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                                                                                                                                                                                                                                                                                                                      AAY36754-Y37949 are encoded by open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma,
                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 1226-1227; 1755pp; English.
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14-JUL-1999
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Corynebacterium glutamicum; metabolic pathway protein; MP protein; fine chemical production; microorganism; organic acid; nucleoside; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin;
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                                                                                                                                                                                                                                                                                                                                                                     Corynebacterium glutamicum; metabolic pathway protein; MP protein; fine chemical production; microorganism; organic acid; nucleoside; nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin; carbohydrate; aromatic compound; cofactor; polyketide; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids from Corynebacterium glutamicum encoding me pathway proteins, useful for producing fine chemicals in microorganisms, including organic acids, nonproteinogenic and purine and pyrimidine bases -
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ĭ Kroeger Β, Schroeder H, Zelder O, Haberhauer Ģ

N-PSDB; 2001-137957/14. AAF72278.

Nucleic acids from Corynebacterium glutamicum encoding pathway proteins, useful for producing fine chemicals i microorganisms, including organic acids, nonproteinoger and purine and pyrimidine bases acids, nonproteinogenic metabolic amino acids

Claim 20; Page 1595-1596; 1737pp; English.

AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic pathway (NP) proteins given in AAB79634 to AAB80211. The C. glutamicum MP nucleic acids are useful for the production of fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic polyketides and

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Best Local Similarity 71.4%;
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                                                                                                                                                                       Substance P is a pain transmitter and the receptor is an effective matching protein of substance P. It may be used as an analgesic, an antiinflammatory drug or an anticonvulsant. It can also be used in
                                                                                                                                          Sequence
                                                                                                                                                                                                                                              New substance P receptor protein and gene - for production of diagnostics and as analgesics, antiinflammatories and anticonvulsants.
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N-PSDB; AAQ12560.
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US-09-257-069-9
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/09257069
Patent No. 6348580
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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45	44	43	42	41	40	39	38	37	36	ω 5	<u>ب</u>	<b>ω</b> 33	32	31	30	29	28
26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	27
76.5	76.5	76.5	76.5	76.5				76.5							76.5		79.4
126	126	107	107	36	36	36	31	31	26	26	26	24	24	24	7	7	958
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US-08-765-783A-77	US-08-765-783A-73	PCT-US94-07659-8	US-08-933-983-76	US-09-112-206-89	US-08-723-425A-89	US-08-146-028-89	US-09-351-296-7	US-08-845-926-7	US-09-112-206-91	US-08-723-425A-91	US-08-146-028-91	US-09-112-206-90	US-08-723-425A-90	US-08-146-028-90	US-09-416-557-82	US-08-765-783A-82	US-08-426-236-4
Sequence 7	Sequence 7:	Sequence 8,	Sequence 76	Sequence 89	Sequence 8	Sequence 89	Sequence 7	Sequence 7,	Sequence 91,	Sequence 91,	Sequence 9:	Sequence 90,	Sequence 90	Sequence 90	Sequence 82	Sequence 82	Sequence 4
77, Appl	73, Appl	Þ	6, Appl	9, Appl	9, Appl	9, Appl	, Appli	, Appli	-	•	1, Appl	-	•	•	-	2, Appl	, Appli

## ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/09/257,069
CURRENT FILING DATE: 199-02-24
PRIOR APPLICATION NUMBER: JP 1998-252921
PRIOR FILING DATE: 1998-09-07
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2:0
SOFTWARE: Patentin Ver. 2:0
CORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Mus
US-09-257-069-9
US-09-257-069-4
                                                                                                                                                                                                                                                                                                                                                                               US-09-257-069-4
                                                                                                                                                                                                                                            Sequence 4, Application US/09257069
PATENT NO. 6348580
GENERAL INFORMATION:
APPLICANT: Medical & Biological Laboratories Co.,Ltd.
APPLICANT: Medical & Monoclonal Antibody Specific for
TITLE OF INVENTION: Phosphatidylinositol-3,4,5-Triphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Medical & Biological Laboratories Co., Ltd.
TITLE OF INVENTION: Monoclonal Antibody Specific for
TITLE OF INVENTION: Phosphatidylinositol-3,4,5-Triphosphate
FILE REFERENCE: M3-008-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: JP PRIOR FILING DATE: 1998-09-0 NUMBER OF SEQ ID NOS: 10
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                                                                                                                                                                                                                                 FILE REFERENCE:
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7; Conserv
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Pred. No. 1.9e+05;
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Best Local Similarity
7; Conserve
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                                                         Sequence 33, Applicat:
Patent No. 6080588
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442110710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
         APPLICANT: Glick, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 94 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037 FILING DATE: 23-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Glick, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (650) 494-0792
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                                                                                         Application US/08881037
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Pred. No.
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RESULT 5
US-08-881-037-34
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Best Local Similarity
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APPLICANT: Glick, Gary D.
APPLICANT: SWAHSON, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/443,540
APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, Antoinette F.
REFERENCE/DOCKET NUMBER: 2034421107:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 99 amino acids
          APPLICATION NUMBER: US/08/
FILING DATE: 23-UN-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
                                                                                                                                                                    COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING STEEM: PC-DOS/MS-DOS
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TYPE: amino acid
STRANDEDNESS: single
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CITY: Palo Alto
STATE: CA
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23-JUN-1997
18-MAY-1995
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85.7%;
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                                                                                   US/08/881,037
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Pred. No.
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CLASSIFICATION:

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US-08-881-037-35
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 Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Glick, Gary D.
APPLICANT: Swanson, Patrick C.
APPLICANT: Swanson, DNA BINDING ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      atent No.
                                                                                                                                                     TELEX:
INFORMATION FOR SEQ ID NO:
                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
                                                                                                                                                                                                   NAME: KONSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 20.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/881,037 FILING DATE: 23-JUN-1997 CLASSIFICATION: 530 PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 08/443,540 FILING DATE: 18-MAY-1995 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442110710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Konski, Antoinette
                                                                                                                                                                                                                                                                        NAME: Konski, Antoinette
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 755 Page
CITY: Palo Alto
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sin
                                                                                  STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                  single
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85.7%;
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85.7%;
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 Score 29;
Pred. No.
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Pred. No. 13;
; DB 3;
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               Length 99;
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Query Match
Best Local Similarity
""" hes 6; Conserv
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                                                                                                                                                                                          TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/187,407
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 0 FILING DATE: 27-JAN-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wylie, Dwane E.
APPLICANT: Wagner, Fred W.
TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore
                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 86
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                    FILING DATE: 14-MAR-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 14-MAR-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 03-JUI
                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 0' FILING DATE: 14-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                          NAME: Carter, Charle
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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50 NAKTLAE 56
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                       1 NAKTLTE 7
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5972656
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                                                            Conservative
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                                                                                                                                     protein
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                                                                         Score 29;
Pred. No.
                                                            Mismatches
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RESULT 8
US-08-881-037-69
; Sequence 69, Application US/08881037
; Patent No. 6080588

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SENERAL INFORMATION:

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US-08-881-037-70
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Best Local Similarity 85.7%;
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                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Glick, Gary D.
APPLICANT: Swanson, Patrick C.
APPLICANT: Swanson, DNA BINDING ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                         itent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
               ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYDE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Ralease #1.0, Version #1.30
CURRENT APPLICATION DATA:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037
FILING DATE: 23-UUN-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: US 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: KORSKI, ARTOINETTE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442110710
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
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CITY: Palo Alto
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NPPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 94304-1018
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APPLICATION NUMBER:
                                                                                                                                              COUNTRY:
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5. 6080588
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US/08/881,037
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Pred. No. 14;
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Best Local Similarity
Whethes 6; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 72,
                                                                                                                     CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UNMEER: US 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Konski, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442110710
TELEPHONE: (550 46 20 20 30 42 210710
                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: KONBKI, ANTOINETE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442110710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEPAX: (650) 494-0792
                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Glick, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
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APPLICATION NUMBER: 18-MAY-:
CLASSIFICATION: 530
STRANDEDNESS:
                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                 FILING DATE: 23-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Palo Alto
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STRANDEDNESS: sir
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                                                                                                            TELEFAX: (650) 494-0792
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                                107 amino acids
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linear
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85.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                    Release #1.0, Version #1.30
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14;
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APPLICANT:

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US-08-397-411-2

; Sequence 2, Application US/08397411

; Patent No. 6129914

; GENERAL INFORMATION:
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US-08-397-411-1
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US-08-881-037-72
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Best Local
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/397,411
FILING DATE: 01-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/859,583
FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                  STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Bispecific Antibody Effective to Treat
TITLE OF INVENTION: B-Cell Lymphoma and Cell Line
                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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STATE: California
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One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                               107 amino acids
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Pred. No. 14;
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                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/859,583
FILING DATE: 27-MAR-1992
ATTORNEY/ACENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 415-326-2422 INFORMATION FOR SEQ ID NO:
                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
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LENGTH: 107 amino acids
TYPE: amino acid
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APPLICATION NUMBER: US.
FILING DATE: 01-MAR-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANM: Teo, J. Yun
TITLE OF INVENTION: Bispecific Antibody Effective to Treat
TITLE OF INVENTION: B-Cell Lymphoma and Cell Line
NUMBER OF SEQUENCES: 14
                                                                                                             TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
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                                                                            CORRESPONDENCE ADDRESS:
                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                               APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
             CITY: Seattle
STATE: Washing
                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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COUNTRY:
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                                                             ADDRESSEE:
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One Market Plaza, Steuart Tower, Suite 2000
                                            3005 First Avenue
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                                                                                                                                                                                            Gordon, Marcia L.
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Hollenbaugh, Dia...
Hollenbaugh, Lisa K.
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                                                             Bristol-Myers Squibb Company
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Different Epitopes of Human gp39 and Methods For Their Use
In Diagnosis and Therapy
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Pred. No. 14;
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COMPUTER READABLE FORM:

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                                                                                     CUASSIFICATION:

APPLICATION: 435

CLASSIFICATION: 435
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; FRAGMENT TYPE: internal
US-08-379-057-27
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NAME: POOT, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ONOI:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 727-3601
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENCTH: 108 amino acids
        ATTORNEY/AGENT INFORMATION:

NAME: POOR, Brian W.

REGISTRATION NUMBER: 32,928

REFERENCE/DOCKET NUMBER: 0N01

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION 1077-3670
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Aruffo, A TITLE OF INVENTION: 1 TITLE OF INVENTION: 1 TITLE OF INVENTION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,057
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                        STREET: J. STREET: Seattle
                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                    STATE: Washington
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TELEPHONE:
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                      3005 First Avenue
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VENTION: Monoclonal Antibodies Specific For
VENTION: Different Epitopes of Human gp39 and Methods For Their Use
 (206)
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Pred. No. 14;
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Best Local Similarity
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                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: POOT, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ONOI:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 727-3670
TELEPHONE: (206) 727-3601
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 6; Conserv
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                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DDS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: US/08/379,057
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
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APPLICANT:
APPLICANT:
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LENGTH: 108 amino acids
TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Seattle
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70 NAKTLAE 76
                               1 NAKTLIE 7
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                                                              Conservative
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Gilliland, Lisa K.
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Different Epitopes of Human gp39 and Methods For Their Use
In Diagnosis and Therapy
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Pred. No.
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Pred. No.
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                                                                                                                                                                                                                    Sequence 2, Application US/08681432 Patent No. 5800991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,411
FILING DATE: 01-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/859,583
FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,233
REFERENCE/DOCKET NUMBER: 011823-004901
                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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APPLICANT:
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APPLICANT: Weiner
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INFORMATION FOR SEQ ID NO:
                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                             NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                 APPLICANT:
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TITLE OF INVENTION: Bispecific Antibody Effective
E-Cell Lymphoma and Cell Line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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                 ADDRESSEE
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o. 6129914
                                                                                                                                                                                                 INFORMATION:
                                                                                                                                                                                                                                                                                                                      50 NAKTLAE 56
                                                                                                                                                                                                                                                                                                                                                      1 NAKTLTE 7
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                                                                                                INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           214 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                HALEY, Boyd E.
KOHLER, Heinz
RAJAGOPALAN, Krishnan
PAVLINKOVA, Gabriela
                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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               BURN, DOANE, SWECKER & MATHIS
Box 1404
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85.7%;
                                                                               NUCLEOTIDE OR NUCLEOSIDE PHOTOAFFINITY COMPOUND MODIFIED ANTIBODIES, METHODS FOR THEIR MANUFACTURE AND USE THEREOF AS DIAGNOSTICS AND
                                                                  THERAPEUTICS
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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Best Local
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APPLICANT: Pastan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/
FILING DATE: 11-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,03
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                              COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEFAX: (415) 543-5043
                                                                ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 15
                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Pastan, Ira H. TITLE OF INVENTION: MONOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                     APPLICATION NUMBER: UPFILING DATE: 19921008 CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                             CITY: San Francisco
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: United States
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One Market Plaza, Steuart Street Tower
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Pred. No.
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                                                                                                                                       RESULT 20
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                                                                       Sequence 6, Application US/08390000A Patent No. 5985883
GENERAL INFORMATION:
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Best Local (
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TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO:
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                           APPLICANT: Sealfon
TITLE OF INVENTION:
TITLE OF INVENTION:
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CORRESPONDENCE ADDRESS:

Annressee: Townsend and Townsend

Annressee: Townsend and Townsend
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LENGTH: 243 amino acids
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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ORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
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DLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Parmelee, Steven W. REGISTRATION NUMBER: 31,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US93/09166
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6; Conserva
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: CA
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AMINO ACID
                                                                                                                                                                                                                                                                                                                                                  amino acid
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INVENTION: MONO
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                                                          Sealfon,
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85.7%;
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                         Cloning and Expression of Gonadotropin-Releasing Hormone Receptor
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                                                          Stuart C.
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Pred. No. 35;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Version #1.25
                                                                                                                                                                                                                                                                           DB 5;
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Query Match
Best Local Similarity
Watches 5; Conserve
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GENERAL INFORMATION:
                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyer, Scott J.
REGISTRATION NUMBER: 25,
SEQUENCE CHARACTERISTICS:
LENGTH: 407 amino acid
                                                                  REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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MOLECULE TYPE:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,000A
                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 212 790-9090
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Misrock, S. Leslie REGISTRATION NUMBER: 18,6 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1155 AVECITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                    TELEPHONE:
                                                                                                                                                                                 APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                 E: Scott J. Meyer, Monsanto Co., A3SD 800 N. Lindbergh Blvd.
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                                                                                        INFUL., Scott J., Scott J.
                                                   (314)694-3117
                                                                                                                                                                  19920805
                                                                                                                                                                                                                                                               Floppy disk
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71.4%;
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Pred. No.
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Query Match
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                                                                                                                     ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-5063
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                                                                                                                                                                                                                                                                                                                             Sequence 5063, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
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SEQ ID NO 4587
LENGTH: 213
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Matches 6; Conserv
                                                                   Query Match
Best Local (
                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
SEQ ID NO 5063
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                                                     Matches
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                                                                                                                                                                                                       CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/134,001C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLETC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                         LENGTH: 4.
TYPE: PRT
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                                                   y Match 82.4%;
Local Similarity 85.7%;
hes 6; Conservative
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Pred. No. 5
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                                                   0; Mismatches
                                                                   Score 28; DB 4;
Pred. No. 1.3e+02;
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Pred. No. 62;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/681,812
FILING DATE: 29-UUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGIGTRATION UNMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI96-07
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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APPLICANT: Bandma
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Gadbois, Ellen L.
APPLICANT: Chao, David M.
TITLE OF INVENTION: TBP-Associated Global Negative Regulator
TITLE OF INVENTION: and Methods of Use Thereof
NUMBER OF SEQUENCES: 7
                                                                                                                                    APPLICANT: Zhang, Hong
TITLE OF INVENTION: NEW TRANSCRIPTION REPRESSOR
NUMBER OF SEQUENCES: 4
                                                                                                                                                                       APPLICANT:
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 COMPUTER READABLE FORM:
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CITY: Lexington
                              COUNTRY:
                                                   STATE:
                                                                CITY: Palo Alto
                                                                                  STREET:
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TOPOLOGY: lin
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                                                                                                   ADDRESSEE:
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5763593
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                                                                                   E: Incyte Pharmaceuticals, Inc 3174 Porter Drive
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617-861-9540
                                 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                       ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELECHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
NFORMATION FOR SEQ ID NO:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
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                                                                                                                               APPLICATION NUMBER: US/08/80
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CLONE: 1244714
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STRANDEDNESS: siz
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SOFTWARE: FastSE(
                                                                                                                    FILING DATE:
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COMPUTER: IF
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LE OF INVENTION: NEW TRANSCRIPTION REPRESSOR
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             415-845-4166
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                                                         PF-0306 US
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Best Local Similarity
Watches 5; Conserve
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                                                   Matches
                                                                Query Match
Best Local
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                                                                                                                                                                                                                         TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/81
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
LIBRARY: SYNORAB01
CLONE: 1620089
                                                                                                                               IMMEDIATE SOURCE:
LIBRARY: GenBa
                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 3174 POI
CITY: Palo Alto
                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                        NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: lir
                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                             ENGTH: 205 amino acid
                                                                                                                                                                                                                                                   CELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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                         1 NAKTLT 6
                                                  Similarity
5; Conserv
NAKTMT 66
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                                                                                                                    : GenBank
1491710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Incyte Pharmaceuticals, Inc
3174 Porter Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bandman, Olga
Goli, Surya K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                   Conservative
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                                                                                                                                                                                               amino acids
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83.3%;
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                                                                79.4%;
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                                                  Score 27; DB Pred. No. 82; 1; Mismatches
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Pred. No.
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                                                                DB 2;
82;
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82;
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RESULT 29
US-08-765-783A-82
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US-08-426-236-4
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Matches
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Patent No. 599452.
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Patent No. 5629188
                                                                                                                                                                                                                                                                                                                  Sequence 82,
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APPLICANT: Shiba,
APPLICANT: Schimme
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SEQUENCE CHARACTERISTICS:
LENGTH: 958 amino acids
                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: BROOK, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                 APPLICANT: Tsuchiya, Masayuki
APPLICANT: Yamazaki, Tatsumi
TITLE OF INVENTION: Reshaped Human Antibody to
TITLE OF INVENTION: Interleukin-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                      NUMBER OF SEQUENCES:
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IITLE OF INVENTION: Human Alanyl-tRNA Synthetase Proteins,

IITLE OF INVENTION: Nucleic Acids and Tester Strains Comprising Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
nes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION:
                                                 ADDRESSEE: MORRISON & FULKSIAN
STREET: 2000 Pennsylvania Avenue, NW, suite 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                  COUNTRY:
                                    STATE:
                                               CITY: Washington
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20006-1888
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Two Militia Drive
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Sato, Koh
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                                                                                                                                                                                                                                           Matsushima, Kouji
Matsumoto, Yoshihiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shiba, Kiyotaka
Schimmel, Paul R.
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                                                                                                                                                                                                                            Yoshiki
                                                                                                                      105
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Pred. No. 4.5e+02;
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                                                                                                                ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/416,557
APPLICATION NUMBER: US/09/416,557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MUTAShige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 3502
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
FILING DATE: 7-March-199
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,9
                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Reshaped Human TITLE OF INVENTION: Interleukin-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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hes 5; Conserv
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STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                      COUNTRY:
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COMPUTER: II
                                                              APPLICATION NUMBER:
                                                                                              CLASSIFICATION:
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                                                                                                                                                                                                                                                                                      Washington
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2000 Pennsylvania Avenue, NW, suite 5500
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                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                                                                                                                                   Tsuchiya, Masayuki
Yamazaki, Tatsumi
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matsushima, Kouji
Matsumoto, Yoshihiro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamada,
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                                                                                                              12-October-1999
                                              7-March-1997
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71.4%;
                                                                                                                                                                                                                                                                                                                                                                                  Reshaped Human Antibody to
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                                                              08/765,783
   29,959
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Pred. No.
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RESULT 32
US-08-723-425A-90
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US-08-146-028-90
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              Sequence 90, Application US/08723425A Patent No. 6165730 GENERAL INFORMATION:
                                                                                                                                                                                           Matches
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Best Local
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: PRO
TITLE OF INVENTION: COR.
TITLE OF INVENTION: IN :
TITLE OF INVENTION: PRO
TITLE OF INVENTION: PRO
NUMBER OF SEQUENCES: 45:
COMPUTER REALDABLE FORM:
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA;
APPLICANT:
                                                                                                                                                                                                                                                                                                        FEATURE:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL:
ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                       NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                     LOCATION:
                                                                                                                                                                                                                                                                                                                                                                  INDIVIDUAL ISOLATE: HCV type 2
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No. 5891640
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202-822-0168
DELEYS, ROBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                         Modified-site 24
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                                                                                                                                                                                                        76.5%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROCESS FOR THE DETERMINATION OF PEPTIDES
CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
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71.4%;
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                                                                                                                                                                                         Score 26; DB
Pred. No. 13;
1; Mismatches
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Pred. No. 1
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US-08-723-425A-90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                              Sequence 90,
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TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 1487
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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TITLE OF INVENTION:
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NUMBER OF SEQUENCES:
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MBDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
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ORIGINAL SOURCE:
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                                                                                                               COMPUTER READABLE FORM:
                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
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1100 NORTH GLEBE ROAD, 8TH FLOOR
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83.3%;
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CORRESPONDING TO IMMUNOLOGICALLY MATTENDIES OR BIOTINYLATED IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES, 1
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US/09/112,206
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Pred. No.
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                                      Version
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13;
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                                                     Matches
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                                                                                Query Match
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TITLE OF INVENTION:
TITLE OF INVENTION:
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TITLE OF INVENTION:
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NAME/KEY:
LOCATION:
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ORIGINAL SOURCE:
INDIVITY:
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NAME/KEY:
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                                                                                                                        NAME/KEY:
LOCATION:
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nes 5; Conserv
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                                                                                                                                                                   LOCATION:
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NARTLT 9
                        NAKTLT 6
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                                                     Conservative
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                                                                                                                                                                                                                                                                linear
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                 76.5%;
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Pred. No. 14;
                                                     Mismatches
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RESULT 35
US-08-723-425A-91
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CENERAL INFORMATION:
                                                                                                                              Sequence 91, Application US/09112206 Patent No. 6210903
                                                                                                                                                                                                                                                                                                                  Matches
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INFORMATION FOR SEQ ID NO:
                                                                                                                GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SALOFF, B.J.
REGISTRATION NUMBER: 36,663
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CORRESPONDENCE ADDRESS:
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                                                                                             APPLICANT
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LOCATION:
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83.3%;
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                     PROCESS FOR THE DETERMINATION OF PEPTIDES

CORRESPONDING TO IMMUNOLOGICALLY IMPARANT EPITOPES AND THEIR (
IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES, I
   PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING
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Pred. No.
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FILING DATE:

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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
ZIP: 2005-5701
ZIP: 2005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                 APPLICATION NUMBER: US/08/845,926
FILING DATE: 04-28-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/598,993
FILING DATE: 09-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
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                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
   APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Nikaido, Marmelstein, Murray & Oram LLP 655 Fifteenth Street N.W. Suite 330
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VENTION: Method for serological typing using
VENTION: type-specific antigens
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JUNG, G nther-Gerhard
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Pred. No. 14;
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                                TELEFAX: (202)638-4810 INFORMATION FOR SEQ ID NO: 7:
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                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
PRIOR APPLICATION DATA:
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ORIGINAL SOURCE:
ORGANISM: Hep
                                                                                                                            APPLICATION NUMBER: DE 1
FILING DATE: 09-FEB-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 22,980
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                           NAME: Murray, Robert B.
REGISTRATION NUMBER: 22,980
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-5000
                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                  FILING DATE:
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JUNG, G nther-Gerhard
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83.3%;
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Pred. No.
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Thebs 5; Conserve
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US-08-723-425A-89
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             Sequence 89, Application US/08723425A

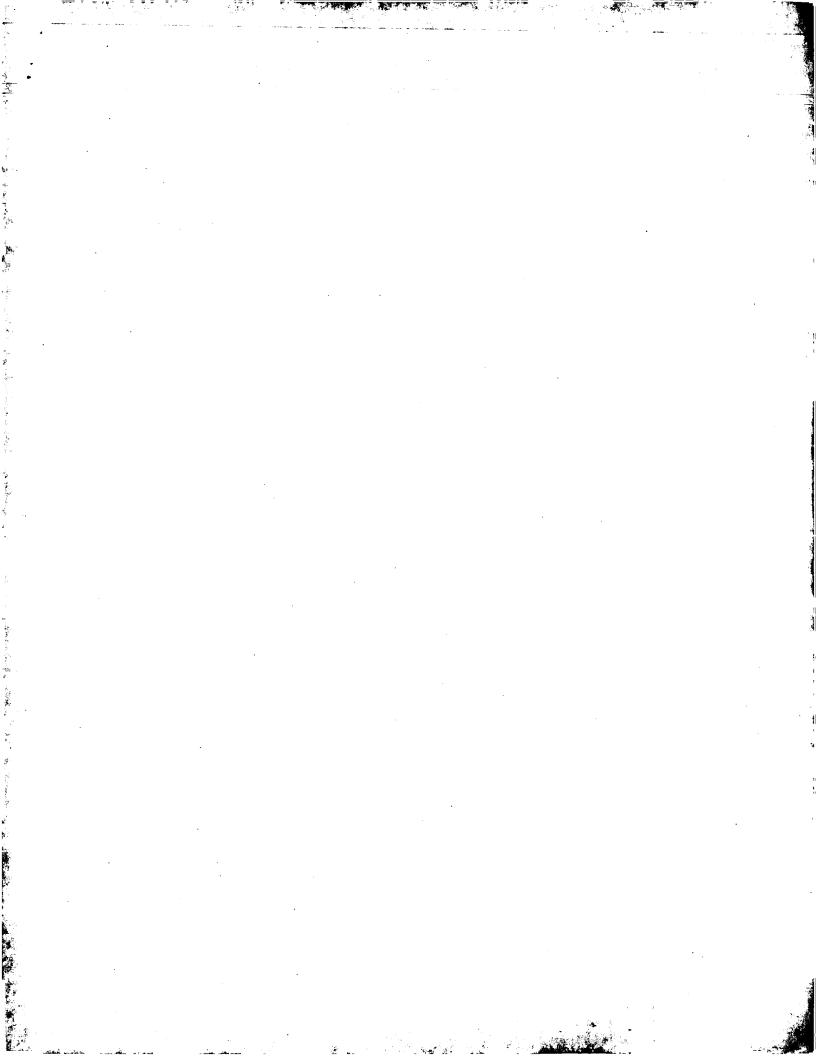
PALENT NO. 6145730

GENERAL INFORMATION:
APPLICANT: DELEYS, ROBERT
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT
TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION
TITLE OF INVENTION: ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING ...
NUMBER OF SEQUENCES: 453
                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 89,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,028
INFORMATION FOR SEQ ID NO: 89:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Atent No. 58910.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: FITTLE OF INVENTION: CONTICUE OF INVENTION: FITTLE OF INVENTION: FITTLE OF INVENTION: FOURBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WOLECULE TYPE: peptide
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                            Local Similarity nes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TOPOLOGY: li
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                                                                                                                                                                                                                                                      14 NARTLT 19
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83.3%;
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83.3%;
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CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIGTINYLATED
PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 26; DB
Pred. No. 17;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                               Score 26; DE
Pred. No. 20;
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Search completed: July 18, Job time: 9.12 secs
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                                                                                                                                                          Query Match
Best Local
                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 89:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/723,425A FILING DATE: CLASSIFICATION: 435 ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                          FEATURE:
NAME/KEY: Modified-site
LOCATION: 36
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: 111541.
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: NIXON & VANDERHYE, P.C. STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR CITY: Arington
                                                                                                                                      Local Similarity
hes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 14
                                                                                                                                                                                                                                                                            LOCATION:
                                                                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                              INDIVIDUAL ISOLATE: HCV type
                                                                     14 NARTLT 19
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83.3%;
                 2003, 15:11:51
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Pred. No.
                                                                                                                                         Mismatches
                                                                                                                                                          20;
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                                                                                                                                        0;
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RESULT 2
US-10-096-246-15
Sequence 15, Application US/10096246
Sequence 15, Application No. US20030100060A1
GENERAL INFORMATION:
APPLICANT: The Minister of National Defence, Government of Canada
RAPLICANT: Pulton, R E
RAPLICANT: Alvi, Azhar E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 6; Conserv
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Sequence 42, Appl
Sequence 466, App
Sequence 10049, A
Sequence 11086, A
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139, App
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11086, A
13898, A
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22, Appl
7, Appli
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                                                                             July 18, 2003, 15:09:56; Search time 18.06 Seconds (without alignments) 46.031 Million cell updates/sec
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Sequence 1
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5.1.6
Compugen Ltd.
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US-10-096-246-15
US-10-096-246-19
US-10-156-761-8682
US-09-738-626-3610
US-10-007-693-139
US-09-881-752A-112
US-09-789-054A-42
US-09-789-054A-42
US-09-789-054A-42
US-09-815-24-11049
US-09-815-242-11049
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US-09-815-242-113898
US-09-738-206-22
US-10-738-200-22
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GenCore version
Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                        protein search, using sw model
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Match Length
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Perfect score:
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Sequence 18, Application US/10096246

Publication No. US20030100060A1

GRNERAL INFORMATION:
GRNERAL INFORMATION:
APPLICANT: The Minister of National Defence, Government of Canada
APPLICANT: Pulton, R E
APPLICANT: Alvi, Azhar E
APPLICANT: Alvi, Azhar E
APPLICANT: Alvi, Azhar E
APPLICANT: Alvi, Azhar E
APPLICANT: Alvi, Azhar E
APPLICANT: Najata, Lealie
TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mor
TITLE OF INVENTION: ScFv Antibody Against Venzuelan Equine Encephalitis Virus (Vee)
TITLE OF INVENTION: 2002-03-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
LENGTH: 101
 Sequence 76, Appl
Sequence 77, Appl
Sequence 77, Appl
Sequence 57, Appl
Sequence 5, Appli
Sequence 67, Appli
Sequence 14, Appl
Sequence 14, Appl
Sequence 693, Appl
Sequence 693, Appl
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Sequence 6983, Appl
Sequence 6983, Appl
Sequence 6983, Appl
Sequence 6983, Appl
Sequence 11065, Appl
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Sequence 11065, Appl
Sequence 12670, Appl
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Sequence 110,
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85.7%; Pred. No. 29;
ive 0; Mismatches 1; Indels
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US-09-738-626-6967
US-09-815-242-10139
US-10-156-761-11065
US-09-738-626-6982
US-09-915-242-12670
US-09-922-217-1093
US-09-977-283A-76
US-09-73-2846-17
US-09-730-857-77
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US-09-977-283A-5
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US-09-977-283A-9
US-09-973-390A-30
US-09-875-456A-14
US-09-875-456A-14
US-09-875-380-693
US-10-213-990-39
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US-10-245-103-110
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US-10-245-143-110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Mouse hybridoma cell line 1A4A1
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GENERAL INFORMATION:
APPLICANT: Kinnersely, Alan M.
APPLICANT: Turancy, Perank J.
TITLE OF INVENTION: Methods for Regulating Plant GABA Production
TITLE OF INVENTION: Methods for Regulating Plant GABA Production
CURRENT APPLICATION NUMBER: US/10/006,852
CURRENT APPLICATION NUMBER: US/02-07-01
PRIOR FILING DATE: 2002-07-01
PRIOR FILING DATE: 2000-11-07
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                         DB.15; Length 302;
96;
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CURRENT FILING DATE: 2000-12-18
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FLING DATE: 2000-04-07
PRIOR FLING DATE: 2000-04-07
PRIOR FLING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN OFF: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VEY: 3.0
SERIOR 1472
                                                                                                                                                                                                                                                                         Score 29;
Pred. No. 9
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Duduence 3610, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Corynebacterium glutamicum
                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-8682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18, Application US/10006852 Publication No. US20030046732A1
                                                                                                                                                                                                                                                                         85.3%;
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APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
                               PRIOR FILING DATE: 2001-08-0
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 8682
LENGTH: 302
                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 85.73
Matches 6; Conservative
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163 DAKTLTE 169
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274 NAKTITD 280
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Best Local Similarity
Matches 5; Conserv
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APPLICANT:
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APPLICANT: Nagata, Leslie
TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of MC
TITLE OF INVENTION: ScFv Antibody Against Venzuelan Equine Encephalitis Virus (Vee)
TITLE OF INVENTION: ScFv Antibody Against Venzuelan Equine Encephalitis Virus (Vee)
CURRENT APPLICATION NUMBER: US/10/096,246
CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin Version 3.1
SEQ ID NO 15.
LENGTH: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Publication No. US20030100060A1
| Publication No. US20030100060A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: The Minister of National Defence, Government of Canada
| APPLICANT: Fulton, R E
| APPLICANT: Alvi, Azhar E
| APPLICANT: Nagata, Leslie
| APPLICANT: Nagata, Leslie
| TITLE OF INVENTION: Gloning, Expression, Sequencing, and Functional Enhancement of MC
| TITLE OF INVENTION: Gloning, Rapid State of Title OF INVENTION (COURTED ADDITION OF TITLE OF INVENTION (COURTED ADDITION OF TITLE OF TITLE OF INVENTION (COURTED ADDITION OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE
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Pred. No. 31;
0; Mismatches 1; Indels
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APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SATAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPRERENCE: 249-2462
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Mouse hybridoma cell line 1A4A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-096-246-19
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PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8682, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.3%;
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Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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US-10-156-761-8682
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US-10-096-246-19
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APPLICANT: Allen, Steve
APPLICANT: Allen, Gun
APPLICANT: Allen, Gun
TITLE OF INVENTION: PLANG GENES ENCODING DR1 AND DRAP1, A GLOBAL REPRESSOR COMPLEX OF
TITLE OF INVENTION: TRANSCRIPTION
FILE REFERENCE: BB1107 US CIP
CURRENT APPLICATION NUMBER: US/09/789,054A
CURRENT FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 09/48558
PRIOR APPLICATION NUMBER: PCT/US98/16688
PRIOR FILING DATE: 1998-08-12
PRIOR APPLICATION NUMBER: 60/055,865
PRIOR APPLICATION NUMBER: 60/055,865
PRIOR APPLICATION NUMBER: 60/055,865
NUMBER OF SEQ ID NOS: 69
SOFTWARE: Microsoft Office 97
LENGTH: 205
LENGTH: 205
LENGTH: 205
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Sequence 466, Application US/09731872

Sequence 466, Application US/09731872

Sequence 466, Application US/09731872

Sequence 100. US20020102604A1

Seneral INFORMATION:

APPLICANT: Bougueleret, Lydie

APPLICANT: Bougueleret, Lydie

APPLICANT: Bougueleret, Lydie

APPLICANT: Bougueleret, Lydie

APPLICANT: Bougueleret, Lydie

APPLICANT: Asverin

TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS

FILE REBERBENE: 78.053.REG

CURRENT FILING DATE: 2000-12-07

PRIOR PILING DATE: 1999-12-08

PRIOR PILING DATE: 1999-12-08

PRIOR PILING DATE: 2000-03-06

NOWHERE OF SEQ ID NOS: 482

SOFTWARE: Patent.pm

SEQ ID NO 466

LENGTH: 500

MANDER DELICATION NOWHER: SEQ ID NOS: 482

SEQ ID NO 466

LENGTH: 500
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83.3%; Pred. No. 1.8e+02;
ive 1; Mismatches 0; IndelB
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83.3%; Pred. No. 4.7e+02;
ive 1; Mismatches 0;
                                                                                                                                                                          Sequence 42, Application US/09789054A Publication No. US20020184659A1 GENERAL INFORMATION:
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Best Local Similarity 83.3
Matches 5; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-09-731-872-466
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91 NAKTLSO 97
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Best Local Similarity
Matches 5; Conserv
                           1 NAKTLTE 7
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61 NAKTMT 66
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                                                                                                                                                      US-09-789-054A-42
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TITLE OF INVENTION: Identification of Polynucleotides
TITLE OF INVENTION: Encoding No. US20020115078A1el Helicobacter Polypeptides in the TITLE OF INVENTION: Genome
FILE REFERENCE: 06132/041002
CURRENT APPLICATION NUMBER: US 09/881,752A
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 08/833,457
NUMBER OF SEQ ID NOS: 370
NUMBER OF SEQ ID NOS: 370
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Pred. No. 80;
2; Mismatches 0; Indels
                                                                                                                                                        Length 502;
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85.7%; Pred. No. 2.3e+02;
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Publication No. US20020146776A1
GENERAL INFORMATION:
APPLICANT: BRAID: Ajay
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT
TITLE OF INVENTION: AND DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.515C2
CURRENT FILING DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 157
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Pred. No. 1.7e+02;
0; Mismatches 1.
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Patent No. US20020115078A1
APPLICANT: Kleanthous, Harold
APPLICANT: Kleanthous, Harold
APPLICANT: M1-Garawi, Amal
APPLICANT: Miller, Charles
APPLICANT: Tomb, Jean-Francois
                                                                                    ) ORGANISM: Lycopersicon esculentum US-10-006-852-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Chlamydia trachomatis
SOFTWARE: Patentin version 3.1
SEQ ID NO 18
LENGTH: 502
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5; Conservative
                                                                                                                                                    Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative
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Matches 6; Conserv
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Best Local Similarity
Matches 5; Conserv
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LENGTH: 100
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LENGTH: 660
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APPLICANT:
                                                                    TYPE: PRT
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Gaps
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APPLICANT: Yanamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,846
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/205,846
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/205,579
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-12-17
PRIOR FILING DATE: 2001-12-17
PRIOR FILING DATE: 2001-12-17
PRIOR FILING DATE: 2001-12-17
PRIOR FILING DATE: 2001-12-16
PRIOR FILING DATE: 2001-12-16
PRIOR FILING DATE: 2001-02-16
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Pred. No. 5.5e+02;
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 11086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
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Pred. No. 5.
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COCATION: (1)...(582)
COTHER INFORMATION: Xaa = Any Amino Acid
US-09-815-242-13898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13898, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                   TYPE: PRT CORGANISM: Haemophilus influenzae US-09-815-242-11086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANY: Zyskind, Judith W.
APPLICANY: Wall, Daniel
APPLICANY: Trawick, John D.
APPLICANY: Carr, Grant J.
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Similarity 71.4%;
5; Conservative
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ORGANISM: Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 79.4
Best Local Similarity 71.4
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-01-03
                                                                                                                                                                                                                                                                                                                                      APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA. 011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/24,578
PRIOR APPLICATION NUMBER: 60/23,625
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
                                                         Sequence 10049, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11086, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
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APPLICATION NUMBER: 60/206,848
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PRIOR APPLICATION NUMBER: 60/207, 727
                                                                                                                                     APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yammoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-815-242-10049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 71.4
Matches 5; Conservative
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SEQ ID NO 10049
LENGTH: 572
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; TITLE OF INVENTION: EPITOPES IN VIRAL ENVELOPE PROTEINS AND SPECIFIC
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST THESE EPITOPES: USE FOR
; TITLE OF INVENTION: DEFECTION OF HCV VIRAL ANTIGEN IN HOST TISSUE
; FILE REFERENCE: 2551-47
; CURRENT APPLICATION NUMBER: US/10/318,200
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: PG/99/645,470
; PRIOR APPLICATION NUMBER: PCT/EP99/02154
; PRIOR APPLICATION NUMBER: EP 98870060.5
; PRIOR APPLICATION NUMBER: EP 98870060.5
; RIGHTING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 22
; LENGTH: 24
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ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
STREET: 655 Fifteenth Street N.W. Suite 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IMP PC compatible
COMPUTER: IMP PC compatible
COMPUTER: IMP PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/196,174
FILING DATE: 17-Jul-2002
CLASSIFCATION AUMBER: US/09/351,296
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/351,296
FILING DATE: CUNKNOWN-
APPLICATION NUMBER: US/09/351,296
FILING DATE: CUNKNOWN-
APPLICATION NUMBER: US/09/351,296
FILING DATE: CUNKNOWN-
APPLICATION NUMBER: US/09/351,296
FILING DATE: UNKNOWN-
APPLICATION NUMBER: US/09/351,296
FILING DATE: UNKNOWN-
APPLICATION NUMBER: US/09/351,296
FILING DATE: US/06/1995
                                                                                                                                                                                                                                                                                                                                                                                                                             76.5%; Score 26; DB 14; Length 24; 83.3%; Pred. No. 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Washington
STRATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMMUNICATION INFORMATION:
TELEPHONE: (202)638-5000
TELEFAX: (202)638-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Conservative
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Best Local Similarity
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STREET: 2000 Pennsylvania Avenue, NW, suite 5500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.5%; Score 26; DB 10; Length 7; 71.4%; Pred. No. 4e+05;
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                                                                                                                                                                   Sequence 82, Application US/09730857
Patent No. US20020083396A1
GENERAL INFORMATION:
MATSUMOTO, Yoshihiro
Yamada, Yoshiki
Sato, Koh
Tsuchiya, Masayuki
Yamazaki, Tatenumi
Yamazaki, Tatenumi
TITLE OF INVENTION:
Interleukin-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRUTER: IBM Compatible
CORRUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/730,857
FILING DATE: O'-Dec-2000
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/416,557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 35029-20001.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 82:
US-09-730-857-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 22, Application US/10318200; Publication No. US200330129746A1; GEBREAL INFORMATION; APPLICANT: MAERTENS, GEERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1999-10-12 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 202-822-0168
TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DELPA, ERIK
BUYSE, MARIE-ANGE
                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                   269 NAKTIAE 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 5; Conserv
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                            1 NAKTLTE 7
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US-10-318-200-22
                                                                                                                                RESULT 14
US-09-730-857-82
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW, suite 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPAtible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NATA:
FILING DATE: 07-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 35029-20001.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEPRAX: 202-822-0168
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Matsushima, Kouji
Matsumoto, Yoshihiro
Yamda, Yoshiki
Sato, Koh
Tsuchiya, Masayuki
Yamazaki, Tatsumi
TITLE OF INVENTION: Reshaped Human Antibody
                                                                                                    Score 26; DB 15;
Pred. No. 1.5e+02;
1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 26; DB 10;
Pred. No. 1.7e+02;
1; Mismatches 1
                   ; TYPE: PRT
; ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-096-246-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE DESCRIPTION: SEQ ID NO: 73:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/416,557
FILING DATE: 1999-10-12
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interleukin-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Signal Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                              Sequence 73, Application US/09730857
Patent No. US20020082396A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                    76.5%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76.5%;
ilarity 71.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 1...19
OTHER INFORMATION
                                                                                 Ouery Match
Best Local Similarity 71.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Washington STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                           50 NAKTLAD 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                     1 NAKTLTE 7
                                                                                                                                                                                                                                                                                                            US-09-730-857-73
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  LENGTH: 108
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Sequence 17, Application US/10096246

Publication No. US20030100060A1

GENERAL INPORMATION:
APPLICANT: The Minister of National Defence, Government of Canada
APPLICANT: Fulton, R E
APPLICANT: APPLICANT: Additional Expression, Sequencing, and Functional Enhancement of MC
TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of MC
TITLE OF INVENTION: ScrV Antibody Against Venzuelan Equine Encephalitis Virus (Vee)
FILE REFERENCE: NEL-0007
CURRENT APPLICATION NUMBER: US/10/096,246
CURRENT APPLICATION NUMBER: 2002-03-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin version 3.1
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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US-09-977-283A-76
; Sequence 76, Application US/0997283A
; Sequence 76, Application US/0997283A
; Publication No. US20030031664A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Guy L.
; TITLE OF INVENTION: Composition and Method for Enhancing Fibrinolysis
; TITLE OF INVENTION: US09.432003
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 08/994,000
; PRIOR FILING DATE: 1997-09-19
; PRIOR FILING DATE: 1996-09-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76
: LENGTH: 107
                                                                                                                                                                                                                                                                    Gaps
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Pred. No. 1.4e+02;
                                                                                                                                                                                                                             DB 15; Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                      Indels
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NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                           Score 26; DB Pred. No. 37; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , LUCATION: (74)...(74)
; OTHER INFORMATION: May be any Amino Acid
US-09-977-283A-76
                                                                                                                                          ORGANISM: Hepatitis C Virus SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                  TYPE: amino acid
STRANDEDNESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                     LENGTH: 31 amino acids
                                                                                                                                                                                                                           76.5%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.5%;
71.4%;
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                        Query Match
Best Local Similarity 83.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50 NAKTLAD 56
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12 NARTLT 17
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US-10-096-246-17
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Sequence 27, Application US/09730857
Patent No. US20020082396A1
GENERAL INFORMATION:
APPLICANT: Mateumoto, Yoshihiro
Yamada, Yoshiki
Sato, Koh
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                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW, suite 5500
CITY: Washington
                                                                                                                                                Sequence 77, Application US/09730857
Fatent No. US2002082396A1
GENERAL INFORMATION:
Matsumoto, Yoshihiro
Yamada, Yashiki
Sato, Koh
Tsuchiya, Masayuki
Yamazaki, Tatenni
Yamazaki, Tatenni
Yamazaki, Tatenni
JITLE OF INVENTION:
Interleukin-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 2006-1888
COMPUTER READABLE PORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEMO FOR Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/730,857
FILING DATE: O'-Dec-2000
CLASSIFICATION AVENOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/416,557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 1999-10-12
ATTORNEY/ABENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECPHONE: 202-887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO: 77:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 126 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 202-822-0168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein FRAGMENT TYPE: internal PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 1...19
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                      69 NAKTLAD 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAKTLAD 75
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Best Local Similarity
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                      1 NAKTLTE 7
                                                                                                                RESULT 20
US-09-730-857-77
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RESULT 21 US-09-730-857-27

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Publication No. US20030031664A1
GENERAL INPORMATION:
TITLE OF INVENTION: Composition and Method for Enhancing Fibrinolysis
FILE REFERENCE: 0609-4320003
CURRENT APPLICATION NUMBER: US/09/977,283A
CURRENT FILING DATE: 2001-10-16
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Pred. No. 1.7e+02;
1; Mismatches 1; Indels
                                                                                                               ADDRESSEE MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW, suite 5500
CITY: Washington
STATE: DC
                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: 1BM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEO for Windows Version 2.0
CURRIN APPLICATION DATA:
FILING DATE: 07-Dec-2000
Tsuchiya, Masayuki
Yamazaki, Tatsumi
YITLE OF INVENTION: Reshaped Human Antibody to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 35029-20001.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/416,557
FILING DATE: 1999-10-12
ATTORNEY/AGENT INFORMATION:
                                                                      Interleukin-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 202-822-0168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.5%;
71.4%;
                                                                                       SEQUENCES: 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
FRAGMENT TYPE: internal
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 1...20
OTHER INFORMATION:
                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 76.5
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 NAKTLAD 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 NAKTLTE 7
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Gaps
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APPLICANT: Millennium Pharmaceuticals Inc.
APPLICANT: Millennium Pharmaceuticals Inc.
APPLICANT: Millennium Pharmaceuticals Inc.
TITLE OF INVENTION: 98359, A. SODIUM CHANNEL BETA 4 SUBUNIT,
TITLE OF INVENTION: AND USES THEREFOR
FILE REPRENCE: MPI2001-106PIRN(M)
CURRENT FALLICATION NUMBER: US/10/142,201B
CURRENT FILING DATE: 2002-05-09
PRIOR FILING DATE: 2001-05-09
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 218
TYPE: PRT
CORANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.5%; Score 26; DB 10; Length 12
71.4%; Pred. No. 1.8e+02;
iive. 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 26; DB 15; Length 21
Pred. No. 3.1e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                             2000-03-01
UMBER: PCT/US98/13966
1998-07-06
UMBER: US 08/889,296
UB97-07-08
                                                                                                                                                                                                                                                                         FILING DATE: 1994-06-21
APPLICATION NUMBER: US 07/814,961
FILING DATE: 1991-12-24
APPLICATION NUMBER: US 09/462,280
                                                                                                                                                                                 BER: US 09/144,611
1998-08-31
BER: US 08/861,306
                                                                                                                                                                                                                                       1997-04-21
MBER: US 08/244,993
1994-06-21
                                                                                                                                                                                                                                                                                                                                                                                                                                    IBER: US 08/411,734
1995-04-03
IBER: US 08/007,996
                                                                                            1998-12-02
ABER: US 60/067,458
                                          US 09/684,254
                                                                                                                                                US 09/453,514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn version 3.0
                                                         2000-10-06
                                                                                                                                 1997-12-04
                                                                                                                                                               1999-12-01
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Best Local Similarity 71.4%;
Matches 5; Conservative 1
                  Query Match
Best Local Similarity 71.4'
Matches 5; Conservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ::|||||
67 DSKTLTE 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 25
US-10-142-201B-8
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TITLE OF INVENTION: METHODS OF USING MAMMALIAN RNASE H AND COMPOSITIONS THEREOF
FILE REFERENCE: ISPH-0521
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PUBLICATION NO. US20030031664A1
GENERAL INFORMATION:
TITLE OF INVENTION: Composition and Method for Enhancing Fibrinolysis
FILE REFERENCE: 6069.432003
CURRENT APPLICATION NUMBER: 08/99/977,283A
CURRENT FILING DATE: 2001-10-16
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/026,356
PRIOR PILING DATE: 1996-09-20
NUMBER OF SEQ ID NOS: 81
SEQ ID NO 9
LENGTH: 127
TYPE: PRT
TYPE: PRT
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71.4%; Pred. No. 1.7e+02;
cive 1; Mismatches 1; Indels
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                                                                                                                                                                                FEATURE:
CTHER INFORMATION: Alpha-2 Antiplasmin Antibody
NAME/KEY: M.SC FEATURE
COCATION: (-12)...(-12)
COTHER INFORMATION: May be either Gly or Ala
US-09-977-283A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Alpha-2 Antiplasmin Antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/799,848 CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 08/934,000
PRIOR FILING DATE: 1997-09-19
PRIOR PRICATION NUMBER: 60/026,356
PRIOR FILING DATE: 1996-09-20
NUMBER OF SEQ ID NOS: 81
SEQ ID NO 5
LENGTH: 127
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Patent No. US20010044145A1
GENERAL INFORMATION:
APPLICANT: Monia, Brett
APPLICANT: Cook, Phillip
APPLICANT: Crooke, Stanley
APPLICANT: Wu, Hongjiang
                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 71.1.
                                                                                                                                                                                                                                                                                                                                                                                                                  70 NAKTLAD 76
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70 NAKTLAD 76
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US-09-977-283A-9
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US-09-799-848-2
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APPLICANT: Wang, Aljun APPLICANT: Clapper, Jonathan D. APPLICANT: Clapper, Jonathan D. APPLICANT: Stolk, John A. APPLICANT: Stolk, John A. APPLICANT: Meagher, Madeleine J. APPLICANT: Meagher, Madeleine J. APPLICANT: Meagher, Madeleine J. TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE FILE REPERENCE: 21012.471C12.
CURRENT APPLICATION NUMBER: US/09/833,263
CURRENT PILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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APPLICANT: Wang, Aljun
APPLICANT: Clapper, Jonathan D.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C13
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: FRAESEQ FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; DB 10; Lengu...
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                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                               4e+02;
                                                                                                                                                                      Score 26; DB 1
Pred. No. 4e+02
1; Mismatches
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Pred. No. 4.1e+
1; Mismatches
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Patent No. US20020110547A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 693, Application US/09922217
Patent No. US20020076414A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Secrist, Heather
Benson, Darin R.
Meagher, Madeleine Joy
Stolk, John A.
Wang, Tongtong
Jiang, Yuqiu
Smith, Carole Lynn
                                                                                                                                                                         76.5%;
71.4%;
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71.4%;
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APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
  NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 268
                                                                                                                                                                         Query Match 76.5
Best Local Similarity 71.4
Matches 5; Conservative
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Best Local Similarity 71.4
Matches 5; Conservative
                                                                                    TYPE: PRT
CRGANISM: Homo sapiens
US-09-875-456A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
CORGANISM: Homo sapiens
US-09-922-217-693
                                                                                                                                                                                                                                                                                                     50 NAETFTE 56
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Patent No. US20020045229A1
GENERAL INFORMATION:
APPLICANT: Qin, Ming
APPLICANT: Qin, Ming
APPLICANT: D'Andrea, Michael
TITLE OF INVENTION: DNAs encoding human betala sodium channel subunit
FILE REFERENCE: ORT-1221
CURRENT APPLICATION NUMBER: US/09/875,456A
CURRENT FILING DATE: 2001-09-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/935,390A
FILING DATE: 22-Aug-2001
CLASSIFICATION - UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/988,671
FILING DATE: 1997-12-11
                                                                                                                                                                                                     Garcia, Pablo
Williams, Lewis T.
Kothakota, Srinivas
TITLE OF INVENTION: Secreted Human Proteins
NUMBER OF SEQUENCES: 38
CORRESPONDER ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Jane E. R. Potter
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 1369.002
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
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MOLECULE TYPE: No. US20020076761Ale
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
                                                                                                      Sequence 30, Application US/09935390A
Patent No. US20020076761A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (510) 923-2718
TELEFAX: (510) 655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                    APPLICANT: Escobedo, Jaime Quianjin, Hu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 71.4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NAKTLTE 7
50 NAETFTE
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US-09-875-456A-14
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TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLECTIDES ENCODING THEM
                                                                                                                                     Length 299;
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                                                                                                                                     Score 26; DB 15; Length 29
Pred. No. 4.5e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 76.5%; Score 26; DB 11; Length 30 Best Local Similarity 71.4%; Pred. No. 4.5e+02; Matches 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
FRIOR PRILAGATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
SOFTWARE: PALENTIN VOX: 3.0
SOFTWARE: PALENTIN VOX: 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 150, Application US/09745763
Patent No. US2000065394A1
GENERAL INFORMATION:
MCCOY, JOHN M.
Invalie, Edward R.
Lavallie, Edward R.
Collins-Racie, Lisa A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT; ORGANISM: Corynebacterium glutamicum US-09-738-626-6409
                                                                                                                                                                                                                                                                                                                                                                                Sequence 6409, Application US/09738626
Publication No. US20020197605A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Merberg, David
Treacy, Maurice
Spaulding, Vikki
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 219
                                                                                                                                                          71.48;
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OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                     Query Match 76.5
Best.Local Similarity 71.4
Matches 5; Conservative
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                                           TYPE: PRT
; ORGANISM: Aspergillus
US-10-213-990-39
                                                                                                                                                                                                                                                                   76 NTKTLSE 82
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87 NGETLTE 93
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                       LENGTH: 299
  SEQ ID NO 39
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APPLICANT: Storms, Reg
APPLICANT: Storms, Reg
APPLICANT: Storms, Reg
APPLICANT: Storms, Reg
APPLICANT: Storms, Reg
TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
TITLE OF INVENTION: ENZYMES AND METHODS OF USE
TITLE OF INVENTION: UNDER: US/10/213,990
CURRENT APPLICATION NUMBER: US/10/213,990
CURRENT FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FASTSEQ for Windows Version 4.0
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CURRENT APPLICATION NUMBER: US/10/025,380
CURRENT FILING DATE: 2001-12-19
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                                                                                                            76.5%; Score 26; DB 11; Length 277; 71.4%; Pred. No. 4.1e+02;
                                                                                                                                                          1; Indels
                                                                                                                                                          1; Mismatches
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 693
LENGTH: 277
                                                                                                                                                                                                                                                                                                                                                         Sequence 693, Application US/10025380 Publication No. US20020182191A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Stolk, John A.
APPLICANT: Wang, Tongtong
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Publication No. US20030082595A1
GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Bussey, Howard
APPLICANT: Storms, Reg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clapper, Jonathan D. Skeiky, Yasir A. W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.48;
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Vedvick Thomas S.
Carter, Darrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jiang, Yuqiu
Smith, Carole L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          King, Gordon E.
Wang, Aijun
                                                                                                         Query Match
Best Local Similarity 71.4
Matches 5; Conservative
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Best Local Similarity 71.4
Matches 5; Conservative
                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , ORGANISM: Homo sapiens
US-10-025-380-693
                                                                                                                                                                                                   1 NAKTLTE 7
| ||:||
63 NEKTVTE 69
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                                                                  US-09-833-263-693
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US-10-025-380-693
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LENGTH: 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamancto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                        APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TAYESHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
APPLICANT: OZAKI, AKI
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR PILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
SOFTWARE: Patentin ver: 3.0
SEQ ID NO 6967
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CURRENT FILING DATE: 2001-03-21
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PELING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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Patent No. US20020061569A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6967
                            Sequence 6967, Application US/09738626
Publication No. US20020197605A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 2000-12-22
APPLICATION NUMBER: 60/269,308
FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 76.5
Best Local Similarity 83.3
Matches 5; Conservative
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Fatent No. US200200523081
GENERAL INFORMATION:
TILLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA.106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/USO0/05882
PRIOR APPLICATION NUMBER: PCT/USO0/05882
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR PILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.5%; Score 26; DB 10; Length 320; 71.4%; Pred. No. 4.8e+02; Live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76.5%; Score 26; DB 10; Length 325; 71.4%; Pred. No. 4.9e+02; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/745,763 FILING DATE: 18-Jun-2000 CLASSIFICATION: <u >- CUNKNOWN-</u>
ATTORNEY/AGENT INFORMATION:
                       ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 150:
US-09-745-763-150
                                                                                                                COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MADIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Sprunger, Suzanne A. REGISTRATION NUMBER: 41,323 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (617) 498-8284
TELEFAX: (617) 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 320 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
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Best Local Similarity 71.4
Matches 5; Conservative
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Matches 5; Conservative
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ORGANISM: Homo sapiens
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63 NIKTVTE 69
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US-09-925-301-969
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PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PALENTIN Ver. 3.0
SEQ ID NO 6982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12670, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Staphylococcus aureus US-09-815-242-12670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                          330 NAKTLAD 336
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US-09-922-217-1093
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                                                                                                                                                                                   76.5%; Score 26; DB 10; Length 416; 83.3%; Pred. No. 6.4e+02;
                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ISHIKAWA, JUN
APPLICANT: BSHIRAWA, HIROSHI
APPLICANT: SHIRAW, TADANOSHI
APPLICANT: SAKAKI, YOSHIVUKI
APPLICANT: SAKAKI, YOSHIVUKI
APPLICANT: SAKAKI, YOSHIVUKI
APPLICANT: HATTORI, MASAHIRA
TILE REPERBNCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-30
PRIOR FILING DATE: 2001-06-30
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 11065
LENGTH: 429
                                                                                                                                                                                                                                1; Mismatches
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10139
LENGTH: 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 11065, Application US/10156761; Publication No. US20030119018A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6982, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , ORGANISM: Streptomyces avermitilis
US-10-156-761-11065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIRO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: SENOH, MIKHRO
APPLICANT: SENOH, MIKHRO
APPLICANT: IKED, MASATO
APPLICANT: IKED, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, UNN
APPLICANT: HORIKAWA, HIROSHI
                                                                                         TYPE: PRT
ORGANISM: Escherichia coli
US-09-815-242-10139
                                                                                                                                                                               Query Match 76.5
Best Local Similarity 83.3
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                       385 NAKTVT 390
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92 DARTLTE 98
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                                                                                                                                                                                                                                                                           1 NAKTLT 6
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US-10-156-761-11065
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   Length 447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Object, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILLE REPRENCE: ELITRA.011A
FILLE REPRENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
                                                               1; Indels
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Best Local Similarity 71.4%; Pred. No. 7.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels
Query Match
76.5%; Score 26; DB 11;
Best Local Similarity 71.4%; Pred. No. 6.9e+02;
Matches 5; Conservative 1; Mismatches 1
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PRIOR APPLICATION NUMBER: 06/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PASCSEQ for Windows Version 4.0
SEQ ID NO 12670
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Sequence 1093, Application US/0992217

Patent No. US20020076414A1

GENERAL INCRMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Lodes, Michael J.

APPLICANT: Secrist, Heather

APPLICANT: Benson, Darin R.

APPLICANT: Benson, Darin R.

APPLICANT: Meagher, Madeleine Joy

APPLICANT: Mang, Yuqiu

APPLICANT: Mang, Yuqiu

APPLICANT: Shid, Carole Lynn

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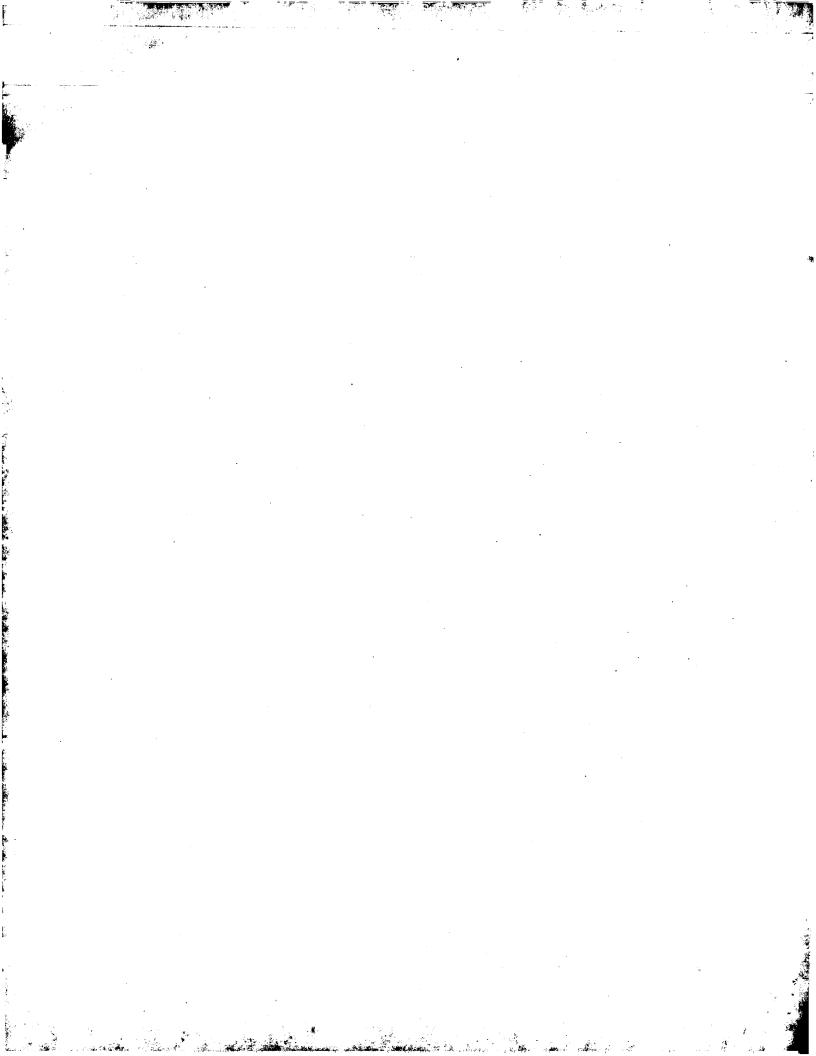
APPLICANT: Mang, Aijun

APPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 76.5
Best Local Similarity 71.4
Matches 5; Conservative
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Search completed: July 18, 2003, 15:35:57 Job time: 19.06.secs

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Gaps



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GenCore version 5.1.6
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OM protein - protein search, using sw model

July 18, 2003, 15:03:05; Search time 9.1 Seconds (without alignments) 73.950 Million cell updates/sec Run on:

US-10-007-790-9 1 NAKTLTE 7 Perfect score: Sequence:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 283224 segs, 96134422 residues Searched:

283224

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
-	31		149	. ~	AC1608	arqinine repressor
8	31	91.2	149	7	AG1245	
٣	29	ď.	62	~	PL0266	-
4	29	85.3	97	7	PH1068	Ig light chain V r
S	29	ů.	86	7	PH1069	g light
9	29	S	101	7	S20810	g kappa
7	29	85.3	106	N	B47329	g kappa chain V
ω	29	S	107	~	PL0080	g kappa
6	29	Ŋ	128	7	S31488	g kappa
10	29	S	211	П	WMBEMA	3.5K protein -
11	29	S	211	-	WMBEMB	. 5K
12	29	S	229	Н	MVECMH	ш
13	29	ß	229	7	H91089	methyl-directed mi
14	29	85.3	229	~	C85935	
15	29	ß	261	N	S72639	hypothetical prima
16	29	S	320	Н	S55244	polyubiquitin 4 -
17	29	ß	351	N	E84096	hypothetical prote
18	29	85.3	407	7	A34357	
19	29	S	407	~	S20304	
20	29	S	416	Ŕ	A99419	hypothetical prote
21	29	Ŋ.	468	~	F97482	
22	29	85.3	484	~	m	protein mel-32 [im
23	29	5.	491	N	-	a)
24	29	ů.	493	N	D98209	
25	29	δ.	493	~	AE3077	
56	29	δ.	494	~	AF2700	a)
27	29	δ.	502	7	617	probable glutamate
28	29	85.3	601	~	T38736	hypothetical prote
29	29	85.3	715	~	C70174	methyl-accepting c

ATP-dependent Clp	hypothetical prote	hypothetical prote	hypothetical prote	conserved hypothet	ribosomal protein	hypothetical prote	26K periplasmic im	periplasmic immuno	. probable echA10 pr	hypothetical prote	speract precursor	hypothetical prote	hypothetical prote	probable cinnamoyl	hypothetical prote
835908	T26774	F97868	A71852	E64663	S18714	H70691	B97619	AI2841	G70553	AG2414	A34543	T27593	T27594	E96792	E86880
7	7	7	~	~	~	~	7	7	7	~	0	7	7	7	7
763	1801	131	181	184	215	236	247	247	268	287	296	304	304	317	328
٣.	m	₹.	₫.	4.	4.	₹.	4.	4.	₫.	4.	4.	4.	4.	4.	4.
85	85	82.4	82.4	82	82	82	82.4	82	82	82.4	82	82.4	82.4	82	82
29	29	28	28	28	28	28	28	28	28	28	28	28	28	28	28
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: 6.5 Duchaud, E.; Duchaud, A.; Baquero, F.; Berche, P.; Bloecker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; D.; Lones 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Matok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Reference number: AB1077; MUID:21537279; PMID:11679669
AC1608
arginine repressor homolog lin1404 [imported] - Listeria innocua (strain Clip11262)
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                                                                                                                                                                                                                                                                                                                A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-149 <GLA>
A.Cross-references: GB.AL592022; PIDN:CAC96635.1; PID:g16413877; GSPDB:GN00178
A.Residuental source: strain Clipl1262
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C,Superfamily: Escherichia coli arginine repressor argR
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Pred. No. 12;
1; Mismatches
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Matches
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arginine repressor homolog lmo1367 [imported] - Listeria monocytogenes (strain EGD-e)

C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #text\_change 14-Dec-2001
C;Date: 27-Nov-2001 #text\_change 14-Dec-2001
C;Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 14-Dec-2001
C;Accession-Nov-2001
S;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; D.; Dominguez-Bernal, G.; Duchaud, E.; Mun, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat A;Authors: Kreft, J.; Kuhn, M.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AG1245
A;Status: preliminary
A;Molecule type: A;Acces: 1-149 cGLA>
A;Residues: 1-149 cGLA>
A;Cross-references: GB:NC\_003210; PIDN:CAC99445.1; PID:g16410783; GSPDB:GN00177

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Ig light chain V region (clone 185-c1) - mouse (fragment)
C.Species: Mus musculus (house mouse)
C.Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C.Accession: PH1069
R.Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 779. 1992
A.Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B Ct A.Reference number: PH0971; MUID:92381444; PMID:1512540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C)Accession: S20810

R)Hoogenboon, H.; Dubois, P.; Raus, J.; Volckaert, G.

Submitted to the EMBL Data Library, September 1990

A)Description: Nucleotide sequences of the variable region cDNAs encoding a murine antibor A)Reference number: S20809

A)Reference number: S20810

A)Reference number: Manary

A)Rolecule type: mRNA

A)Rolecule type: mRNA
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: B47329
R;Brinkmann, U.; Gallo, M.; Brinkmann, E.; Kunwar, S.; Pastan, I.
Proc. Natl. Acad. Sci. U.S.A. 90, 547-551, 1993
A;Title: A recombinant immunotoxin that is active on prostate cancer cells and that is A;Reference number: A47329; MUD:93133825; PMID:8421689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2003
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A;Residues: 1-106 <BRI>
A;Experimental source: Balb/c
A;Note: sequence modified after extraction from NCBI backbone
A;Note: sequence extracted from NCBI backbone (NCBIN:122874)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
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85.7%; Pred. No. 22;
iive 0; Mismatches
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Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-98 <TIL>
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-May-1997
C;Accession: PLO266
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic A;Accession: PLO26
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H1068
Ig light chain V region (clone $17.166) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1068
R;Tillan, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c A;Accession: PH1068
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A;Residues: 1-97 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]Fl
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
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                                                                                                                                                                                                         Length 149;
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               A,Experimental source: strain EGD-e
C,Genetics:
A,Gene: lmoll367
C,Superfamily: Escherichia coli arginine repressor argR
                                                                                                                                                                                                     Score 31; DB 2;
Pred. No. 12;
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Pred. No. 22;
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F:45-53/Region: complementarity-determining 3
F:54-62/Region: framework 4
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C; Keywords: immunoglobulin
F; 16-89/Domain: immunoglobulin homology <IMM>
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Pred. No.
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85.7%;
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85.7%;
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85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-62 <SHL>
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A;Note: host Gallus gallus (chicken)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 08-Apr-1994
C;Accession: J$0389
R;Ihara, T; Kato, T; Kato, Gdd, S.; Ishihama, A.; Hirai, K.
Nirus Genes 3, 127-140, 1989
A;Title: Comparison of the sequence of the secretory glycoprotein A (gA) gene between Md: A;Reference number: A22818; MUID:90142542; PMID:2559540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NyAlternate names: UL45h protein
C;Species: Marek's disease virus
A;Note: host Gallus gallus (chicken)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999
C;Accession: B22818; JQ2207
R;Ihara, T.; Kato, A.; Ueda, S.; Ishihama, A.; Hirai, K.
Nirus Gomparison of the sequence of the secretory glycoprotein A (gA) gene between Md:
A;Title: Comparison of the sequence of the protein A;Reference number: A22818; MUID:90142542; PMID:2559540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: B22818
A;Molecule type: DNA
A;Residues: 1-211 <IHA>
A;Residues: 1-211 <IHA>
A;Experimental source: strain Md5
B;Yanagida, N.; Yoshida, S.; Nazerian, K.; Lee, L.F.
J. Gen. Virol. 74, 1837-1845, 1993
A;Fitle: Nucleotide and predicted amino acid sequences of Marek's disease virus homologue
A;Reference number: JQ2199; MUID:93389438; PMID:8397281
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C;Species: Bscherichia coli
C;Species: Bscherichia coli
C;Species: Bscherichia coli
C;Species: Bscherichia coli
C;Spaces coli
C;Accession: H65065; A27506
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Status: preliminary; nucleic acid sequence not shown; translation not shown A, Molecule type: DNA A, Molecule type: DNA A, Residues: 1-229 < LLAT> A, Residues: 1-229 < LLAT> A, Residues: 1-229 < RESIDENS SERVICES: 1-289 < RESIDENS SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERVICES SERV
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A;Residues: 1-211 <YMN>
A;Residues: 1-211 <YMN>
A;Cross-references: GB:L10283; NID:g388703; PIDN:AAA03152.1; PID:g388710
A;Experimental source: strain GA
C;Superfamily: turkey herpesvirus 23.5K protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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Pred. No. 47;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
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Pred. No. 47;
0; Mismatches
                                                                                                                                                                                                                                                                                 A;Accession: JS0389
A;Molecule type: DNA
A;Residues: 1-211 <IHA>
C;Superfamily: turkey herpesvirus 23.5K protein
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Similarity 85.7%;
6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 NAKTLVE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 6; Conserv
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig kappa chain V region (E4) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 21-Jan-2000
C;Accession: PL0080
R;Meek, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.; Ca
A;Title: Structural characterization of antiidiotypic antibodies; evidence that Ab2s are
A;Reference number: PL0080; MUID:89094248; PMID:2492056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:X58596; GB:Y00794; NID:g51574; PIDN:CAA41471.1; PID:g938255
A;Experimental source: strain BALB/c
A;Note: 106-Leu is translated from the codon CUN
A;Note: the sequence shown here is from the V kappa region of an antiidiotypic monoclona
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig kappa chain precursor V region (F11) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S31488
R;Bespalov, I.A.; Shiyanov, P.A.; Lukashevich, L.V.; Lunev, V.E.; Tribush, S.S.; Gaponov abbmitted to the EMBL Data Library, December 1992
A;Reference number: S31488
A;Accession: S31488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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85.7%; Pred. No. 29;
.ive 0; Mismatches 1; Indels
                                                                                                                                Length 106;
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23.5K protein - Marek's disease virus (type 1, strain BC-1)
C;Species: Marek's disease virus
                                                                                                                                Score 29; DB 2;
Pred. No. 24;
0; Mismatches
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Pred. No. 24;
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                C;Keywords: heterotetramer; immunoglobulin F;16-90/Domain: immunoglobulin homology <IMM>
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85.7%;
                                                                                                                            Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                          50 NAKTLAE 56
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Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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A; Residues: 1-107 <MEE>
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"Specials: Thermoanaerobacterium thermosulfurigenes
C;Specials: Thermoanaerobacterium thermosulfurigenes
C;Specials: Thermoanaerobacterium thermosulfurigenes
C;Date: 29-uul-1997 #sequence_revision 29-Aug-1997 #text_change 08-Oct-1999
C;Accession: S72639
R;Matuschek, M.; Sahm, K.; Bahl, H.
R;Matuschek, M.; Sahm, K.; Bahl, H.
R;Matuschek, M.; Sahm, K.; Bahl, H.
R;Matuschek, M.; Sahm, K.; Bahl, H.
R;Matuschek, M.; Sahm, K.; Bahl, H.
R;Matuschek, M.; Sahm, K.; Bahl, H.
R;Matuschek, M.; Sahm, K.; Sahm, K.;
R;Matuschek, M.; Sahm, K.;
R;Matuschek, M.; Sahm, K.;
R;Matuschek, M.; Sahm, K.;
R;Matuschek, M.; Sahm, K.;
R;Satus: Preliminary
A;Residues: 1-261 *MAT>
A;Residues: 1-261 *MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:U50951; NID:g1542972; PIDN:AAB08043.1; PID:g1542976
C;Genetics:
A;Gene: sight
C;Superfamily: Lyme disease spirochete probable RNA polymerase sigma factor; transcriptic
F;30-255/Domain: transcription initiation factor sigma katF homology <KTF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dolyubiquitin 4 - Arabidopsis thaliana polyubiquitin 4 - Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S55244; S61069
C;Accession: S55244; S61069
B;Callis, J; Carpenter, T; Sun, C.W.; Vierstra, R.D.
A;Title: Structure and evolution of genes encoding polyubiquitin and ubiquitin-like protes A;Reference number: S55242; MUID:95229071; PMID:7713442
                                                                                                                                                                                                                                                                                                                                                                                                           - Thermoanaerobacterium thermosulfurigenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.3%; Score 29; DB 2; Length 261;
85.7%; Pred. No. 59;
ive 0; Mismatches 1; Indels
                                                                                        Length 229;
                                                                                                                                                  1; Indels
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A, Residues: 1-76' I', 78-111,'V',113-212,'M',214-320 «CAF»
A, Residues: 1-76' I', 78-111,'V',113-212,'M',214-320 «CAF»
A, Cross-references: BMB:L10536
C, Superfamily: polyubiquitin 4; ubiquitin homology
C, Keywords: nucleus; polyprotein; protein degradation
F, 1-76/Poomatin: ubiquitin homology «UBH1»
F, 77-152/Porduct: ubiquitin homology «UBH2»
F, 77-152/Porduct: ubiquitin homology «UBH2»
F, 77-152/Porduct: ubiquitin homology «UBH3»
F, 153-228/Poomatin: ubiquitin homology «UBH3»
F, 153-228/Poomatin: ubiquitin homology «UBH3»
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R;Callis, J.; Carpenter, T.; Sun, C.W.; Vierstra, R.D.
submitted to the EMBL Data Library, June 1995
                                                                                           ..
7
                                                                                                                                               0; Mismatches
                                                                                        Score 29;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical primary sigma factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 85.7-
6; Conservative
                                                                                     Query Match 85.3
Best Local Similarity 85.7
Matches 6; Conservative
                           C; Superfamily: mutator mutH
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A;Accession: S61069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217 NLKTLTE 223
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A;Residues: 1-320 <CAL>
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   A; Gene:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: C5593
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Mature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: GB:AE005174; NID:g12517320; PIDN:AAG57943.1; GSPDB:GN00145; UWGP:Z41; Skeperimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    methyl-directed mismatch repair [imported] - Escherichia coli (strain 0157:H7, substrain
                     Ricrafstrom, R.H.; Hoess, R.H.

Nucleic Acids Res. 15, 3073-3084, 1987

Airlie: Nucleotide sequence of the Escherichia coli muth gene.

Airlie: Nucleotide sequence of the Escherichia coli muth gene.

Airlie: Nucleotide sequence of the Escherichia coli muth gene.

Airlie: Nucleotide sequence of the Escherichia coli muth gene.

Airlie: Nucleotide sequence of the Escherichia coli muth gene.

Airlie: Nucleotide sequence of the Escherichia coli muth gene.

Airlie: Nucleotide sequence of the Codon CTG for residue 83 as Val

Cicomment: Two temperature-sensitive mutants have also been isolated and sequenced.
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A,Residues: 1-229 <HAY>
A,Cross-references: GB:BA000007; PIDN:BAB37111.1; PID:g13363160; GSPDB:GN00154
A,Experimental source: strain O157:H7, substrain RIMD 0509952
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Pred. No. 52;
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A; Experimental source: strain K-12, substrain MG1655
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C; Superfamily: mutator mutH
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A; Molecule type: DNA
A; Residues: 1-229 <STO>
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Matches 6; Conser
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A;Gene: mutH
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Matches
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A;Cross-references: GB:X62934; NID:g54206; PIDN:CAA44707.1; PID:g54207
R;Cook, G.A.; Elliott, D.; Metwali, A.; Blum, A.M.; Sandor, M.; Lynch, R.; Weinstock, J.N.
J. Immunol. 152, 1830-1835, 1994
A;Title: Molecular evidence that granuloma T lymphocytes in murine schistosomiasis mansor A;Reference number: 156216; MUID:94165478; PMID:8120392
A;Reference 156216
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R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-V John J.; Chan-V John J.; Lagan, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P. surett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
                                                                                                                                                                                                                                                                                                                                                                       NiAlternate names: NK-1 receptor; substance P receptor C;species: Mus musculus (house mouse)
C;species: Mus musculus (house mouse)
C;date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 02-Jun-2000
C;Accession: $20304; I56216; T73044
R;Sundelin, J.B.; Provvedini, D.M.; Wahlestedt, C.R.; Laurell, H.; Pohl, J.S.; Peterson, Bur. J. Bolochen. 203, 625-631, 1992
A;Title: Molecular cloning of the murine substance K and substance P receptor genes. A;Reference number: $20303; MUID:92137253; PMID:1370937
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C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001
                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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A;Experimental source: tissue granuloma
C;Superfamily: neurokinin 1 receptor
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 63-290 <COO1>
A;Cross-references: GB:L27826; NID:g450286; PIDN:AAA17891.1; PID:g480776
A;Experimental source: tissue brain
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                                Length 407;
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                                                                                      0; Indels
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A; Accession: A99419
A; Status; preliminary
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                             Score 29; DB:
Pred. No. 92;
2; Mismatches
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Pred. No.
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71.4%;
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                                                                                      Conservative
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                             Query Match
Best Local Similarity
Matches 5; Conserv
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A;Molecule type: mRNA
A;Residues: 1-407 <SUN>
                                                                                                                                               1 NAKTLTE 7
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                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: E84096
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BAB07292.1; GSPDB:GN00
A;Experimental source: strain C-125
C;Genetics:
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SiYokota, Y.; Sasai, Y.; Tanaka, K.; Fujiwara, T.; Tsuchida, K.; Shigemoto, R.; Kakizuka
J. Biol. Chem. 264, 17649-17652, 1989
A;Title: Molecular characterization of a functional cDNA for rat substance P receptor.
A;Reference number: A34357; MUID:90036822; PMID:2478537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 19-May-2000
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 19-May-2000
C;Accession: A38692; A34357; A40089
R;Hershey, A.D.; Dykema, P.E.; Krause, J.E.
J. Biol. Chem. 266, 4366-4374, 1991
A;Title: Organization, structure, and expression of the gene encoding the rat substance A;Reference number: A38692; MUID:91154239; PMID:1705552
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                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein BH3573 [imported] - Bacillus halodurans (strain C-125)
                                                                                                                 Gaps
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C;Keywords: G protein-coupled receptor; glycoprotein; membrane protein
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                                                        Score 29; DB 1; Length 320;
Pred. No. 72;
                                                                                                                 Indels
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N;Alternate names: NK-1 receptor; substance P receptor
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Pred. No. 79;
                                                                                                                 1; Mismatches
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A;Cross-references: GB:M31477
F;229-305/Domain: ubiquitin homology <UBH4>
                                                     85.3%;
                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Hershey, A.D.; Krause, J.E. Science 247, 958-962, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NASTLTE 116
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HAKTLTE 10
                                                                                Best Local Similarity
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A; Residues: 1-407 < YOK>
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Best Local Similarity
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Molecule type: DNA
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                                                        Query Match
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Matches

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C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002
C;Accession: AH3416
E;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, P.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessc Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens; A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aldehyde dehydrogenase dhas [imported] - Agrobacterium tumefaciens (strain CS8, Cereon)
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Accession: D98209
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume A;Reference number: A97359; PMID:11743194
A;Accession: D98209
A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: GB:AE007870; PIDN:AAK89198.1; PID:g15159016; GSPDB:GN00170
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C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
C;Accession: AB3077
C;Accession: AB3077
C;Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClelle; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aldehyde dehydrogenase dhaS [imported] - Agrobacterium tumefaciens (strain CS8, Dupont)
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A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:11743193
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A;Experimental source: strain 16M
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A;Map position: linear chromosome
C;Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology
   nucleosidase (EC 3.2.2.4) [imported] - Brucella melitensis (strain 16M)
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Pred. No. 1.1e+02;
0; Mismatches 1; Indels
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85.3%; Score 29; DB 2; Length 491

Best Local Similarity 71.4%; Pred. No. 1.1e+02;

Matches 5; Conservative 2; Mismatches 0; Indels
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C;Keywords: glycosidase; hydrolase
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Best Local Similarity 85.7%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                            A Status: preliminary
A Molecule type: DNA
A, Residues: 1-491 < KUR>
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C.Accession: B88483
R.Anconymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A.Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A.Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A.Reference number: A75000; MUID:99069613; PMID:9851916
A.Note: see websites genome wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele A.Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                                                                                                                         amp nucleosidase [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C;Species: Agrobacterium tumefaciens
C;Species: 30-5ep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C;Accession: F97482
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
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A;Cross-references: GB:chr III; PIDN:AAB53830.1; PID:g485099; GSPDB:GN00021; CESP:mel-32
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A;Molecule type: DNA
A;Residues: 1-468 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK86815.1; PID:g15156023; GSPDB:GN00169
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Species: Caenorhabditis elegans
Bate: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
                                                                                                                             Gaps
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0
                                                          Score 29; DB 2; Length 416;
Pred. No. 94;
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Pred. No. 1.1e+02;
0; Mismatches 1; Indels
                                                                                                                          Indels
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C;Species: Caenorhabditia בחריבים
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                                                                                                                       1; Mismatches
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;Superfamily: glycine hydroxymethyltransferase
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A,Map position: circular chromosome
C;Superfamily: aconitate hydratase
                                                          85.3%;
ilarity 85.7%;
Conservative
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Best Local Similarity 71.4%;
Matches 5; Conservative
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Best Local Similarity 85.7%;
Matches 6; Conservative
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NAKTITD 272
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                                                                                Local Similarity
                                                                                                                                                                                                                        SAKTLTE 9
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Status: preliminary
Molecule type: DNA
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A; Map position:
C; Superfamily: c
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                                                                Query Match
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ò 셤 Genetics:

RESULT 23 AH3416

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methyl-accepting chemotaxis protein (mcp-2) homolog - Lyme disease spirochete C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999
C;Acceson. C70174
S;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Bowman, C.; Garland, S.; Fujli, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Authors: Smith, H.O.; Venter, J.C.
A;Aitle: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Accession: C70174
A;Ateference number: A70100; MUID:98065943; PMID:9403685
A;Accession: C70174
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-715 < KLE>
A;Accession: C70174
A;Residues: 1-715 < KLE>
A;Esterences: GB:AED01161; GB:AE000783; NID:g2688515; PIDN:AAC66955.1; PID:g268852; A;Experimental source: strain B31
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                                                                                                                                                                                                                                              Pypothetical protein SPAC3H1.04c - fission yeast (Schizosaccharomyces pombe)
Cispecies: Schizosaccharomyces pombe
Cipate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
CiAccession: T38736
RiGentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
A;Reference number: 221808
A;Reference number: 221808
A;Reference number: 221808
A;Reference number: 221808
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-601 <GEN>
A;Residues: 1-601 <GEN>
A;Residues: 1-601 <GEN>
A;Resperimental source: strain 972h-; cosmid c3H1
C;Genetics: Care
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Pred. No. 1.6e+02;
0; Mismatches 1; Indels
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Best Local Similarity 85.7%;
Matches 6; Conservative (
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Best Local Similarity 100
Matches 6; Conservative
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                                                                                                 351 NAKVĽTE 357
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A,Map position: 1
A,Introns: 549/3
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                                       NAKTLTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMP nucleosidase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C;Accession: AF2700
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I. Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A.Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable glutamate decarboxylase - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 28-May-1999
C;Accession: S6177
R;Callego, P.P.; Whotton, L.; Picton, S.; Grierson, D.; Gray, J.E.
Plant Mol. Biol. 27, 1143-1151, 1995
A;Title: A role for glutamate decarboxylase during tomato ripening: the characterisation
A;Reference number: S56177; MUID:95284363; PMID:7766895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; PMID:11743193
A,Accession: AF2700
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                                                                                                                        A;Cross-references: GB:AE008689; PIDN:AAL45035.1; PID:g17742698; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
C;Genetics:
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A;Cross-references: GB:AE008688; PIDN:AAL42020.1; PID:g17739395; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                      C;Genetics:
A;Gene: dhaS
A;Map position: linear chromosome
C;Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology
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                                                                                                                                                                                                                                                                                                                                                   Length 493
                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
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Best Local Similarity 71.4
Matches 5; Conservative
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292 NAKTITD 298
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A;Accession: AE3077
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-493 <KUR>
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Best Local Similarity
Matches 6; Conserv
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A; Residues: 1-502 <GAL>
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A;Gene: amn
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FiAIm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; J Nature 397, 176-180, 1999
Affitle: Genomic sequence comparison of two unrelated isolates of the human gastric patht A;Reference number: A71800; MUID:99120557; PMID:9923682
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A, Status: pyeliminary
A, Molecule type: DNA
A, Residues: 1-181 <ARN>
A, Residues: GB: AE001535, GB: AE001439; NID: G4155664; PIDN: AAD06656.1; PID: G415567(
A, Experimental source: strain J99
C, Genetics:
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C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Accession: E64663

R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne)
Son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.h A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: E64663
A;Satus: preliminary; nucleic acid sequence not shown; translation not shown
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C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 13-Aug-1999
C;Accession: S18714; S25569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Variety: strain J99
C,Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
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Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein jhp1076 - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
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Score 28; DB;
Pred. No. 50;
1; Mismatches
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Pred. No. 69;
0; Mismatches
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82.48;
71.48;
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Query Match 82.4
Best Local Similarity 71.4
Matches 5; Conservative
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14 NGKTITE 20
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Matches 6; Conserv
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Matches 6; Conserv
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C; Superfamily: endopeptidase Clp ATP-binding chain
C; Superfamily: endopeptidase Clp ATP-binding chain
C; Superfamily: endopeptidase; molecular chaperone; nucleotide binding; P-loop; serine prot
F; Reynords: ATP, hydrolase; moleculae-binding motif B
F; 248-253/Region: nucleotide-binding motif B
F; F; 11-518/Region: nucleotide-binding motif A (P-loop)
F; 580-585/Region: nucleotide-binding motif B
F; 180-781 Region: nucleotide-binding motif R
F; 180-781 Region: nucleotide-binding motif R
F; 180-781 Region: nucleotide-binding motif R
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C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001
C;Datession: F97868
R;Ogata, H; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Rc Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
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A,Molecule type: DNA
A,Residues: 1-1801 «MIL»
A,Cross-references: EMBL:AL032634; PIDN:CAB54418.1; GSPDB:GN00019; CESP:Y39G8C.b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein RC1350 [imported] - Rickettsia conorii (strain Malish 7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
Accession: T26774
                                                                                                                                                  A;Cross-references: EMBL:X62333; NID:g296463; PIDN:CAA44207.1; PID:g296464
C;Genetics:
A;Gene: clpL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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85.7%; Pred. No. 4.2e+02;
tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 763;
A; Reference number: S35907; MUID: 93247497; PMID: 8387149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein Y39G8C.b - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 29; DB 2; I
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ubmitted to the EMBL Data Library, October 1998
Reference number: 220263
Accession: T26774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 85.3
Best Local Similarity 85.7
Matches 6; Conservative
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Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         565 NANTLTE 571
                                    A;Accession: S35908
A;Molecule type: DNA
A;Residues: 1-763 <HUA>
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Residues: 1-131 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession: F97868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Map position:
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A,Gene: RC1350
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C;Accession: A12841
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClelli ; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cybecies: Mycobacterium tuberculosis (strain H37RV)
Cybecies: Mycobacterium tuberculosis
Cybecies: Mycobacterium tuberculosis
Cybecies: Mycobacterium tuberculosis
Cybecies: Mycobacterium tuberculosis
Cybecesion: G70553
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Huthors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome & A;Reference number: A7050; MuID:98295987; PMID:9634230
A;Reference number: A7050; MuID:98295987; PMID:9634230
A;Reference number: Droin in Shown
A;Molecule type: DNA
A;Residues: 1-268 <COL>
                                                                                     A;Title: Genome Sequence of the plant Pathogen and Biotechnology Agent Agrobacterium tume A;Fitle: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume A;Reference number: A97359; PMID:11743194
A;Recession: B97619
A;Residues: 1-247 <KUR>
A;Residues: 1-247 <KUR>
A;Residues: 1-247 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK87907.1; PID:g15157303; GSPDB:GN00169
C;Genetics: A;Recession: Chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  periplasmic immunogenic protein [imported] - Agrobacterium tumefaciens (strain C58, Dupor
   R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
A;Reference number: AB2277; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Reaiduea: 1-247 «KUR»
A;Cross-references: GB:AE008688; PIDN:AAL43151.1; PID:g17740627; GSPDB:GN00186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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100.0%; Pred. No.....
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.4%; Score 28; DB 7 100.0%; Pred. No. 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Experimental source: strain C58 (Dupont)
C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Gene: pp26
A, Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 82.4
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 AKTLTE 188
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A, Status: preliminary
A, Molecule type: DNA
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Matches
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A; Cross-references: EMBL:X60305; NID:958408; PIDN:CAA42850.1; PID:958413
A; Cross-references: EMBL:X60305; NID:958408; PIDN:CAA42850.1; PID:958413
A; Cross-references: EMBL:X60305; NID:958408; PIDN:CAA42850.1; PID:958413
A; Cross-references: DSM 2476
A; Cross-reference was submitted to the EMBL Data Library, September 1991
B; Klenk, H.P.; Schwass, V.; Lottspeich, F.; Zillig, W.
Nucleic Acids Res. 20, 4659, 1992
A; Klenk, H.P.; Schwass, V.; Lottspeich, F.; Zillig, W.
A; Keference number: 825562; MUID:93027167; PMID:1408768
A; Accession: 825569
R,Klenk, H.P.; Schwass, V.; Zillig, W. Nucleic Acids Res. 19, 6047, 1991
A,Title: Nucleotide sequence of the genes encoding the L30, S12 and S7 equivalent ribosc
A,Reference number: S18710; MUID:92051399; PMID:1840672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein Rv2821c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-010-1998 #sequence_revision 17-Ju1-1998 #text_change 20-Jun-2000
C;Accession: H70691
R;Collor, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature: 393, 537-544, 1998
A;Authors: Sqares, R.; Sulscon, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Rieference numbering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
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A;Cross-references: GB:Z81331; GB:AL123456; NID:G3261650; PIDN:CAB03665.1; PID:G1648899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B97619
26K periplasmic immunogenic protein precursor (28K outer membrane protein) AGR_C_3922
C;Species: Agrobacterium tumefaciens
C;Species: 30-8ep-2001 #sequence_revision 30-8ep-2001 #text_change 11-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-197,'S',199-213,'RA' <KLE2>
A;Cross-references: EMBL:X67313; NID:g48138; PIDN:CAA47728.1; PID:g48146
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
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                                                                                                                                    A,Accession: $18714
A,Status: nucleic acid sequence not shown; translation not shown
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C;Superfamily: Escherichia coli ribosomal protein S7
C;Keywords: protein biosynthesis; ribosome
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82;
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100.0%; Pred. No. >...
0; Mismatches
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C;Superfamily: hypothetical protein MJ1669
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Best Local Similarity 100.
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Best Local Similarity
Matches 6; Conserv
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RESULT 37

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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. B, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; WUID:21595285; PMID:11759840
A;Cross-references: GB:29584; GB:AL123456; NID:g3261774; PIDN:CAB09030.1; PID:g2117180 A;Experimental source: strain H37Rv C;Genetics: C;Genetics: A;Gene: echalo C;Superfamily: naphthoate synthase; enoyl-CoA hydratase homology E;35-187/Domain: enoyl-CoA hydratase homology <ECH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 40

Ag2414

hypothetical protein all4871 [imported] - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp.

A)Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002

C;Accession: AG2414
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-287 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB76570.1; PID:g17134008; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all4871
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Pred. No. 1e+02;
0; Mismatches 1; Indels
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Matches 6; Conservative
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Search completed: July 18, 2003, 15:10:46 Job time : 10:1 secs

223 NAKRLTE 229

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SEQUENCE OF 63-290 FROM N.A.
STRAIN=CBA; TISSUE=T-cell, and Brain;
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[1]
SEQUENCE FROM N.A.
MEDLINE=90142542; PubMed=2559540;
MEDLINE=90142542; PubMed S., Ishihama A., Hirai K.;
"Comparison of the sequence of the secretory glycoprotein A (gA) gene in Md5 and BC-1 strains of Marek's disease virus type 1.";
Virus Genes 3:127-140(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                              SEQUENCE FROM N.A.
MEDLINE=93389438; PubMed=8397281;
Yanagida N., Yoshida S., Nazerian K., Lee L.F.;
Yanagida n., Yoshida S., Nazerian K., Lee L.F.;
"Nucleotide and predicted amino acid sequences of Marek's disease
"Nucleotide and predictes amplax virus major tegument proteins.";
J. Gen. Virol. 74:1837-1845(1993).
-: SIMILARITY: BELONGS TO THE UL45 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97426617; PubMed=9278503; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Bscherichia.
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                                                                                                                                                                                                                                                                                                                                                                                               Score 29; DB 1; Length 211;
Pred. No. 19;
0; Mismatches 1; Indels
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"Nucleotide sequence of the Escherichia coli mutH gene.";
Nucleic Acids Res. 15:3073-3084(1987).
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Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                    23507 MW; FFDF3AA525AE38E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1988 (Rel. 06, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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REVISIONS TO 82; 129-130 AND 135.
STRAIN=K12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=87174827; PubMed=3031619;
                                                                                                                                                                                                                                                                                                                       PIR; B22818; WMBEMB.
PIR; JQ2207; JQ2207.
InterPro; IPR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                 85.3%;
                                                                                                                                                                                                                                                                                                EMBL; D90001; BAA14053.1; -. EMBL; L10283; AAA03152.1; -.
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SEQUENCE 211 AA; 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli
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P06722;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR004230; MutH.
Pfam; PF02976; MutH; 1.
DNA repair; Hydrolase; Endonuclease; 3D-structure; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                          relationship of Muth to restriction endonucleases.";
EMBO J. 17:1526-1534 [1998).
-!- FUNCTION: SEQUENCE-SPECIFIC ENDONUCLEASE THAT CLEAVES UNMETHYLAT
GATC SEQUENCES. IT IS INVOLVED IN DNA MISMATCH REPAIR.
-!- MISCELLANEOUS: TWO INDEPENDENTLY ISOLATED TEMPERATURE SENSITIVE
ALLELES OF THE MUTH GENE HAVE BEEN SEQUENCED (TS AND TS28).
                                                                                                                                                                                                  mismatch repair and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Sundelin J.B., Provvedini D.M., Wahlestedt C.R., Laurell H.,
Pohl J.S., Peterson P.A.;
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Pred. No. 21;
"The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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D -> N (IN TS28).
; 1F21EED4BB1A97A1 CRC64;
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                                                                                                                                                                Ban C., Yang W., "Structural basis for MutH activation in E.coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                  X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS)
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EMBL; U16361; AAB59986.1; -.
EMBL; U29581; AAB40478.1; -.
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                                                                                                                                     MEDLINE=98151376; PubMed=9482749;
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228 AA; 25396 MW;
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85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EcoGene; EG10624; mutH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDB; 1AZO; 20-MAY-98.
PDB; 2AZO; 20-MAY-98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188 NAKALTÉ 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A27506; MVECMH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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Substance-P receptor (SPR) (NK-1 receptor) (NK-1R)
              TAC1R.
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TRANSMEM
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   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                -!- FUNCTION: THIS IS A RECEPTOR FOR THE TACHYKININ NEUROPEPTIDE SUBSTANCE P. IT IS PROBABLY ASSOCIATED WITH G PROTEINS THAT ACTIVATE A PHOSPHAIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.-: SUBCELLULAR LOCATION: Integral membrane protein.-: MISCELLULAR LOCATION: Integral membrane protein.-: THE RANK ORDER OF AFFINITY OF THIS RECEPTOR TO TACHYKININS IS: SUBSTANCE P. SUBSTANCE K. NEUROMEDIN K. -: SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. HIGHEST TO OTHER TACHYKININS RECEPTORS.
MEDLINE=94165478; PubMed=8120392; Cook G.A., Elliott D., Metwali A., Blum A.M., Sandor M., Lynch R. Weinstock J.V.; Medistock J.V.; Molecular evidence that granuloma T lymphocytes in murine schistosomiasis mansoni express an authentic substance P (NK-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (CYTORLASMIC N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                  EMBL; X62934; CAA44707.1; -...
EMBL; L27828; AAA17892.1; -...
EMBL; L27826; AAA17892.1; -...
EMBL; L27826; AAA17891.1; -...
PIR; S20304; S20304.
MGD; MG1:98475; Tacri.
InterPro; IPR000276; GPCR_Rhodpsn.
Refan; PP00001; 7tm 1; 1.
PRINTS; PR00237; GPCRHODOPSN.
RPROSITE; PS50227; GPROTEIN_RECEP_F1_2; 1.
RPROSITE; PS50227; GPROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmenbrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85.3%; Score 29; DB 1; Length 407; 71.4%; Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                 Phosphorylation, Lipoprotein, Palmitate.
DOMAIN 1 31 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL) 5 (POTENTIAL).
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451B6D475A6659A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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(Rel. 14, Last sequence update)
(Rel. 36, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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P14600;
01-APR-1990 (1
01-APR-1990 (1
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TRANSMEM
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TRANSMEM
DOMAIN
                                                          receptor.
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Matches
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NKIR RAT
ID NKIR
AC P146
DT 01-A
DT 01-A
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                                                                                                                                                                                                      MEDLINE=91154239; PubMed=1705552;
Hershey A.D., Dykema P.E., Krause J.E.;
"Organization, structure, and expression of the gene encoding the rat
                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=90036822; PubMed=2478537;
Yokota Y., Saeai Y., Tanaka K., Fujiwara T., Tsuchida K.,
Shigemoto R., Kakizuka A., Ohkubo H., Nakanishi S.;
"Molecular characterization of a functional cDNA for rat substance P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.

- FUNCTION: THIS TA RECEPTOR FOR THE TACHYKININ NEUROPEPTIDE STUBSTANCE P. IT IS PROBABLY ASSOCIATED WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.-SUBCELLULAR LOCATION: Integral membrane protein.

- SUBCELLULAR LOCATION: Integral membrane protein.

- MISCELLANEOUS: THE RANK ORDER OF AFFINITY OF THIS RECEPTOR TO TACHYKININS IS: SUBSTANCE P. SUBSTANCE K. NEUROMBDIN K.

- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

HIGHEST TO OTHER TACHYKININS RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hershey A.D., Krause J.E.;
"Molecular characterization of a functional cDNA encoding the rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITÉ; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Phosphorylation; Lipoprotein; Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      z (FOIENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor.";
J. Biol. Chem. 264:17649-17652(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                    substance P receptor.";
J. Biol. Chem. 266:4366-4374(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-Sprague-Dawley;
MEDLINE-90161991; PubMed=2154852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M64236; AAA42176.1; -.
EMBL; M64222; AAA42176.1; JOINED.
EMBL; M64233; AAA42176.1; JOINED.
EMBL; M64234; AAA42176.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M64234; AAA42176.1; JOINED.
EMBL; M64235; AAA42176.1; JOINED.
EMBL; JO5097; AAA42175.1; -.
EMBL; M31477; AAB59726.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00001; 7tm 1; 1. PRINTS; PR00237; GPCRRHODOPSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       substance P receptor.";
Science 247:958-962(1990)
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31
54
64
86
106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR, A34357; A34357.
PIR, A38692; A38692.
PIR, A40089; A40089.
                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REVISION TO 213.
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InterPro; IPR001030; Aconitase N.

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE 5202 / DSM 1617 / P2;

MEDLINE-2132295; PubMed=11427726;

She O., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

A Meors A.J. Erauso G., Fletcher C., Gordon P.M.K.,

Thi-Ngoc H.P., Redder P., Schen C., Kozera C.J. Medin N., Peng X.,

Thi-Ngoc H.P., Redder P., Schen K.E., Theriault C., Tolstrup N.,

Charlebois R.L., Doolittle W.F., Duguet M., Gassterland T.,

Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";

Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).

I. FUNCTION: Catalyzes the isomerization between 2-isopropylmalate

and 3-isopropylmalate, via the formation of 2-isopropylmaleate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- SUBUNIT: Heterodimer of leuC and leuD (By similarity).
-!- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY. LEUC 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sulfolobus solfataricus.
Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 29; DB 1; Length 407;
Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)
18opropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
PALMITATE (POTENTIAL).
N -> D (IN REF. 3).
ADF885A0BF55IC96 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2)0 = 2-
                           CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                             S (FOIENIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                 (POTENTIAL)
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                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                     7 (POTENTIAL)
CYTOPLASMIC (
3 (POTENTIAL)
                                                                                                                                                  CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       097VZ;
15-UNN-2002 (Rel. 41, Created)
15-UNN-2002 (Rel. 41, Last seq
15-UNN-2002 (Rel. 41, Last and
                                                                                                                                                                                                                                                                                                                                                                                                                                               46366 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.3%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  391 NSKTMTE 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
LEU2_SULSO
AC 097V72;
DT 15-JUN-2002
DT 15-JUN-2002
DT 15-JUN-2002
DT 15-JUN-2002
DE 3-isopropylma
GN 15-JUN-2002
DE 3-isopropylma
GN 201folobus:
OX MCBI_TAXID=2
RN ARJECTOR A:
RA ARAYEZ M.J.
RA ARAYEZ M.J.
RA Heikampo-de J.
RA ARAYEZ M.J.
RA Heikampo-de J.
RA GARTELL R.A:
RA GARTELL R.A:
RA GARTELL R.A:
RA GARTELL R.A:
RA GARTELL R.A:
RA GARTELL R.A:
RA GARTELL R.A:
RA GARTELL R.A:
RA GARTELL R.A:
RA GARTELL R.A:
RA GARTELL R.A:
CC T.I. CATALYTI
CC I. CATALYTI
CC I. CATALYTI
CC I. SUBUNIT:
CC II. SIMILARI
CC This SWISS-I
CC DELWEEN IN MCC THE EUROPEAN
CC HE EUROPEAN
CC GENERAL S.
CC HE EUROPEAN
CC GROWELL S.
CC GROWELL S.
CC GROWELL S.
CC GROWELL S.
CC GROWELL S.
CC GROWELL S.
CC CT.I. SUBLIARI
CC CT.I. SUBLIARI
CC CT.I. SUBLIARI
CC CT.I. SUBLIARI
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EMBL; AE006845; AAK42608.1; -.

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SEQUENCE FROM N.A.

STRAIN=cv. Ailsa Craig; TISSUE=Pericarp;

MEDLINE=95284365; PubMed=7766855;

Mallogo P.P., Whotton L., Picton S., Grierson D., Gray J.E.;

Mallogo P.P., Motton L., Picton S., Grierson D., Gray J.E.;

"A role for glutamate decarboxylase during tomato ripening: the characterisation of a cDNA encoding a putative glutamate decarboxylase with a calmodulin-binding site.";

Tacatotisation of a cDNA encoding a putative glutamate of STALYZES THE PRODUCTION OF GABA. THE CALMODULIN-BINDING CO.!- FUNCTION: CATALYZES THE PRODUCTION OF GABA. THE CALMODULIN-BINDING CO.!- FUNCTION: PROPER CO. CORTROL OF GABA

BIOSYNTHESIS (BY SIMILARITY).

--- CATALYTIC ACTIVITY: L-glutamate = 4-aminobutanoate + CO(2).

--- CATALYTIC ACTIVITY: L-glutamate = COFACTOR: PYRIDOXAL PHOSPHATE.

--- COFACTOR: PYRIDOXAL PHOSPHATE.

--- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND).

TYRDC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                             Complete proteome.
(BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR002129; Pyridoxal_deC.
PREM: PF00282; pyridoxal_deC; I.
PROSITE; PS00392; DDC_GAD HDC. YDC; FALSE NEG.
Lyase, Decarboxylase; Pyridoxal phosphate; Calmodulin-binding.
Lyase, Decarboxylase; Pyridoxal phosphate; Calmodulin-binding.
PYRIDOXAL PROSPHATE (BY SIMILARITY).
CALMODULIN-BINDING (BY SIMILARITY).
SEQUENCE 502 AA; 56785 MW; LC5F9BD0084272A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
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Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                       Score 29; DB 1; Length 416;
Pred. No. 38;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                   45253 MW; 5A342E12C6B8B796 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Glutamate decarboxylase (EC 4.1.1.15) (GAD) (ERT DI).
Lycopersicon esculentum (Tomato).
                                                                                      PRODUCTION PRODUCTION TO THE PROSTUE; PSO1450; ACONITASE 1; FALSE NEG. PROSTUE; PSO1244; ACONITASE 2; PALSE NEG. Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S; METAL 299 1295 IRON-SULFUR (4FE-4S)
                                                                                                                                                                                                                                                              (4FE-4S)
(4FE-4S)
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85.7%; Pred. No. 46;
ive 0; Mismatches
                                                                                                                                                                                                                                                              IRON-SULFUR
IRON-SULFUR
                                                                                                                                                                                                                                                                                                                                                                                                 85.3%;
85.7%;
                    Pfam; PF00330; aconitase; PRINTS; PR00415; ACONITASE. ProDom; PD000511; Aconitase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
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                                                                                                                                                                                                                                                                                                    360
                                                                                                                                                                                                                                                                                                                                416 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DCE_LYCES
P54767;
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                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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DCE_LYCES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      601 AA; 69428 MW; 8E2857C8A35DB72E CRC64;
                                                                                                                                                                             Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes, Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
ATP-dependent protease ATP-binding subunit clpL.
CLPL.
                                                                                               Hypothetical protein C3H1.04c in chromosome I SPAC3H1.04C.
                           (Rel. 33, Created)
(Rel. 33, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              763 AA
                                                                                                                                                          pombe (Fission yeast)
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                                                                                                                                                          Schizosaccharomyces
                                                                                                                                                                                                                                      Schizosaccharomyces.
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Best Local Similarity
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                        01-FEB-1996 (
01-FEB-1996 (
15-JUN-2002 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical
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CLPL_LACLA
ID _CLPL_LACLA
AC Q06716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                        GLYC_CAEEL STANDARD; PRT; 507 AA.
P50432; Q95QXB;
01-COT-1996 (Rel. 34, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
Serine hydroxymethyltransferase (EC 2.1.2.1) (Serine methylase)
GLY-ine hydroxymethyltransferase) (SHMT) (Glycosylation related 1).
GLY-1 OR MEL-32 OR C55D11.11.
Caenorhabditis elegans.
NAPARANA NEMBATANA Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBDATT: HOWOTETRAMER (BY SIMILARITY).
-!- ALTERNATIVE PRODUCTS: 2 isoforms, a and b (shown here); may be produced by alternative splicing.
-!- SIMILARITY: BELONGS TO THE SHMT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PYRIDOXAL PHOSPHATE (BY SIMILARITY). MISSING (IN ISOFORM A). 693B380E77BB07DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INTERCONVERSION OF SERINE AND GLYCINE.
-!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + glycine H(2)O = tetrahydrofolate + L-serine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
-!- PATHWAY: KEY ENZYME IN THE BIOSYNTHESIS OF PURINES, LIPIDS, HORMONES AND OTHER COMPONENTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Pred. No. 46;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00464; SHWT; 1.
PROSITE; PS00096; SHWT; 1.
Transferase; Pyridoxal phosphate; One-carbon metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wormbep; C05D11.11a; CE01130.
WormPep; C05D11.11b; CE29661.
InterPro; IPR001085; Gly_HyMetransf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3, AND ALTERNATIVE SPLICING.
R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 23 M
507 AA; 55764 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U00048; AAB53830.1; -. EMBL; U00048; AAL27228.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85.3%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       359 NAKTLAE 365
                                                   351 NAKVLTE 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P07511; 1CJ0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=Bristol N2;
NAKTLTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 NAKTLTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YAN4_SCHPO
ID YAN4_SCHPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                               the birdprent profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                     FUNCTION: ESSENTIAL FOR EFFICIENT PROCESSING OF 165 RRNA. PROBABLY PART OF THE 30S SUBUNIT PRIOR TO OR DURING THE FINAL STEP IN THE PROCESSING OF 165 FREE 30S RIBOSOMAL SUBUNITS. IT COULD BE SOME ACCESSORY PROTEIN NEEDED FOR EFFICIENT ASSEMBLY OF THE 30S SUBUNIT. RIMM IS NEEDED IN A STEP PRIOR TO RBFA DURING THE MATURATION OF 165 RRNA. HAS AFFINITY FOR FREE RIBOSOMAL 30S SUBUNITS BUT NOT FOR 70S RIBOSOMES (BY SIMILARITY). SIDILARITY: BELONGS TO THE RIMM FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pylori.";
Nature 388:539-547(1997).

-I FUNCTION: ESSENTIAL FOR EFFICIENT PROCESSING OF 16S RRNA. PROBABLY
PART OF THE 30S SUBUNIT PRIOR TO OR DURING THE FINAL STEP IN THE
PROCESSING OF 16S FREE 30S RIBOSOMAL SUBUNITS. IT COULD BE SOME
ACCESSORY PROTEIN NEEDED FOR EFFICIENT ASSEMBLY OF THE 30S
SUBUNIT. RIMM IS NEEDED IN A STEP PRIOR TO REFA DURING THE
MATURATION OF 16S RRNA. HAS AFFINITY FOR FREE RIBOSOMAL 30S
SUBUNITS BUT NOT FOR 70S RIBOSOMES (BY SIMILARITY).

-1- SUBCELLULAR LOCATION: CYCOPIDASMIC (POCENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=26695 / Arcc 700392;
MEDLINE=97394467; PubMed=9252185;
MEDLINE=97394467; PubMed=9252185;
MTomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
McKenney K., Firzecrald L.M., Lee N., Adams M.D., Hickey E.K.,
Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
Cotton M.D., Weidman J.M., Pujii C., Bowman C., Watthey L., Wallin E.,
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 28; DB 1; Length 181;
Pred. No. 28;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rRNA processing; Complete proteome.
SEQUENCE 181 AA; 20395 MW; DE56382F515B1E4A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
17-OCT-2001 (Rel. 40, Last annotation update)
18-OCT-2009ble 165 rRNA processing protein rimM.
18-OCT-2009ble 165 rRNA PINGENA PROCESSING PROFESSING PROFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 AA
                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE001535; AAD06656.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.4%;
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Pfam; PF01782; RimM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173 NAKTLLE 179
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIMM HELPY
025767;
     Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                          Plasmid pUCL22.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                           MOI. Microbiol. 7:957-965(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                   Huang D.C., Huang X.F., Novel G., Novel M.;
"Two genes present on a transposon-like structure in Lactococcus
lactis are involved in a Clp-family proteolytic activity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
0
                                                                                                                                                                                                                                                                                                                                                                                       85.3%; Score 29; DB 1; Length 763; 85.7%; Pred. No. 70;
  Lactococcus lactis (subsp. lactis) (Streptococcus lactis)
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ATP (POTENTIAL).
ATP (POTENTIAL).
; E92CCF2F629D9C14 CRC64;
                                                                                                                                                                                                                                                                                                                                  ATP-DEPENDENT PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Last sequence update)
Probable 16s rRNA processing protein rimm.
RIMM OR JHP1076.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 181 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00870; CLPAB 1; FALSE NEG.
PROSITE; PS00871; CLPAB 2; FALSE NEG.
Chaperone; ATP-binding; Repeat; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          centr.
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InterPro; IPR003595; AAA_ATPase centr
InterPro; IPR0019270; Chaprnin_ClpA/B.
Pfam; PF00004; AAA; 1.
PRINTS; PR00300; CLPPROTEASEA.
PPCDOM; PD000739; GSPII_E; 1.
SWART; SM00382; AAA; 2.
                                                                                                                                                                              MEDLINE=93247497; PubMed=8387149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86018 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188
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Best Local Similarity
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NP BIND
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Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 AKTLTE 7
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P11761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SAPR_STRPU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92051399; PubMed=1840672;
Klenk H.-P., Schwass V., Zillig W.;
"Nucleotide sequence of the genes encoding the L30, S12 and S7
equivalent ribosomal proteins from the archaeum Thermococcus celer.";
Nucleic Acids Res. 19:6047-6047(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Klenk H.-P., Schwass V., Lottspeich F., Zillig W.; "Nucleotide sequence of the genes encoding the three largest subunits of the DNA-dependent RNA polymerase from the archaeum Thermococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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-!- FUNCTION: PROTEIN S7 BINDS SPECIFICALLY TO PART OF THE 3' END OF
16S RIBOSOMAL RNA (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDILINE-5317672; PubMed=7916630; MEDILINE-5317672; PubMed=7916630; Klenk H.-P., Schwass V., Zillig W.; "Nucleotide sequence of the genes encoding proline tRNA(UGG) and threonine tRNA(GGU) and consensus promoter model of Thermococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -! - SIMILARITY: BELONGS TO THE S7P FAMILY OF RIBOSOMAL PROTEINS.
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Pred. No. 28;
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                                                                                                                                                                                                                                                                                                                                processing, Complete proteome.
ENCE 184 AA; 20792 MW; BB25C2A140488110 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93027167; PubMed=1408768;
                                                                                                                                                                                                                         EMBL; AE000621; AAD08193.1; -.
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01-DEC-1992 (Rel. 24, Last sem
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SEQUENCE OF 196-215 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          85.7%;
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                                                                                                                                                                                                                                                                          InterPro; IPR002676; RimM.
Pfam; PF01782; RimM; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-1992 (Rel. 24, 30-MAY-2000 (Rel. 39,
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=DSM 2476;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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Echinoidea, Euechinoidea, Echinacea, Echinoida, Strongylocentrotidae,
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Ramarao C.S., Burks D.J., Garbers D.L.;
"A single mRNA encodes multiple copies of the egg peptide speract.";
Biochemistry 29:3383-3388(1990).
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Hansbrough J.R., Garbers D.L.;
"Speract. Putification and characterization of a peptide associated
"Speract. Putificates spermatczea.";
J. Biol. Chem. 256:1447-1452(1981).
-!- FUNCTION: CANES SITMULATION OF SPERM RESPIRATION AND MOTILITY
THROUGH INTRACELLULAR ALKALINIZATION, TRANSIENT ELEVATIONS OF
CAMP, CGMP AND CLACIUM LEVELS IN SPERM CELLS, AND TRANSIENT
ACTIVATION AND SUBSEQUENT INACTIVATION OF THE MEMBRANE FORM OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Garbers D.L., Watkins H.D., Hansbrough J.R., Smith A., Misono K.S.; "The amino acid sequence and chemical synthesis of speract and of
                                                                                                                                                                                                                                                                                                                                                                                        .;
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                                                                                                                                                                                                                                                                                                                                         82.4%; Score 28; DB 1; Length 215; 100.0%; Pred. No. 33; 10; ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                     T - > S (IN REF. 2).
SR - > RA (IN REF. 2).
6269A731ACE34230 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1991 (Rel. 19, Last sequence update)
1-AMR-1992 (Rel. 21, Last annotation update)
Speract precursor (Sperm-activating peptide)
Strongylocentrotus purpuratus (Purple sea urchin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: SMALL TO A.PUNCTULATA RESACT.
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                                                                                                     HSSP, P17291; IRSS.
InterPro; IRR00225; Ribosomal_S7.
Prom; PF0017; Ribosomal_S7; 1.
TIGRFAMs; TIGR01028; S7 SE A; 1.
PROSITE; PS00052; RIBOSOMAL_S7; FALSE_NEG.
Ribosomal protein; rRNA-binding.
CONFLICT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol. Chem. 257:2734-2737(1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=82142387; PubMed=7061446;
                                                                                                                                                                                                                                                                              214 215 S
215 AA; 24393 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1989 (Rel. 12, Created)
01-AUG-1991 (Rel. 19, Last seq
EMBL; X60305; CAA42850.1; -. EMBL; X67313; CAA47728.1; -. EMBL; X63317; CAA48463.1; -. PIR; S18714; S18714; S29858;
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PRINTS: PR00237; GPCRRHODOPSN
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-!- FUNCTION: THIS IS A RECEPTOR FOR THE TACHYKININ NEUROPEPTIDE SUBSTANCE P. IT IS PROBABLY ASSOCIATED WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- MISCELLANBOUS: THE RANK ORDER OF AFFINITY OF THIS RECEPTOR TO TACHYKININS IS: SUBSTANCE P > SUBSTANCE K > NEUROMEDIN K.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
HIGHEST TO OTHER TACHYKININS RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cavia porcellus (Guinea pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Caviidae, Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gorbulev V., Akhundova A., Luzius H., Fahrenholz F.;
"Molecular cloning of substance P receptor cDNA from guinea-pig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 296;
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                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                            (POTENTIAL)
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15-JUL-1998 (Rel. 36, Last annotation update)
Substance-P receptor (SPR) (NK-1 receptor) (NK-1R).
TACRI OR TACIR.
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Pred. No. 45;
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SPERACT-LIKE.
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0; Mismatches
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or send an email to license@isb-sib.ch).
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EMBL; J02896; AAA30080.1; ALT_INIT.
PIR; A25724; A25724.
PIR; A34543; A34543.
PEPTIDE 135 144 SPERAC
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Pfam; PF00001; 7tm_1; 1.
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01-APR-1993 (Rel. 25, Last seq
15-JUL-1998 (Rel. 36, Last ann
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S19198, S19198.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        296 AA;
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Best Local Similarity
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AC D30547;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIBOSOMES (BY SIMILARITY).
SUBUNIT: SIGNAL RECOGNITION PARTICLE CONSISTS OF A SMALL CYTOPLASMIC RNA (GC-RNA) MOLECULE AND PROTEIN FFH (BY SIMILARITY).
CYTOPLASMIC RNA FAW DOMAIN STRUCTURE: THE G-DOMAIN BINDS GTP; THE M-DOMAIN BINDS THE RNA AND ALSO BINDS THE SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M., Prichmann J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L., Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M., Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C., Saidek J.M., Schence 270:397-403(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  I- FUNCTION: NECESSARY FOR EFFICIENT EXPORT OF EXTRA-CYTOPLASMIC PROTEINS. BINDS TO THE SIGNAL SEQUENCE WHEN IT EMERGES FROM THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE SRP FAMILY OF GTP-BINDING PROTEINS.
                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
PSO0237; G PROTEIN RECEP F1 1; 1.
PS50262; G-PROTEIN RECEP F1 2; 1.
n coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 16
SR54 MYGGE

ID SR54 WYGGE
STANDARD; PRT; 446 AA.

P 47224;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Signal recognition particle protein (Fifty-four homolog)
GN FFH OR MG048.
                                                                               EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                         6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
                                                                                                                                      2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                             F8C5D31C4BB45E6B CRC64;
                                                                                                                                                                                                                 4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                             (POTENTIAL).
                                                                                                1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                   S (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                               PALMITATE (POTENTIAL)
                                                                                                                                                                            3 (POTENTIAL).
CYTOPLASMIC (P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY
                                                               Phosphorylation; Lipoprotein; Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-ATCC 33530 / G-37;
MEDLINE-96026346; PubMed=7569993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 46257 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82.4%;
71.4%;
                                           G-protein coupled receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Conservative
                                                                                   31
54
64
86
86
1128
1148
1169
                                                                                                                                                                                                                                                                                                            283
308
407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      391 NSKTVTE 397
                                                                                                                                                                                                                                                                                                                                                                                                                                               407 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 NAKTLTE 7
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Gaps

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Indels

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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF395541; AAK83888.1; -.
InterPro; IPR001909; KRAB.
InterPro; IPR000822; Znf_C2H2.
Pfam; PF00096; zf-C2H2; I2.
Pfam; PF01352; KRAB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            604 AA; 68743 MW;
                                                                                             STANDARD;
    5; Conservative
                                    | ||:||
108 NGKTITE 114
                        1 NAKTLTE 7
                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                Z300 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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ZN_FING
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                                                                                  Z300_HUMAN
    Matches
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    and for commercial
             (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Structure of betaine aldehyde dehydrogenase at 2.1-A resolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein Sci. 7:2106-2117(1998).
-!- CATALYTIC ACTIVITY: Betaine aldehyde + NAD(+) + H(2)0 = betaine
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBLOWIT: HOMOTETRAMER.
-!- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
PDB; 1445; 08-APR-98.
PDB; 118PW; 19-AUG-98.
InterPro; IPR002086; Aldehyde_dehydr.
Pfam; PF0011; aldedh; 1.
PROSITE; PS00067; ALDEHYDE_DEHYDR_CLU; 1.
PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
Oxidoreductase; NAD; 3D-structure.
NP_BIND 241 246 NAD (ADP PART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.4%; Score 28; DB 1; Length 503; 71.4%; Pred. No. 77;
                                                                                                                                                                                                                                                                  DB 1; Length 446;
                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                        G-DOMAIN.
M-DOMAIN.
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
    Usage by
                                                                                                    Pfam; PF00448; SRP54; 1.
Pfam; PF02881; SRP54 N; 1.
Pfam; PF02881; SRP54 N; 1.
Procom; PD000819; SRP54; 1.
PROSITE; PS00300; SRP54; 1.
PROSITE; PS00300; SRP54; 1.
Signal recognition particle; GTP-binding; RNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1CB2FB92FA89E577 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Betaine aldehyde dehydrogenase (EC 1.2.1.8) (BADH).
Gadus callarias (Baltic cod).
modified and this statement is not removed. entities requires a license agreement (See Por send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                Score 28; DB 1
Pred. No. 68;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   503 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Liver;
MEDLINE=99006561; PubMed=9792097;
                                                                     InterPro; IPR000897; SRP54.
InterPro; IPR004125; SRP54_SPB.
InterPro; IPR004780; SRP_sub.
                                                                                                                                                                                                                                            50199 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54367 MW;
                                                                                                                                                                                                                                                                82.4%;
71.4%;
                                         EMBL; U39684; AAC71264.1; -.
HSSP; O07347; 1FFH.
                                                                                                                                                                                                                                                                                     5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                         293
446
1113
192
249
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19 NAQTITE 25
                                                                                                                                                                                                                                           446 AA;
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                                                                                                                                                                             Complete proteome.
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Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                           1 NAKTLTE 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=8053;
                                                               FIGR; MG048;
                                                                                                                                                                                                                                                                                                                                                                                  DHAB GADCA
P56533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eklund H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NP BIND
ACT SITE
ACT SITE
SEQUENCE
                                                                                                                                                                                                 DOMAIN
NP BIND
NP BIND
                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                        DHAB_GADCA
                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                            RESULT 17
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PROSITE; PS0028; ZINC_FINGER_C2H2_1; 12.
PROSITE: PS0157; ZINC_FINGER_C2H2_2; 12.
Transcription regulation; Zinc-finger; Metal-binding; Nuclear protein; DNA-binding; Repeat; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Gou D.-M., Li W.-X., Gao L., Sun Y.;
"A human zinc finger gene, ZNF300.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAY FUNCTION AS A TRANSCRIPTION FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -> H (IN DBSNP:1988688)
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EABCF821E9FAC441 CRC64;
                          096RE9;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
115-JUN-2002 (Rel. 41, Last annotation update)
Zinc finger protein 300.
604 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KRAB.
ZINC FINGERS.
C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FINGER PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C2H2-TYPE.
C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C2H2-TYPE
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Gaps

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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kempken F., Meinhardt F., Esser K.;
"In organello replication and viral affinity of linear,
"In organello replication and viral affinity of linear,
extrachromosomal DNA of the ascomycete Ascobolus immersus.";
Mol. Genet. 218:523-530 (1989).
-!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- MISCELLANEOUS: THIS DNA POLYMERASE REQUIRES A PROTEIN AS A PRIMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY. STRONG, TO DNA POLYMERASE OF OTHER FUNGAL AND PLANTS MITOCHONDRIAL PLASMIDS.
                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid pAI2.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Pezizomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROBLE: PS00116; DNA POLYMERASE B; 1..
Transferase; DNA-directed DNA polymerase; DNA replication; DNA-binding; Plasmid; Mitochondrion.
SEQUENCE 1202 AA; 138279 MW; 51D41FCEBDBF2CDE CRC64;
                                                                                                                                                                                                                           Nonstructural protein; Noncapsid protein; DNA replication;
                                                                                                                                                                                                                                                                                                                           82.4%; Score 28; DB 1; Length 849; 100.0%; Pred. No. 1.3e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                   631 ATP (POTENTIAL).
97543 MW; D4FA0980B0BE152E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Probable DNA polymerase (EC 2.7.7.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1202 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pezizales; Ascobolaceae; Ascobolus.
                                                                                                                                            EMBL; M37899; -; NOT ANNOTATED CDS.
PIR; A40784; UYPVAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002064; DNA_pol_B.
InterPro; IPR004868; DNA_pol_B_2.
Pfam; PF03175; DNA_pol_B_2; I.
SWART; SM00486; POLEC; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=2/1;
MEDLINE=90066356; PubMed=2573821;
                                                                                                                                                                                     InterPro; IPR001257; Parvo_NS1.
Pfam; PF01057; Parvo_NS1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X15982; CAA34106.1; -. PIR; S05362; S05362.
                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                   624 6
849 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   553 AKTLTE 558
                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=5191;
                                                                                                                                                                                                                                                                                                                                                                                                             2 AKTLTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mitochondrion.
                                                                                                                                                                                                                                                ATP-binding.
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P22374:
                                                                                                                                                                                                                                                                                                                                                                       ;
9
                                                                                                                                                                                                                                                                                    SEQUENCE
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Matches
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-!- FUNCTION: SEEMS NECESSARY FOR VIRAL DNA REPLICATION, PLAYS AN IMPORTANT ROLE IN THE REGULATION OF CARBID GENE EXPRESSION. IT IS COVALENTLY BOUND TO THE S'TERMINI OF VIRAL DNA, AND CAN INFLUENCE DNA PACKAGING. NSI IS ALSO BELIEVED TO POSSESS THE TOPOISOMERASE I TYPE NICKING ACTIVITY, AND CYTOTOXIC ACTIVITY.

-!- SIMILARITY: BELONGS TO THE PARVOVIRUSES NONCAPSID PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Afanasiev B.N., Galyov E.E., Buchatsky L.P., Kozlov Y.V.; "Nucleotide sequence and genomic organization of Aedes densonucleosis
                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Viruses; ssDNA viruses; Parvoviridae; Densovirinae; Brevidensovirus.
NCBI_TaxID=10808;
                                                                                                                                                                                                                                              Mycoplasma pneumoniae.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2104;
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01-AUG-1992 (Rel. 23, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1).
                                                                                                                                                                                                                                                                                                                                                                                          Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.4%; Score 28; DB 1; Length 839; 85.7%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein; Complete proteome.
SEQUENCE 839 AA; 99912 MW; 3E3523E18BCDFECC CRC64;
                                                                                                                                                                       Hypothetical protein MG422 homotation update)
MPN620 OR MP222.
                                                                                                      839 AA
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                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     pneumoniae.";
Nucleic Acids Res. 24:4420-4449(1996).
                                                                                                                                                                                                                                                                                                        [1] SEQUENCE FROM N.A. STRAIN=ATCC 29342 / M129; MEDLINE=97105885; Pubwed=8948633; MEDLINE=97105 H. Plager
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=92024090; Pubmed=1833875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE000022; AAB95870.1; -.
                                                                                                      STANDARD;
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    152 NSKTVTE 158
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Y422 MYCPN
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Pred. No. 13; 0; Mismatches

85.7%;

6; Conservative

22 NAKTNTE 28

1 NAKTLTE 7

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Best Local Similarity
Matches 6; Conserv
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MEDLINE=97394467; PubMed=9252185;

MEDLINE=97394467; PubMed=9252185;

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Garmel G., Tummino P.J., Caruso A., Uria Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter pylori (Campylobacter pylori), and
Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria, Proteobacteria, epsilon subdivision, Helicobacter group,
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Nature 397:176-180(1999)
-!- SIMILARITY: BELONGS TO THE L33P FAMILY OF RIBOSOMAL PROTEINS.
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      Length 1202;
                                                                       0; Indels
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      Score 28; DB 1; Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 35, Last sequence update) (Rel. 40, Last annotation update)
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                                                                           Mismatches
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Pfam; PF00471; Ribosomal L33; I.
ProDom; PD002595; Ribosomal L33; 1.
TIGRPAMS; TIGR01023; PDMG Dact; 1.
PROSITE; PS00582; RIBOSOMĀL L33; 1.
Ribosomal protein; Complete proteome.
SEQUENCE 52 AA; 6066 MW; 66BAC829C1
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01-NOV-1997 (Rel. 35, Last sem
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      82.48;
71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50S ribosomal protein L33. RPMG OR HP1204 OR JHP1127.
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                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                       5; Conservative
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Best Local Similarity
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P56055;
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                                                                       Matches
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DB 1; Length 52;

Score 27;

79.48;

Query Match

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A Kunst F., Ogasawara N., Absertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Barevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Barevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Bruschier L., Brans A., Braun M., Briganell S.C., Bron S., Brouilet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Brouilet S., Bruschi C.V., Connerton I.F., Cummings N.J., Daniel R.A., A. Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Britz C., Fujita M., Pujita Y., Fuma S., Galizzi A., Galleron N., A. Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Guy B.J., Hagad K., Haiech J., Harwood C.R., Henaut A., A. Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Axbayashi Y., Koetter P., Koningstein G., Krogh S., Kunano M., Klein C., Robyashi Y., Koetter P., Koningstein G., Krogh S., Kunano M., Andlia N., Levine A., Liu H., Masuda S., Mauel C., Medigue C., Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., Persecan E., Pujic P., Purnalle B., Rapoport G., Rey M., Reynolds S., Ragor U., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M., Raconi E., Purnalle B., Rapoport G., Rey M., Reynolds S., Schroeter R., Scoffone F., Scorleich S., Schroeter R., Scoffone F., Scorkoka A., Tacconi E., Takagi T., Takamashi H., Takemaru K., Takemaru K., Takemaru K., Takemaru M., Tamakoshi A., Tanakoshi A., Tanakoshi A., Tanakoshi A., Tarakaj T., Weitzenegger T., Wambutt R., Wambutt R., Wambutt R., Wambutt R., Wambutt R., Wambutter R., Wambutter R., Wambutter R., Wambutter R., Wambutter R., Wambutter R., Wambutter R., Wambutter R., Wambutter R., Wambutter R., Wambutter R., Wambutter R., Wambutter R., Wandheler R., Wandheler R., Wandheler R., Wandheler R., Wandheler R., Wandheler R., Wandheler R., Wandheler R., Wandheler R., Wandheler R., Wandheler R., Wandheler R., Wandheler R., Wandheler R., Wandheler R., Wandheler R., Wandheler R., Wandheler R., 
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-!- CATALYTIC ACTIVITY: Cleavage of N-terminal leader sequences from secreted proteins precursor.
-!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
-!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
LEPU BACSU STANDARD; PRT; 187 AA.

142959;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Signal peptidase I U (EC 3.4.21.89) (SPase I) (Leader peptidase I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamane K., Kumano M., Kurita K.; "The 25 degrees-36 degrees region of the Bacillus subtilis chromosome: determination of the sequence of a 146 kb segment and
                                                                                                                                                                                                                                                                                                                                                    Akagawa E., Kurita K., Sugawara T., Nakamura K., Yamane K.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                     Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
NCDI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=168;
MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97124189; PubMed=8969502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    identification of 113 genes.";
Microbiology 142:3047-3056(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                Bacillus subtilis.
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Best Local Similarity
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58 NAKTIT 63
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HMUV_YERPE
ID HMUV_YERPE
AC Q56993;
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MEDLINES97124195; PubMed=8969508;
Mizuno M., Masuda S., Takemaru K.-I., Hosono S., Sato T., Takeuchi M.,
Kobayashi Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Systematic sequencing of the 283 kb 210 degrees-232 degrees region of
the Bacillus subtilis genome containing the skin element and many
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 27; DB 1; Length 187;
Pred. No. 48;
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to the EMBL/GenBank/DDBJ databases.
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Bacilius subtilis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
NCBL_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0727; LEADERPTASE,
PROSITE; PS00501; SPASE I 1; 1
PROSITE; PS00760; SPASE I 2; 1.
PROSITE; PS00761; SPASE I 3; 1.
Transmembrane; Hydrolase; Protease; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31C48774CF6A849B CRC64;
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Last annotation update)
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BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
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InterPro; IPR000508; SigPTase.
InterPro; IPR000223; SigPTase_S26A.
Pfam; PF00461; Peptidase_S26, 1.
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88 BY
21183 MW;
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I LEADER PEPTIDASE FAMILY
                                                                                                                                                                                                                                                                                   EMBL; D38161; BAA07353.1; -. EMBL; D50453; BAA09032.1; -. EMBL; Z99106; CAB12209.1; -. HSSP; P00803; 1B12.
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Submitted (SEP-1995)
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STRAIN=168 / JH642;
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2 NAKTIT 7
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Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Chois S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., RA Beniam K.D., Errington J., Pabret C., Ferrari E., Foulger D., Fantam K.D., Errington J., Fabret C., Ferrari E., Foulger D., Finan S., Galser P., Goffeau A., Golightly E.J., Grandi G., Glaser P., Goffeau A., Golightly E.J., Grandi G., Aniseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A., Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Joris B., Karamata D., Kasahara Y., Klaerner Blanchard M., Klein C., R.A., Kobayashi Y., Koetter P., Kohingstein G., Krogh S., Kumano M., Kobayashi Y., Koetter P., Woningstein G., Krogh S., Kumano M., Medigue C., R.A. Medina N., Mellado R.P., Mizumo M., Mosell D., Nakai S., Noback M., Portectalle D., Porwollik S., Persoctt A.M., RA Prescan E., Pulic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Ralect M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y., Sekowska A., Seros B., Schroeter R., Soffene F., Sato T., Scanlan E., Schleetelle D., Porwollik S., Shin B.S., Soldo B., RA Fosto T., Scanlan E., Schleeter R., Soffene F., Rak Sekiguchi J., Sakowska A., Seros J., Tarakashi H., Takemaru K., Yatekuchi M., Tamakoshi A., Tanaka T., Tarakashi H., Weitzenegger T., RA Tosato V., Uchlyama S., Vandenbol M., Vannier F., Vasumoto K., Yata K., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Whiters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Whiters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Wetter S., Shin Bacillus B., Shin Bacillus B., Rubellis, R., Wedler E., Wedler E., Wedler E., Vashikawa H., Danchin A., The Complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no, way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Pred. No. 59;
1; Mismatches 0; Indels
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229 AA; 25549 MW; 110310C897BD8691 CRC64;
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01-NOV-1997 (Rel. 35, Last sequence update)
115-JUN-2002 (Rel. 41, Last annotation update)
Hemin transport system ATP-binding protein hmuV.
HMUV OR YPO0279.
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STRAIN-KIM6;
MEDLINE-96386041; PubMed=9026634;
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SubtiList; BG11414; spoIIIAG.
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15 NANTITE 21
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Best Local Similarity
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                                                                                                                                                                                                               MEDLINE-21470413; Pubmed-11586360;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.,
"Genome sequence of Yersinia pestis, the causative agent of plague.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 413:523-527(2001).
-!- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM
FOR HEMIN. PROBABLY RESPONSIBLE FOR ENERGY COUPLING TO THE
TRANSPORT SYSTEM.
Hornung J.M., Jones H.A., Perry R.D.; "The hmu locus of Yersinia pestis is essential for utilization of free harmin and haem-protein complexes as iron sources."; Mol. Microbiol. 20:725-739(1996).
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15-JUN-2002 (Rel. 41, Last annotation update)
ADP,ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: Inner membrane-associated (Potential)
-!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
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Inner membrane; Iron transport; Transport; ATP-binding;
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NP BIND 44 51 ATP (POTENTIAL).
SEQUENCE 266 AA; 29658 MW; 4A7DEB955583CB27 CRC64;
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InterPro; IPR003593; AAA ATPase.
InterPro; IPR003439; ABC_transportr.
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ProDom; PD000006; ABC transportr; 1.
SMART; SM00382; AAA; 1.
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                                                                                                                                                                                           STRAIN=CO-92 / Biovar Orientalis;
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01-NOV-1997 (Rel. 35, Last seq
15-JUN-2002 (Rel. 41, Last ann
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SEQUENCE FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                 RK STRANNSYS, WELLANDSYSON RATAINSYSON RATAINSYSON RAY MEDLINE-21848401; PubMed=11859360; Basham D., Bowman S., Sequros U., Peat N., Hayles J., Basham D., Bowman S., Brown D., Brown S., Chillingworth T., Churcher C.M., RA Brooks K., Brown D., Enown S., Chillingworth T., Churcher C.M., RA Brooks K., Brown D., Davis P., Feltwell T., Fraser A., Racherles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., RA Monory P., Moule S., Mingall K., Murphy L., Niblett D., Odell C., RA Stevens K., Stavens K., Stavens K., Stevens K., Stavens K., Stevens K., Whitchead S., Wodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Wodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Wodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Wodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Goffeau A., Cadieu E., Rieger M., Schaefer M., Mulbert H., Reinhardt R., Purlar S., RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Lehrach H., Reinhardt R., Hurst S.M., Locas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Locas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Letrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Ra Shpakovski G.V., Ussery D., Barrell B.G., Nurse P., Rather Strandston S., Armstrong J., Porsburg S., Nurse T. FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MINGATINE MEMBRANA.

- I- FUNCTION: CHIRCH MEMBRANA.
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                                carrier of Schizosaccharomyces pombe by functional complementation in Saccharomyces cerevisiae.";
Gene 171:113-117(1996).
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-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
"Cloning of the gene encoding the mitochondrial adenine nucleotide
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PRINTS, PR002054, MITOCHARIER, 2.
PROSITE, PS00215; MITOCH CARRIER; 2.
Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
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InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
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Best Local Similarity
Matches 5; Conserv
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TIGR; VC1921; -
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CLPX VIBCH
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                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=91172845; PubMed=1706527;
Darmer D.; Schmutzler C., Diekhoff D., Grimmelikhuijzen C.J.P.;
Darmer D.; Schmutzler C., Diekhoff D., Grimmelikhuijzen C.J.P.;
Primary structure of the precursor for the sea anemone neuropeptide
Antho-RFamide (<Glu-Gly-Arg-Phe-NH2).";
Proc. Natl. Acad. Sci. U.S.A. 88:2555-2559(1991).
-I- FUNCTION: NOT KNOWN BUT IT COULD ACT AS A TRANSMITTER AT
NEUROMUSCULAR SYNAPSES.
-I- TISSUE SPECIFICITY: NEURONS ASSOCIATED WITH SMOOTH MUSCLE FIBERS.
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Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
Nynantheae; Hormathiidae; Calliactis.
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(G-165
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01-JUN-1994 (Rel. 29, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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ANTHO-RFAMIDE.
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SIGNAL 1 26 POTTENTIAL
                                                                                                                                                                                Antho-RFamide neuropeptides precursor.
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InterPro; IPR002544; FARP.
Pfam; PF01581; FARP; 15.
                                                                                STANDARD;
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120
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                                                                             FMRA C
                                    RESULT 27
FMRA_CALPA
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STRAIN=El Tor N16961 / Serotype Ol;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 406:477-483 (2000).

-!- FUNCTION: ATP-dependent specificity component of the Clp protease.

It directs the protease to specific substrates. Can perform chaperone functions in the absence of clpP (By similarity).

-!- SUBUNIT: Hererodimer of clpP and clpX (By similarity).

-!- SIMILARITY: BELONGS TO THE CLPX CHAPERONE FAMILY.
                                                                                                                                                                                                                                                            Gaps
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                                GROUP)
GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                            ;
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(G-257 PROVIDE AMIDE G
(G-267 PROVIDE AMIDE G
(G-276 PROVIDE AMIDE G
(G-285 PROVIDE AMIDE G
                                                                                                                                                                                          Score 27; DB 1; Length 334;
Pred. No. 86;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79.4%; Score 27; DB 1; Length 426; 71.4%; Pred. No. 1.1e+02; ive 2; Mismatches '0; Indels

      Pfam; PF00004; AAA; 1.

      SMART; SM0382; AAA; 1.

      TIGFFAMS; TIGR00382; AAA; 1.

      TIGFFAMS; TIGR0038; DIX; 1.

      Chaperone; ATPP

      TIG

      ATYPE

      12

      ATP

      POTENTIAL)

      SEQUENCE

      426 AA; 46490 MW; 9EA336B942EFA9D4 CRC64;

                                                                                                                               438E182C736EB583 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ATP-dependent Clp protease ATP-binding subunit clpX.
CLPX OV VUJ921.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              426 AA
                                AMIDATION
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Interpro, IPR003959; AAA ATPase_centr.
Interpro, IPR004487; ClpX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE004268; AAF95069.1; -.
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Σ
                                                                                                                                                                                             79.48;
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   256
266
275
284
39781 N
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Best Local Similarity 71.4
Matches 5; Conservative
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Length 442;

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POLYSACCHARIDE.
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           Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                       Capk protein.
                                                                                                                                                    STAAU
  Query Match
                                                                                                                                     CAPK_STAAU
ID CAPK_STA
AC P39860;
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                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=ATCC 35210 / B31;
STRAIN=ATCC 35210 / B31;
Brast. C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlayage A.R., Quackenbush J., Salzberg S., Hanson M.,
van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
Utterback T., Watthey L., MoDonald L., Artiach P., Bowman C.,
Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                          Dunn J.J., Butler-Loffredo L., Kieleczawa J., Medalle J., Luft B.J., Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 18-207 FROM N.A.
STRAIN=ATCC 35210 / B31;
Limberger R.J., Slivienski L.L.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: BELONGS TO THE FLAGELLA BASAL BODY ROD PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R -> I (IN STRAIN HB19).
D -> Y (IN STRAIN HB19).
V -> I (IN STRAIN HB19).
N -> S (IN STRAIN HB19).
W; 561AC092B72C69BE CRC64;
                                                                                                                                                                                                                                                                                                                                              Old I.G.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                        Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
                                                                                          FLGE BORBU STANDARD; PRT; 442 AM. 044767; Q44899; Q44734; 01-NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       interPro; IPR001444; Flag bb_rod.
Pfam; PF00460; flg_bb_rod; 1.
PROSITE; PS00588; FLAGELIA_BB_ROD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U43739; AAA85606.1; -.
EMBL; L43849; AAA87351.1; -.
EMBL; AE001137; AAC66665.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Flagella; Complete proteome.
                                                                                                                                                             Flagellar hook protein flgE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 390:580-586(1997).
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=ATCC 35210 / B31;
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281 NSKTLSE 287
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SEQUENCE FROM N.A.
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                                                                                                                                                                              OR BB0283.
                                                                                                                                                                                                                                                                                                                                 STRAIN=HB19;
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SEQUENCE
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                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Sequence analysis and molecular characterization of genes required for the biosynthesis of type 1 capsular polysaccharide in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYP ECOLI STANDARD; PRT; 572 AA.
P16559; 055430; P78272;
01-AUG-1990 (Rel. 35. Created)
01-OCT-1994 (Rel. 36. Last sequence update)
16-OCT-2001 (Rel. 40. Last sequence update)
Prolyl-trna synthetase (EC 6.1.1.15) (Proline--trna ligase) (ProRS)
PROS OR DRPA OR B0194.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF 1-12.
MEDLINE=90370122; PubMed=2203971;
Stain G., Delarue M., Poof O., Gangloff J., Moras D.;
"Partition of tRNA synthetases into two classes based on mutually exclusive sets of sequence motifs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Score 27; DB 1; Length 442
Pred. No. 1.1e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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SEQUENCE 449 AA; 52510 MW; 3806354020A95E26 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Firmicutes, Bacillales, Staphylococcus, NCBI_TaxID=1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79.4%; Score 27; DB 1; 1
71.4%; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                              01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
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79.4%;
ilarity 83.3%;
Conservative 1
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Best Local Similarity
Local 5; Conserve
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244 NAETLTD 250
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SYP_HAEIN
P43830;
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                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                   Zhou Z., Syvanen M.;
"Identification and sequence of the drpA gene from Escherichia coli.";
J. Bacteriol. 172:281-286(1990).
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

STRAIN=K12 / W1110;

Takemoto K., Mori H., Murayama N., Kataoka K., Yano M., Itoh T.,

Yamamoto Y., Inokuchi H., Miki T., Hatada E., Fukuda R., Ichihara S.,

Mizuno T., Makino K., Nakata A., Yura T., Sampei G., Mizobuchi K.;

Mizumatic sequencing of the Escherichia coli genome: analysis of the

"Systematic sequencing of the Escherichia coli genome: analysis of the

4.0 - 6.0 min (189, 987 - 281,416bp) region.";

Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Link A.J., Robison K., Church G.M.;
"Comparing the predicted and observed properties of proteins encoded in the genome of Escherichia coli K.12.";
Electrophoresis 18:1259-113(1997).
-!- CATALYTIC ACTIVITY: ATP + L-proline + tRNA(Pro) = AMP + diphosphate + L-prolyl-tRNA(Pro).
-!- SUBUNIT: HOMODIME..
-!- SUBCELLULAR LOCATION: Cytoplasmic..
-!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                          [3]
SUGENCE FROM N.A.
STRAIN=K12 / MG1655,
MEDIJURE=97426617, PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Kiley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                               STRAIN=K12; STRAIN=K12; STRAIN=K12; SChramm S., Duncan M., Allen E., Araujo R., Aparicio A., Chung E., Davis K., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lashkari D., Lew H., Lin D., Namath A., Oefner P., Roberts D.,
                                                                                                                                                                                                      "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Miyamoto K.;
Submitted (APR-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-2DPAGE; P16659; COLI.
BCOGGERG; EG10770; proS.
InterPro; IPR002106; AAthNA ligaseII.
InterPro; IPR004154; HGTP_anticodon.
            [2]
SEQUENCE FROM N.A.
MEDLINE=90094229; PubMed=1688424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-12.
STRAIN=K12 / EMG2;
MEDLINE=97443975; PubMed=9298646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X55518; CAA39134.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M97858; AAA24420.1; -. EMBL; M32357; AAA23710.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE000128; AAC73305.1;
EMBL; D8338; BAA77870.1; -
EMBL; U70214; AAB08622.1; -.
EMBL; D15661; BAA03654.1; -.
PIR; JV0110; YPEC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-155 FROM N.A.
Nature 347:203-206(1990)
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- CATALYTIC ACTIVITY: ATP + L-proline + tRNA(Pro) = AMP +
diphosphate + L-prolyl-ENA(Pro).
-i- SUBUNIT: HOMODIMER (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: Cytoplaemic.
-i- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                 Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                   ML -> IV (IN REF. 1 AND 4).
QL -> HV (IN REF. 2).
QASHBFQVLAQS -> RPLTNSCWRR (IN REF. 2).
Q -> S (IN REF. 3 AND 5).
PG -> RA (IN REF. 2).
MISSING (IN REF. 2).
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STRAINE-87 7 KN20.

MEDIANE-975 250630; PubMed=7542800;

Pleischmann R.D., PubMed=7542800;

Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shillys R., Liu L.-I., Glodek A., Kellay J.M., Weldman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fitchman J.L., Geoghagen N.S.M., Genem C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 41, Last annotation update)
Proly1-tRNA synthetase (EC 6.1.1.15) (Proline--tRNA ligase) (ProRS)
PROS OR HI0729
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Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 71.4%; Score 27; DB 1; Length 572; Similarity 71.4%; Pred. No. 1.5e+02; 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                             MISSING (IN REF. 2).
KOIKG -> ETD (IN REF. 4).
2514448F3BC5F1D3 CRC64;
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                                                 PEGM; PF00587; ERNA-synt 2b; 1.
PEAM; PF03129; HGTP anticodon; 1.
PRINTS; PR01046; TRNASYNTHPRO.
TIGREAMS; TIGRO0409; proS fam II; 1.
PROSITE; PS50862; AA TRNA_LIGASE_II;
InterPro; IPR002314; tRNA-synt_2b.
InterPro; IPR002316; tRNA-synt_pro.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        63733 MW;
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TIGR; HI0729; -.
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128
216
205
205
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572
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259 NAKTIAE 265
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127
205
205
205
516
518
568
572 AA;
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CONFLICT 26
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CONFLICT 205
CONFLICT 205
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Best Local Similarity
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modified and this statement is not removed.
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InterPro; IPR002937; Amino_oxidase.
InterPro; IPR00624; Glycosidase.
InterPro; IPR000205; NAD_binding.
Pfam; PF01593; Amino oxidase; 1.
Pfam; PF02027; RolB_RolC; 1.
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MEDLINE=92033088; PubMed=1932811;
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                                                                                                                       EMBL; J04454; AAA34499.1; -.
EMBL; X91258; CAA62646.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Camilleri C., Jouanin L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Agrobacterium rhizogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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221 NSKTLTK 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 NAKTLTE 7
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Q09109;
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ACT_SITE
SEQUENCE
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=S288C / AB972;

A Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,

A Johnston M., Andrews S., Hillier L., Jier M., Johnson D.,

RA Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.,

A Johnston L., Langeron Y., Latreille P., Le T., Mardis B., Menezes S.,

Miller N., Mhan M., Pauley A., Peluso D., Rifken L., Riles L., Riles L., Raich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Vaudin M.,

RA Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Vaudin M.,

RA Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Vaudin M.,

RA Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Vaudin M.,

RA Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Vaudin M.,

RA Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Vaudin M.,

RA Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Vaudin M.,

RA Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Vaudin M.,

RA Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Vaudin M.,

RA Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Vaudin M.,

RA Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Vaudin M.,

RA Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Vaudin M.,

RA Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Vaudin M.,

RA Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Vaudin M.,

RA Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Vaudin M.,

RA Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Vaudin M.,

RA Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Vaudin M.,

RA Taich A., Trevaskis E., Vignati D., William L., William L., William L., William L., William L., William L., William L., William L., William L., William L., William L., William L., William L., William L., William L., William L., William L., William L., William L., William L., William L., William L., William L., William L., Willi
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InterPro; IPR002106; AAtRNA ligaseII.
InterPro; IPR004154; HGTP anitocdon.
InterPro; IPR00450; ProS_fam_II.
InterPro; IPR002316; tRNA-synt_2b.
InterPro; IRR002316; tRNA-synt_pro.
Pfam; PF00587; tRNA-synt_pro.
Pfam; PF00587; tRNA-synt_pro.
Pfam; PF00587; TRNA-SYNTHPRO.
TIGRPAM; TIGR00409; proS_fam_II; 1.
PRINTS; PR01046; TRNASYNTHPRO.
PROSITE; PS50862; AA TRNA_LIGAGE II; 1.
PROSITE; PS50862; AA TRNA_LIGAGE II; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=89123268; PubMed=2536698;
Hosaka K., Kodaki T., Yamashita S.;
"Cloning and characterization of the yeast CKI gene encoding choline
Kinase and its expression in Eccherichia coli.";
J. Biol. Chem. 264:2053-2059(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                             Length 572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
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Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                       572 AA; 63975 MW; 5BF0F81162368583 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             79.4%; Score 27; DB 1; I
71.4%; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1991 (Rel. 17, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) Choline kinase (EC 2.7.1.32).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258 NAKTIAE 264
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                Complete proteome. SEQUENCE 572 AA;
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P20485;
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                                  (See http://www.isb-sib.ch/announce/
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-!- PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF AUXINS FROM TRYPTOPHAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The TR-DNA region carrying the auxin synthesis genes of the Agrobacterium rhizogenes agropine-type plasmid pRiA4: nucleotide sequence analysis and introduction into tobacco plants."; Mol. Plant Microbe Interact. 4.155-162[1991].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oxidoreductase; Monōoxygenase; Auxin biosynthesis; T-DNA; Plasmid.
SEQUENCE 749 AA; 83178 MW; 8B7793970206F97B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHORYLATION (POTENTIAL).
PHOSPHORYLATION (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.4%; Score 27; DB 1; Length 582; 71.4%; Pred. No. 1.5e+02; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 27; DB 1; Length 749;
Pred. No. 1.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
10-NOV-1995 (Rel. 32, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Tryptophan 2-monooxygenase (EC 1.13.12.3).
                                  entities requires a license agreement ((or send an email to license@isb-sib.ch)
                                                                                                                                                                                                               EMBL, 273305; CAA97704.1; --
EMBL, 133881, AAB82296.1; --
FIR, A32034, A32034.
SGD, S0004123, CKI1.
InterPror, IPR002573; Choline kinase.
Fram, PP01633; Choline kinase, 1.
Transferase, Kinase, Phosphorylation.
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NCBI_TaxID=4932;
                                            RPB2_YEAST
P085<u>1</u>8; Q12738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZN FING
CONFLICT
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                        YEAST
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  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diphosphate + L-alanyl-tRNA(Ala).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0980; TRNASYNTHALA.
TIGREAMS; TIGR00344; alaS; 1.
PROSITE; PS50860; AA_TRNA_LIGASE_II_ALA; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Alanyl-tRNA synthetase, cytoplasmic (BC 6.1.1.7) (Alanine--tRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [2]
SEQUENCE FROM N.A.
MEDLINE=97051586; PubMed=8896263;
MEDLINE=0Mcdermott A.G., Hand N.J., Goulding S.G., Wolfe K.H.;
"Sequence of 29 kb around the PDR10 locus on the right arm of Saccharomyces cerevisiae chromosome XV: similarity to part of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79.4%; Score 27; DB 1; Length 958; 71.4%; Pred. No. 2.5e+02; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- CATALYTIC ACTIVITY: ATP + L-alanine + tRNA(Ala) = AMP
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Ripmaster T.L., Schimmel P.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R -> S (IN REF. 1).

KDQ -> RTK (IN REF. 1).

FE -> LQ (IN REF. 1).

W; 50FD31C2E2D40F32 CRC64;
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0
                                                                                                                                                                                             958 AA
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001106; AAtRNA_ligaseII.
InterPro; IPR001156; DHHA1.
InterPro; IPR0021156; ERNA-synt_2c.
Pfam; PF014II; ERNA-synt_2c; IPfam; PF02272; DHHA1; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107277 MW;
                                                                                                                                                                                                                                   01-FEB-1995 (Rel. 31, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, U18672; AAC49007.1; -.
EMBL; 249821; CAA89980.1; -.
EMBL, Z75243; CAA99658.1; -.
SGD; SO005862; ALA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Conservative
  5; Conservative
                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chromosome I.";
Yeast 12:999-1004(1996).
                                                                                    88
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                                                              ||::|||
82 NARSLTE
                                          1 NAKTLTE
                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                          ligase) (AlaRS).
ALA1 OR YOR335C.
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P40825;
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                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ayadi A. Bordones, Camasses A., Madania A., Poch O.,
Ayadi A., Bordones, Camasses A., Madania A., Poch O.,
Tarassov I.A., Winsor B., Martin R.P.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-: FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
SUBSTRAIES.
                                                        01-00V-1997 (Rel. 36, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1999 (Rel. 35, Last annotation update)
15-JUL-1999 (Rel. 36, Last annotation update)
NNA-directed RNA polymerase II 140 kDa polypeptide (EC 2.7.7.6) (B150)
(RNA polymerase II subunit 2).
RPB2 OR RP022 OR RPB150 OR YOR151C.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

    {RNA} (N).
    SUBUNIT: RNA POLYMERASE II CONSISTS OF 12 DIFFERENT SUBUNITS.
    THIS SUBUNIT IS THE SECOND LARGEST COMPONENT OF RNA POLYMERASE II.
    SUBCELLULAR LOCATION: Nuclear.
    MISCELLANEOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES ARE FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE II FOR SS AND TRNA GENES.
    SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sweetser D., Nonet M., Young R.A.; "Prokaryotic and eukaryotic RNA polymerases have homologous core
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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PROSITE; PS01166; RNA POL BETA; 1.
Transferase; DNA-directed RNA polymerase; Transcription; Zinc; Zinc-finger; Nuclear protein.
ZNG-finger; Nuclear Protein.
ZN FING 1163 1185 C4-TYPE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 27; DB 1; Length 1224;
Pred. No. 3.2e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1163 1185 C4-TYPE (POTENTIAL).
1003 1006 AEGI -> RRRY (IN REF. 1).
1224 AA; 138751 MW; BABD03212C0A583E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 84:1192-1196(1987)
PRT; 1224 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=87147239; Pubmed=3547406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A25884; A25884.
SGD; S0005677; RPB2.
InterPro; IPR001572; RNA_pol_B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M15693; AAA68096.1; -. EMBL; U55020; AAC49637.1; -. EMBL; Z75059; CAA99357.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79.4%;
83.3%;
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STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=S288c / FY1678;
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Best Local Similarity
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RESULT 37

||| :|| 858 NAKAITE 864

1 NAKTLTE 7

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FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
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                                                                                                                                                                                                                                                               IG KAPPA CHAIN V-V REGION K2.
                                                                                                                                                                                                                                                                                                                                                                                                    12581 MW; 4F41E3D40C539DEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-077-1996 (Rel. 34, Created)
01-077-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218 AA
                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sodium channel beta-1 subunit precursor. SCNIB.
                                                                                                                                                                                                                                                                                                        FRAMEWORK-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biol. Chem. 269:7571-7578(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=93357746; PubMed=8394762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hum. Mol. Genet. 2:745-749(1993).
                                                                                                                                                                                            Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
SIGNAL 1
                                                                                                                      EMBL; V00778; CAA24155.1; -.
                                                                                                                                                   HSSP, P01607, 1REI.
InterPro, IPR003006, Ig_MHC.
InterPro, IPR003596, Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
                                                                                                                                     PIR; A01918; KVMSK2.
                                                                                                                                                                                                                                                                                                                                                                      43 1
115 1
115 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 NAKTLAD 76
                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 NAKTLTE 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CIB1 HUMAN
Q07699;
                                                                                                                                                                                                                                                                                                                                                                                      NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                      DISULFID
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DOMAIN
DOMAIN
DOMAIN
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CIB1 HUMAN
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                         DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T., Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G., Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E., Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., Haselkorn R., Kyrpides N., Overbeek R.; The genome sequence of the facultative intracellular pathogen Brucella melitensis."; U.S.A. 99:443-448(2002).
-- SIMILARITY: BELONGS TO THE L33P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plasmacytoma kappa V-region genes";
J. Biol. Chem. 255:3691-3694 (1980).
-!- MISCELLANBOUS: THE GENE WAS ISOLATED AND SEQUENCED SEPARATELY FROM
TWO DIFFERENT SOURCES, EMBRYOS AND CULTURED PLASMACYTOWA CELLS
THAT SECRETE THE SIMILAR KAPPA CHAIN MOPC 149.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                      Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
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Nishioka Y., Leder P.;
"Organization and complete sequence of identical embryonic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 26; DB 1; Length 55;
Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4D9A995A363C4621 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-V region K2 precursor (Fragment).
                                                            Last sequence update)
Last annotation update)
                 55 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE009701; AAL53903.1; -.
InterPro; IPR001705; Ribosomal L33.
TIGRRAMs; TIGR01023; rpmG bact; 1.
PROSITE; PS00582; RIBOSOMĀL L33; PALSE_NEG.
Ribosomal protein; Complete proteome.
SEQUENCE 55 AA; 6400 MW; 4D9A995A363C46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=16M / ATCC 23456 / Biotype 1;
MEDLINE=20020109; PubMed=11756688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.5%;
57.1%;
                                                                                        50S ribosomal protein L33. RPMG OR BMEI10661.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Conservative
               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                     Brucellaceae; Brucella.
NCBI_TaxID=29459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                        Brucella melitensis.
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26 NSRTMTE 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                         Q8YC71;
15-JUN-2002
15-JUN-2002
                                                                          15-JUN-2002
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              BRUME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE-Skeletal muscle, and Heart;
MEDLINE-94171787, PubMed-8125980,
Makita N., Bennett P.B. Jr., George A.L. Jr.,
"Voltage-gated Na+ channel beta 1 subunit mRNA expressed in adult human skeletal muscle, heart, and brain is encoded by a single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=51154833; PubMed=7851891;
Makita N., Slaan-Brown K., Weghuis D.O., Ropers H.H.,
George A.L. Jr.;
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                                 WEDLINE=98361163; PubMed=9697698;

WEDLINE=98361163; PubMed=9697698;

WEDLINE=98361163; PubMed=9697698;

WA MAILACH R., Saar K., Reis A., Johnson E.W., Sutherland G.R.,

WA MAILACH R., Saar K., Reis A., Johnson E.W., Sutherland G.R.,

A Berkovic S.F., Mulley J.C.;

The Ebrile seizures and generalized epilepsy associated with a mutation

RT "Febrile seizures and generalized epilepsy associated with a mutation

RT "Febrile seizures and generalized epilepsy associated with a mutation

RT "Febrile Sizon(1998).

L Nat. Gener. 19:366-370(1998).

C -- FUNCTION: CRUCIAL IN THE ASSEMBLY, EXPRESSION, AND FUNCTIONAL

MODULATION OF THE HETEROTHERENC COMPLEX OF THE SODIUM CHANNEL.

C THE BETA-1 SUBINIT CAN MODULATE MULTIPLE ALPHA SUBUNIT

ISOFORMS FROM BRAIN, SKELFTL MUNSCLE, AND HEART.

C SUBUNIT: THE SODIUM CHANNEL CONSISTS OF A PORE-FORMING ALPHA

SUBUNIT, BETA-1 AND BETA-2 SUBUNITS. BETA-1 IS NONCOVALENTLY

ASSOCIATED WITH ALPHA, WHILE BETA-2 IS COVALENTLY LINKED BY
                                                                                                                                                                                                                                                                                                         -!- DISEASE: DEFECTS IN SCN1B ARE A CAUSE OF GENERALIZED EPILEPSY WITH FEBRILE SEIZURES PLUS (GEFS+), A DISEASE CHARACTERIZED BY. A HIGHLY VARIABLE PHENOTYPE COMBINING FEBRILE SEIZURES, GENERALIZED SEIZURES OFTEN PRECIPITATED BY FEVER AT AGE 6 YEARS OR MORE, AND PARTIAL SEIZURES, WITH A VARIABLE DEGREE OF SEVERITY.
-!- SIMILARITY: BELONGS TO THE IMMUNOCLOBULIN SUPERFAMILY.
-!- SIMILARITY: CONTAINS I IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN SKELETAL MUSCLE, HEART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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SODIUM CHANNEL BETA-1 SUBUNIT.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 26; DB 1; Length 218;
Pred. No. 94;
         voltage-gated Na+ channel beta 1 subunit gene (SCN1B).";
Genomics 23:628-634(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TId=VAR 010165.
09B812FA3F9E9018 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE C2-TYPE DOMAIN.

POTENTIAL.

N-LINKED (GLCNAC. ) (P
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'Genomic organization and chromosomal assignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C -> W (IN GEFS+).
/FTId=VAR 010165.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, L10338, AAA60391.1; --
EMBL, L16242, AAA61277.1; --
EMBL, U12193, AAB97608.1; --
EMBL, U12189, AAB97608.1; JOINED.
EMBL, U12190, AAB97608.1; JOINED.
EMBL, U12191, AAB97608.1; JOINED.
EMBL, U12192, AAB97608.1; JOINED.
GENEW, HGNC.10586; SCN1B.
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Similarity 71.4%;
5; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                              AND BRAIN.
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Bacteriol. 171:1075-1086(1989).

-!- FUNCTION: THE KEY ENZYMATIC REACTIONS IN NITROGEN FIXATION ARE CATALYZED BY THE NITROGENAEZ COMPLEX, WHICH HAS 2 COMPONENTS: THE IRON PROTEIN (COMPONENT 2) AND A COMPONENT 1 WHICH IS EITHER A MOLYBDENUM-IRON PROTEIN, A VANADIUM-IRON, OR AN IRON-IRON PROTEIN.

-!- CATALYTIC ACTIVITY: 8 reduced ferredoxin + 8 H(+) + N(2) + 16 ATP - 10 COFACTOR: BINDS ONE 4FE-4S CLUSTER PER DIMER.

-!- COFACTOR: BINDS ONE 4FE-4S CLUSTER PER DIMER.

-!- SUBUNIT: HOWODIMER.

-!- SUBUNIT: HOWODIMER.

-!- STREAM OF A STREAM OF A STREAM OF A STROGENASE.

-!- SIMILARITY: BELONGS TO THE NIFH / BCHL / CHLL FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Joerger R.D., Jacobson M.R., Premakumar R., Wolfinger E.D., Bishop P.B.; "Wolfootide sequence and mutational analysis of the structural genes (anfHDGK) for the second alternative nitrogenase from Azotobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Nitrogenase component II)
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IRON-SULFUR (4FE-4S) (BY SIMILARITY)
IRON-SULFUR (4FE-4S) (BY SIMILARITY)
6D262472F925SBBB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Azotobacter.
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                                                                                                                                                                                                                                        01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Nitrogenase iron protein 3 (EC 1.18.6.1) (Nitrogenase (Nitrogenase reductase).
                                                                                                                                                                                        275 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, M23528; AAA82508.1; -.
PIR, A32057; A32057.
HSSP; P00459; 1N2C.
InterPro, IPP000392; NitrogenaseII.
Pfam; PF00142; fer4 NifH; 1.
PRINTS; PR00091; NITROGNASEII.
                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=89123105; PubMed=2644222;
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275 AA; 29885 MW;
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                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                            Azotobacter vinelandii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223 NKKTVTE 229
                                                50 NAETFTE 56
1 NAKTLTE 7
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Matches 5; Conser
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P16269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vinelandii.
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SEQUENCE
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Gaps

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1; Indels

1; Mismatches

Matches

Search completed: July 18, 2003, 15:07:19 Job time : 5.34 secs

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Q92R69 Q95QX8 O51542

QBUGNO

Q8Y153 Q9U5M9 Q8R5Z3

054952 Q92FX7 Q9A1C0

Q9FKW3 Q8Y237 P71631

O06542 Q8YMR2

Q8UDG4

Q9ENI9 Q9C9KB Q9SFX4 Q8XWH9

Q9CE05

Q93QI0 Q94382 Q94383

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X MEDLINE=97121482; PubMed=8962148; MEDLINE=97121482; PubMed=8962148; MEDLINE=97121482; PubMed=8962148; Faron D.W., Adams T.H., Keller N.P.; Procom D.W., Adams T.H., Keller N.P.; Recondary metabolism."; Proco. Natl. Acad. Sci. U.S.A. 93:14873-14877(1996). Rembl. U75347; Ada14941. -.. InterPro; IPR001227; Ac transferase. RiterPro; IPR001227; Ac transferase. RiterPro; IPR00555; Fatty, acid synth. RiterPro; IPR00555; Fatty, acid synth. RiterPro; IPR005539; MaoC dehydratas. Rembl. Procost Sci. Rembl. Rembl. Procost Sci. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl. Rembl
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fatty acid synthase, beta subunit.
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Similarity 85.7%;
6; Conservative
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|NAKTMTE 643
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Best Local Similarity
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79.863 Million cell updates/sec
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                                                                                                 July 18, 2003, 15:02:40 ; Search time 18.06 Seconds
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            5.1.6
Compugen Ltd.
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            GenCore version (c) 1993 - 2003
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Maximum Match 100%
Listing first 45 summaries
                                                                     protein search, using sw model
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Q92BY8
Q8Y7B9
Q9NYW8
Q8SWP7
Q9L643
Q8X6K2
P77996
Q9FHQ6
Q9FHQ6
Q97VY2
Q8USF8
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1: Sp archea:*
2: Sp_bacteria:*
3: Sp_fung:*
4: Sp_fung:*
5: Sp_invertebrate:*
5: Sp_mammal:*
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Score 32; DB 3; Length 2091; Pred. No. 2.8e+02; 1; Mismatches 0; Indels

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STRAIN=EGD-E / SEROVAR 1/2A;
MEDLINE=21537279; PubMed=11679669;
MEDLINE=21537279; PubMed=11679669;
MEDLINE=21537279; PubMed=11679669;
Glaster P., Frangeul L., Buchrieser C., Rusnick C., Amend A., Charbit A., Chercuani F., Couve E., de Daruvar A., Dehoux P., Charbit A., Chercuani F., Couve E., de Daruvar A., Dehoux P., Entian E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O., Entian E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O., Entian K.-D., Fshih H., Gamcz-Lopez N., Hain T., Hauf J., Jackson D., Jones L., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G., Jones E., Maitcurnam A., Mata Vicente J., Ng E., Nacjari H., Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A., Charder P., Parche P., Bloecker H., Brandt P., Chakraborty T., Charbit A., Chetounani P., Couve E., de Dartwar A., Dehoux P., Domann E., Domann E., Domann E., Domann E., Domann E., Domann E., Domann E., Durant L., Dussurget O., Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P., Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D., Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G., Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H., Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R., Raguez-Boland J.-A., Voss H., Wehland J., Cossart P.,
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                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
Listeriaceae; Listeria.
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Bacteria, Pirmicutes; Bacillus/Clostridium group; Bacillales;
Listeriaces; Listeria.
NCBI_TaxID=1639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.2%; Score 31; DB 16; Length 149; 85.7%; Pred. No. 34;
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EMBL; ALS96168; CAC96635.1; -
ListLilst; LINO1404; -.

Literilst; LINO1404; -.

Fam: PF01316; Arg_repressor; 1.

Pfam; PF01316; Arg_repressor; 1.

ProDom; PD07402; Arg_repressor; 1.

ProDom; PD07402; Arg_repressor; 1.

ProDom; PD07402; Arg_repressor; 1.

ProDom; PD07402; Arg_repressor; 1.

ProDom; PD07402; Arg_repressor; 1.

SEQUENCE 149 AA; 16811 MW; 364222B56ADDE1BF CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein lmo1367.
                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Hypothetical protein lin1404.
                               149 AA
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                                                                                                 Created)
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STRAIN=CLIP 11262 / SEROVAR 6A;
PubMed=11679669;
                           Q92BY8
Q92BY8;
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 85.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                     Listeria innocua.
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Q8Y7B9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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85.7%; Pred. No. 34;
ive 1; Mismatches 0; Indels
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Cossart P.,
                                                                                                                                                                                     EMBL; ALS91978; CAC9945.1; -.
ListLilist; LM001367; -.
ListLilist; LM001367; -.
Pidam; PF00114; Arg_repressor; 1.
Probom; PF002863; Arg_repressor C; 1.
Probom; P007402; Arg_repressor C; 1.
Hypochetical protein; Complete proteome.
SEQUENCE 149 AA; 16778 MW; 25622476E092E1A1 CRC64;
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                                         Vazquez-Boland J.-A., Voss H., Wehland J., C. "Comparative genomics of Listeria species."; Science 294:849-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1251 AA.
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01-OCT-2000 (TrEMBLrel. 15, Last seq
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Best Local Similarity 85.7
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nes 6; Conservative
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SEQUENCE FROM N.A.

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SEQUENCE FROM N.A.

SEQUENCE TRAIN=0157:H7 / RIMD 0509952;

MEDLIME=21156231; PubMed=11258796;

HAYABH T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., HAYABH T., C.G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

Ida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,

Kuhara S., Shiba T., Hattori M., Shinagawa H.;

Ruhara S., Shiba T., Hattori M., Shinagawa H.;

Complete genome sequence of enterohemorrhagic Escherichia coli

O157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 811-22(2001).

EMBL; ARO03563; BAB37111.1;

NR EMBL; ARO03563; MutH.

PROME PROSPOSO MUTH.

PROME PROSPOSO MUTH.

REMBL; ARO03664; MutH; 1.

MC Complete proteome.
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Perna N.T., Plunkett G. III, Burland V., Mau B., Glaener J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533 (2001).
                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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85.7%; Pred. No. 1.5e+02;
.ive 0; Mismatches 1; Indels
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01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                       01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261 AA.
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Bacteria, Firmicutes; Bacillus/Clostridium
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                                                                                                                            PRT;
                                                                                                                                                                                                                                             Methyl-directed mismatch repair.
MUTH OR Z4149 OR ECS3688.
Escherichia coli 0157:H7.
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Best Local Similarity
Matches 6; Conserv
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  23 NAKTLT 28
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EMBL, AL391737; CAD24904.1; -. Hypothetical protein.

SEQUENCE 1251 AA; 144573 MW; 2302875E5350DA11 CRC64;
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Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
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Pred. No. 4.8e+02;
1; Mismatches 0; Indels
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                                                                                                                                                Encephalitozoon cuniculi.
Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.
NCBI_TaxID=6035;
                                                                                                                                                                                                                                                                                                 Genoscope;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
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Pfam; PF00699; Urease_beta; 1.
ProDom; PD0021326; Urease_beta; 1.
TIGRPAMs; TIGR00192; urease beta; 1.
SEQUENCE: 106 AA; 11678 MW; 39783E13202349D3 CRC64;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypotherical protein ECU01_0350.
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Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21, Last ann
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Best Local Similarity 85.7°,
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1205 NAKTLSE 1211
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Q9L643;
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STRAIN=EM1;

Length 229;

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SEQUENCE FROM N.A.

STRAIN=ATCC 35092 / DSM 1617 / P2;

STRAIN=21312956; PubMed=11427726;

She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

"The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";

Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
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                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N., Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
3-1sopropylmalate dehydratase, large subunit (isopropylmalate isomerase) (IPMI) (leuC) (EC 4.2.1.33).
                                                                                                        Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.3%; Score 29; DB 17; Length 416;
85.7%; Pred. No. 2.7e+02;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 351;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 85.3%; Score 29; DB 16; Length 35 Best Local Similarity 85.7%; Pred. No. 2.3e+02; Matches 6; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0415; ACONITASE.
ProDom; PD000511; Aconitase N; 1.
Lyase; Complete proteome.
SEQUENCE 416 AA; 45253 MW; 5A342E12C6B88796 CRC64;
01-MAR-2002 (TrEMBLrel. 15, Last sequence update) Hypothetical protein BH3573.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       416 AA
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Sulfolobus solfataricus.
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                                                                                             Bacillus halodurans.
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Best Local Similarity
6, Conserve
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3 SAKTLTE 9
                                                                                                                                                      NCBI_TaxID=86665;
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Q97VY2
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           Matuschek M., Sahm K., Bahl H.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES
-!- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES
THEN IS RELEASED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE SIGMA-70 FACTOR FAMILY.
EMBL: U50951; AAB08043.1; --
HSSP; PO0579; 1SIG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=COLUMBIA;
MEDLINE=99397451; PubMed=10470850;
Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Kotani H.,
Kaneko T., Tabato S.;
"Structural analysis of Arabidopsis thaliana chromosome 5. IX.
Sequence features of the regions of 1,011,550 bp covered by seventeen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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85.7%; Pred. No. 2.1e+02;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                              Length 261;
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PRINTS; PR00046; SIGMA70FCT.
PROSITE; PS00716; SIGMA70_1; 1.
PROSITE; PS00716; SIGMA70_2; 1.
DNA-binding; DNA-directed RNA polymerase; Sigma factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALLEGICO, ALCONO DESCRIPTION A.
PRINTS, PROD348; UBIQUITIN.
SMART, SMO0213; UBO, 4.
PROSITE, PSC00299; UBIQUITIN 1; 2.
PROSITE; PSC0053; UBIQUITIN 2; 4.
SEQUENCE 322 AA; 36256 MW; 8E1D215E50085A99 CRC64;
                                                                                                                                                                                                                                                                                     Transcription regulation.
SEQUENCE 261 AA, 30627 MW, A99F6038F2842242 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                          85.3%; Score 29; DB 2; I
85.7%; Pred. No. 1.7e+02;
iive 0; Mismatches 1;
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01-OCT-2000 (TrEMBLrel. 15, Created)
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EMBL; AB018107; BAB08310.1; -.
HSSP; P02248; 1UBI.
                                                                                                                                                                      InterPro; IPR000943; Sigma_70.
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Best Local Similarity 85.7°
6; Conservative
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Best Local Similarity
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Q9K701 RESULT 10 Q9K701 ID Q9K703 AC Q9K703 DT 01-OC7

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QBUSF8; QBUSFB

DDT ACCOUNT OF THE PROPERTY OF

RESULT 12 Q8U5F8

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STRAIN=13 / TYPE A;
PubMed=11792842;
Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
"Complete genome sequence of Clostridium perfringens, an anaerobic
flesh-eater.";
                                                                                                                             Clostridium perfringens.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
Clostridiales; Clostridiaceae; Clostridium.
NCBI_TaxID=1502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria, Proteobacteria, gamma subdivision, Pasteurellaceae,
Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85.3%; Score 29; DB 16; Length 472; 100.0%; Pred. No. 38+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 475;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               472 AA; 51056 MW; CF8FB1C27533FE99 CRC64;
                                                     01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Probable glutamate gamma-aminobutyrate antiporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) Hypothetical protein PM0735.
                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
EMBL; AP003192; BAB81766.1; -.
InterPro; IPR00293; AA/rel_prmeasel.
InterPro; IPR004641; Permease.
Pfam; PF00324; aa_permeases; 1.
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Pred. No. 3.1e+02;
0; Mismatches 1,
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                    472 AA
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STRAIN=PM70;
MEDLINE=21145866; PubMed=11248100;
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Local Similarity 85.7%;
nes 6; Conservative (
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                    PRELIMINARY;
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STRAIN=13 / TYPE A;
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SEQUENCE 472 AA
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Q8XIQ4
ID Q8XIQ4
AC Q8XIQ4;
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Matches
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Bukaryota, Viridiplantae; Streptophyta; Bmkryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-21608551; PubMed=11743194;
MEDLINE-21608551; PubMed=11743194;
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Cielo C., Slater S.,
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AGR C 1649.

Agrobacterium tumefaciens (strain C58 / ATCC 33970).

Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
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Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB070748; BAB86923.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58."; Science 294:2323-2328(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 85.3%; Score 29; DB 16; Length 468; Similarity 71.4%; Pred. No. 3e+02; 5; Conservative 2; Mismatches 0; Indels
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SEQUENCE 468 AA; 51681 MW; 5CD479AF05DFD15F CRC64;
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                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                        PRELIMINARY;
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266 NAKTITD 272
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**Q8S9A4** 

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Matches

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289 NAKTITD 295
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Query Match
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Q8XTA0
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STRAIN=16M / ATCC 23456 / BIOTYPE 1;
MEDLINE=20020109; PubMed=11156688;
MEDLINE=20020109; PubMed=11156688;
DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T., Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G., Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E., Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., Hagius R., Kyrpides N., Overbeek R.; Intracellular pathogen Brucella melitensis.;
                                                                                                                                                                                                                                                                             STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
MEDLINE=21082930; PubMed=11214968;
Maneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., "Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                    Rhizobium loti (Mesorhizobium loti).
Bacteria, Proteobacteria, alpha subdivision, Rhizobiaceae group,
Phyllobacteriaceae, Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Brucellaceae; Brucella.
NCBI_TaxID≂29459;
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                                         01-OCT-2001 (TrEMBLrel. 18, Last sequence update) 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
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EMBL; AE005569; AAL52499.1; -
InterPro; IPR000845; PNP UDP.
Pfam; Pfam; PNP UDP.
Hydrolase; Glycosidase; Complete proteome.
SEQUENCE 491 AA; 54760 MW; 7AE3118EFCC17FB0
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                   01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2001 (TrEMBLrel. 18,
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Best Local Similarity 71.4:
Matches 5; Conservative
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285 NAKTITD 291
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Best Local Similarity
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SEQUENCE 487 AA;
                                                                                             AMP nucleosidase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nester E.W.;
"The genome of the natural genetic engineer Agrobacterium tumefaciens C58.";
                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-Z1608550, The Numbed=11743193; Words D.E., Kitajima J.P., Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okuta V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Elsen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A. Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A. Saymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D., Shang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Nester E.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                  Agrobacterium tumefaciens (strain CS8 / ATCC 33970).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.3%; Score 29; DB 16; Length 49
85.7%; Pred. No. 3.2e+02;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            493 AA; 52866 MW; 3AD4B8D13BCC7467 CRC64;
                                                        (TrEMBLrel. 21, Created)
(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UJN-2002 (TrEMBLrel. 21, Last annotation update)
Probable AMP nucleosidase protein (EC 3.2.2.4).
AMN OR RSP0214 OR RS05213.
Ralstonia solanacearum (Pseudomonas solanacearum).
   493 AA
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                                                     01-JUN-2002 (TrEMBLrel. 21, Cre 01-JUN-2002 (TrEMBLrel. 21, Las 01-JUN-2002 (TrEMBLrel. 21, Las Aldehyde dehydrogenase.

DHAS OR ATU4241 OR AGR_L_1241.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE009353; AAL45035.1; -. EMBL; AE008260; AAK89198.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 294:2317-2323(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
PRELIMINARY;
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Gaps

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500 AA.
                                            (TrEMBLrel. 19, Created)
  PRT;
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                                                                                                                                                                                                                                                                                   MEDLINE=21396507; PubMed=11481430;
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MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         investigating biology. The C Science 282:2012-2018(1998).
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    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 NAKTITD 304
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les 5; Conserv
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                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                        NCBI_TaxID=382;
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                                          01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                     STRAIN=1021
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Q95QX8;
    Q92R69
Q92R69;
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MEDLINE=21608560; Pubmed=11743193;

MOOD D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

Mood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,

A Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

Rutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,

A Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,

A Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,

A Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,

A Nester E.W.,

The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                       Arlat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
Chandler M., Choisen N., Claudel-Renard C., Cunnac S., Demange N.,
Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
A Weissenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
"Mature 415:497-502(2002)
"In RemBi, AL646077, CAD17365.1;
"In InterPro; IPR002106; AAtRNA ligaseII.
Refero; IPR002106; AAtRNA ligaseII.
Refero; IPR00345; FNP UDP 1; 1.
Refero; PS00339; AATRNA LIGASE II. 2; UNKNOWN 1.
Refero; Glycosidase; Plasmid; Complete protecome.
W Hydrolase; Glycosidase; Plasmid; Complete protecome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
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Pred. No. 3.2e+02;
2: Mismatches 0; Indels
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       494 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                        71.4%; Pred. ...
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                                     STRAIN-GM11000;
MEDLINE-21681879; Pubmed-11823852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 294:2317-2323(2001).
EMBL; AE009065; AAL42020.1; -.
Complete proteome.
SEQUENCE 494 AA; 54526 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 85.3%;
Similarity 71.4%;
5; Conservative
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292 NAKTITD 298
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292 NAKTITD 298
                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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[1]
SEQUENCE FROM N.A.
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Best Local Similarity
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RESULT 20 QBUGNO

Matches

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RESULT 21 Q92R69

Matches

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Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                         Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J., Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.; Sinorhizobium meliloti strain 1021."; Brock. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Probable AMP nucleosidase protein (EC 3.2.2.4)
AMN OR R01042 OR SMC02386.
Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria, Proteobacteria, alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85.3%; Score 29; DB 16; Length 50 71.4%; Pred. No. 3.2e+02; ive 2; Mismatches 0; Indels
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Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; U00048; AAL27228.1; -.
InterPro; IPR001085; Gly_HyMetransf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The sequence of C. elegans cosmid C05D11."; Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR000845; PNP UDP.
Pfam; PF01048; PNP UDP 1; 1.
Hydrolase; Glycosidase; Complete proteome.
SEQUENCE 500 AA; 55385 WW; 0B4C31860A6A4538 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 55.8 kDa protein.
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1 NAKTLT
                 NCBI_TaxID=305;
                                                                                 SEQUENCE
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Q9USM9;
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Q8R5Z3;
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SETARIA=ATCC 35210 / B31;

MEDLINE=98065943; PubMed=9403685;

Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,

Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,

Dougherty B., Tomb J.F., Fleischmann R.D., Richardson D.,

Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,

Van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,

Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,

Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
                                                                                                                                                                                                                                                 Gaps
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
probable bacteriophage-related protein.
RSC0839 OR RSO4987.
Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria, Proteobacteria, beta subdivision; Ralstonia group,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 715;
                                                                                                                                                                             Length 507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
Pfam; PF00464; SHWT; 1.
PROSITE; PS00096; SHMT; UNKNOWN_1.
Hypothetical protein.
SEQUENCE S07 AA; 55764 MW; 693B380E77BB07D8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  051542 PRELIMINARY; PRT; 715 AA.
051542;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Methyl-accepting chemotaxis protein (MCP-2).
                                                                                                                                                                      85.3%; Score 29; DB 5; I
85.7%; Pred. No. 3.3e+02;
:ive 0; Mismatches 1;
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85.7%; Pred. No. 4.6e+02;
ative 0; Mismatches 1;
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InterPro; IPR00360; HAMP.
Pfam; PR0672; HAMP; 1.
Pfam; PF00015; MCPsignal; 1.
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EMBL; AE001161; AAC66955.1; -.
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Matches 6, Conservative
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SMART; SM00283; MA; 1.
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                                                                                                                                                                                                                                                                                                                                                                            359 NAKTLAE 365
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"The multigene family of the tobacco hornworm V-ATPase: novel subunits
"The multigene family of the tobacco hornworm V-ATPase: novel subunits
B.C. D. H and putative isoforms.";
B.Ochim. Biophys. Acta 1467:369-379 (2000).
EMBL; AJ249190; CAB55500.1;
InterPro; IPR002490; V_ATPase_sub116.
Pfam; PF01496; V_ATPase_sub16.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Sphingiodea; Sphingidae; Sphinginae; Manduca.
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                                                                 Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Artiguenave M., Ellault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Cloudel-Fenard C., Cunnac S., Demange N. Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Welseenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
Nature 415:497-502(2002).
Complete proteome.
SEQUENCE 765 AA; 84779 MW; OAB174490618272E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2002 (TrEMBLrel. 20, Last annotation update)
Vacuolar ATPase subunit a (EC 3.6.1.35).
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Last sequence update)
Last annotation update)
box family)
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100.0%; Pred. No. 4.9e+02;
iive 0; Mismatches 0;
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                       STRAIN=GM11000;
MEDLINE=21681879; PubMed=11823852;
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
DNA/RNA helicase (DEAD/DEAH)
FN1974.
                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
ses 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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TISSUE=MIDGUT;
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Q8R5Z3
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SEQUENCE FROM N.A
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Carcinogenesis 17:1561-1566(1996).

-! FUNCTION: NOT KNOWN, MAY REGULATE GENE EXPRESSION. MAY PLAY A ROLE

-! SUBCELLULAR LOCATION AND DIFFERNITALION

-! SUBCELLULAR LOCATION: NUCLEAR (FOOTENTIAL).

-! SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.

EMBL; S82504; -; NOT ANNOTATED CDS.

EMBL; S82502; -; NOT ANNOTATED CDS.

EMBL; S82502; -; NOT ANNOTATED CDS.

EMBL; S82501; -; NOT ANNOTATED CDS.

EMBL; S82501; -; NOT ANNOTATED CDS.

EMBL; S82500; AAB37501.1; -

RILEPTO; IPRO01375; BRCT.

RILEPTO; IPRO01375; BRCT.

RILEPTO; IPRO0134; Zf Zing.

Pfam; PF00097; Zf C3HC4; 1.

PR PRINTS; PR00493; BRSTCHACKI.
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01-JUN-1998 (TERMELrel. 06, Created)
01-JUN-1998 (TERMELrel. 06, Last agenece update)
01-JUN-2002 (TERMELrel. 21, Last annotation update)
Breast cancer type 1 susceptibility protein (Breast and ovarian cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. .
STRAIN=SPRAGUE-DAWLEY;
MEDLINB=99111389; PubMed=9892727;
Bennett L.M., Brownlee H.A., Hagavik S., Wiseman R.W.;
"Sequence analysis of the rat brcal homolog and its promoter region.";
Mamm. Genome 10:19-25(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                    SEQUENCE FROM N.A.
STRAIN=ATCC 25586;
MEDLINE=21886394; PubMed=11889109;
MEDLINE=21886394; PubMed=11889109;
MEDLINE=21886394; Vanderson I., Ivanova N., Reznik G., Los T., Lykidis A., Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L., Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A., Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R., "Genotein M., Kyrpides N., Overbeek R.; "Genome sequence and analysis of the oral bacterium Fusobacterium nucleatum strain ATCC 25586.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 8-222 FROM N.A.
STRAIN-WISTAR-KYOTO; TISSUB-SPLEEN;
MEDLINE-96138532; PubMed-8761410;
Chen K.S., Shepel L.A., Haag J.D., Heil G.M., Gould M.N.;
"Cloning, genetic mapping and expression studies of the rat Brcal
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                                                                                                                                                                                                                                                                                                                                                                                                                                   85.3%; Score 29; DB 16; Length 942;
85.7%; Pred. No. 6.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                         110580 MW; B3F40B0AAE05C0B2 CRC64;
  Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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EMBL; AE010499; AAL94064.1; -.
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SEQUENCE 942 AA; 110580 1
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Matches 6; Conserv
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                                            NCBI_TaxID=76856;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
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Pred. No. 1.2e+03;
0; Mismatches 1; Indels
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Rickettsiaceae; Rickettsieae; Rickettsia.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Similarity to type I'restriction enzyme M subunit.
RC1350.
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01-UNN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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EMBL; AE008681; AAL03888.1; -.

InterPro; IPR001899; Gram pos_anchor.

InterPro; IPR00356; N6 DNA_Mtase.

Pfan; PF02384; N6 Mtase; 1.

PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
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NCBI_TaxID=1314;
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981 NRKTLTE 987
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STRAIN=MALISH 7;
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"Structural analysis of Arabidopsis thaliana chromosome 5. V. Sequence features of the regions of 1,381,565 bp covered by twenty one physically assigned P1 and TAC clones.";

DNA Res. 5:131-145(1998).
Gaps
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MEDLINE=9834145; PubMed=9679202;
Kaneko I., Kotani H., Nakamura Y., Sato S., Asamizu E., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Saguier P., Laver M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Mincker P., Levy M., Welssenbacch J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
Nature 415,497-502(2002).
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Bacteria, Proteobacteria, beta subdivision, Ralstonia group,
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85.7%; Pred. No. 2.5e+02;
ive 0; Mismatches 1; Indels
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Pred. No. 2.4e+02;
0; Mismatches 1; Indels
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SEQUENCE 227 AA; 25127 MW; 3C2B273B4272D491 CRC64;
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InterPro; IPR001345; PG/BPGM_mutase.
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MEDLINE=21681879; PubMed=11823852;
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PROSITE; PS00175; PG MUTASE; 1.
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176 NAMTLTE 182
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Best Local Similarity
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01-MAR-2002 (
01-MAR-2002 (
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P71631;
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P71631
ID P7163
AC P7163
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                                              MEDINE=21192684; PubMed=11295296;
Perretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Scarte S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
"Complete genome sequence of an M1 strain of Streptococcus pyogenes.", Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
EMBL, AE006499; AAX33403.1; ...
InterPro: IPR003607; ME_Pplase_HDc.
SMART; SM00471; HDC; 1...
Hypochacical protein; Complete proteome.
SEQUENCE 166 AA; 20033 MW; 0A82100E7CA83904 CRC64;
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Kim J.-H.F., Wei Z.-M., Beer S.V.;

"Complementation groups II and III of the Erwinia amylovora hrp gene

cluster are required for secretion of harpin.";

Phytopathology 85:1163-1163(1995).
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Kim J.F., Wei Z.M., Beer S.V.;
"The hrpA and hrpC operons of Erwinia amylovora encode components of
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Chalcone isomerase-like protein.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                        Score 28; DB 16; Length 166;
Pred. No. 1.8e+02;
0; Mismatches 1; Indels
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100 0%; Pred. No. 2.1e+02; Indels
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                              STRAIN=SF370 / ATCC 700294 / SEROTYPE M1;
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J. Bacteriol. 179:1690-1697(1997).
EMBL; U56662; AAB49176.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                   82.4%;
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01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
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Query Match
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6; Conservative
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Best Local Similarity
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SEQUENCE FROM N.A.
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Q46622;
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O9FKW3
DD O9FKW
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STRAIN=CDC 1551 / OSHKOSH;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                    Harris D.,
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MEDLINE=2160856; PubMed=11743193;
MEDLINE=2160856; PubMed=11743193;
MEDLINE=2160856; PubMed=11743193;
Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                               Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D. Gordon S.V., Eighmeier K., Gas S., Barry C.E. III, Teksia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., Stutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                               Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Periplasmic immunogenic protein.
PP26 OR ATU2162 OR AGR_C_3922.
Agrobacterium tunefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; Z81311; CAB03665.1; ---
EMBL; AR007114; AAK47213.1; ---
                                                                                                                                       Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tuberculist; Rv2821c; -.
Hypothetical protein; Complete proteome.
SEQUENCE 236 AA; 25773 MW; 1728D20400321017 CRC64;
                     (TrEMBLrel. 02, Last sequence update) (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 Similarity 100.0%; Pred. No. 2.6e+02; 6; Conservative 0; Mismatches 0;
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  02, Created)
                                                                                                                                                                                                                                                                            MEDLINE=98295987; PubMed=9634230;
                                                                  Hypothetical protein Rv2821c.
RV2821C OR MTCY16B7.21 OR MT2888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                               Mycobacterium tuberculosis.
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01-FEB-1997
01-FEB-1997
01-MAR-2002
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Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fletschmann R.D., Alland D., Eisen J.A., Haft D., Hickey E.,
Feterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
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Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Guroll B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
Houmiel K., Gordon J., Vaudin M., lartchouk O., Epp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
"Genome sequence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens C58.";
                                                                                                            Nester E.W.;
"The genome of the natural genetic engineer Agrobacterium tumefaciens
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
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MEDLINE=9292997; PubMed=9634230;
Gole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Hornsby T., Jagels K., Kroph A., McLean J., Moule S., Hamlin N., Holroyd Shorne S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Sulston J.E., Taylor K., Skelton S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
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100.0%; Pred. No. 2.7e+02;
.ive 0; Mismatches 0; Indels
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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01-JUL-1997 (TrEMBLrel. 04, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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EMBL; AE009166; AAL43151.1; -.
EMBL; AE008132; AAK87907.1; -.
                                                                                                                                                                                                                             Science 294:2317-2323(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
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                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lactococcus lactis.
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales; Streptococcaceae; Lactococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sanz Y., Lanfermeijer F.C., Hellendoorn M., Kok J., Konings W.N.,
Poolman B.;
"Localization of the Leptospira interrogans metF gene on the CII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Two homologous oligopeptide binding protein genes (oppA) in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82.4%; Score 28; DB 2; Length 294; 100.0%; Pred. No. 3.2e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                          Length 293;
                                                                                                                                                                                                                                                       1; Indels
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
EMBL, AFP45305, AAKS6894.1;
InterPro, IPR000515; BPD_transp.
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Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
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SEOUENCE 294 AA; 33003 MW; B3AB6171C614F4B2 CRC64;
                                                                                                                                       Pfam; PF02219; MTHFR; 1. _ SEQUENCE 293 AA; 32610 MW; B997A57B4DD3F4A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                        82.4%; Score 28; DB 2; I
llarity 85.7%; Pred. No. 3.2e+02;
Conservative 0; Mismatches 1;
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                     secondary chromosome.";
FEMS Microbiol. Lett. 191:259-263 (2000)
EMBL, $23561; AAF64321.1;
HSSP; P00394; 185T.
InterPro; IPR003171; Mehydrof_redctse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2002 (TrEMBLrel. 20, Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1997 (TrEMBLrel. 02, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1997 (TrEMBLrel. 02,
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                                                                                                                                                                                                                                  Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                     1 NAKTLTE 7
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ZC47.3a protein.
ZC47.3A.
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Q93QI0;
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Q94382;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsumo A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.; Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
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85.7%; Pred. No. 3.1e+02;
iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690;
                                                                                        InterPro, IPR001753; EnCoA_hydrtse.
Pfam; PR00178; ECH; I.
Hypothetical protein; Isomerase; Complete proteome.
SEQUENCE 268 AA; 27649 MW; 8EFABFFIGIFDBDC0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 protein; Complete proteome.
287 AA; 31891 MW; 7625C0A12CC3E82A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Spirochaetales; Leptospiraceae; Leptospira.
NCBI_TaxID=173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein All4871.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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01-OCT-2000 (TEMBLrel. 15, Last sequence
01-MR-2002 (TEMBLrel. 20, Last annotation)
5,10 methylene tetrahydrofolate reductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AP003597; BAB76570.1; -.
InterPro; IPR002123; Acyltransferase.
Pfam; PF01553; Acyltransferase; 1.
Hypothetical protein; Complete proteor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=21595285; PubMed=11759840;
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SEQUENCE FROM N.A.
MEDLINE=20480680; PubMed=11024273;
BOUTHY P., Saint Gixons I.;
                       AE006996; AAK45434.1;
  EMBL; Z95584; CAB09030.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 85.7
nes 6; Conservative
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                                          TIGR; MT1175; -.
TubercuList; Rv1142c;
                                                                                                                                                                                                                                                                                                                                             223 NAATLTE 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223 NAKRLTE 229
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Best Local 8
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QBYMR2;
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08YMR2
AC Q8YMR
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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"Genome sequence of the nematode C.elegans: A platform for investigating biology.";
Science 28:2012-2018(11998).
EMBL; Z81141; CABO3492.1;
InterPro; IPR001801; F-box.
InterPro; IPR001810; F-box.
Pfam; PF0046; F-box; 1.
R Pfam; PF0046; F-box; 1.
R SMART; SM00256; RBOX; 1.
R PROSITE; PS50181; RBOX; 1.
                              'Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 304;
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MCMurray A.A.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                         investigating biology.";
Science 282:2012-2018(1998).
EMBL; 28141; CAB03491.1; -.
InterPro; IPR001910; F-box.
Pfam; PF01827; DUF38; 1.
Pfam; PF00426; F-box; 1.
SMART; SM00256; FBOX; 1.
PROSITE; PS50181; PBOX; 1.
SRQUENCE 304 AA; 35542 MW; OBEC3888A963909B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
2C47.3B protein.
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 82.4%; Score 28; DB 5; I Best Local Similarity 85.7%; Pred. No. 3.3e+02; Matches 6; Conservative 0; Mismatches 1;
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Murine PIP3 recogn Light chain variab Murine PIP3 recogn Anti-DNA antibody Anti-DNA antibody Anti-DNA antibody Anti-DNA antibody Anti-DNA antibody VH and VL of MAb P

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AAY87662

3B10xF5-2 bispecif 8019 VK antibody. Murine 15B8 light Murine 15B8 light Amino acid sequence Anti-human gp39 MA Predicted sequence Humanised MAD 39-1 Sequence of the sh Mouse MAD 2G12 L Light (KADDA) Chai Recombinant mouse Murine MC-1 antibo Murine Muman PTHrP mouse Human PTHrP mouse Human PTHrP mouse Human anti-placent Humanised iblo antibody li	ρ ω ψ · · · · · · · · · · · · · · · · · ·
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This invention describes a novel antibody specifically recognizing phosphatichidylinostice. 4.5-triphosphate (PPR3). The antibody of the invention is used in immunogenic compositions in which a dead salmonella genus microbe is used as an adjuvant and mixed with PIP3. The antibody can be used in an immunosasay contraining a step in which the above antibody or its variable region is reacted with PIP3 present in a sample and the bond based on their immunological reaction. The method can determine PIP3 eaally in a high sensitivity. This sequence represents the murine PIP3 recognizing monoclonal antibody variable region light chain complementarity determining region, CDR3 described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hybridoma antibodies have been produced with the spleen cells of BALB/c mouse that had received multiple injections of mercuric ions reacted with glutathione to produce a mercuric ion coordinate covalent compound which was covalently bound to keyhole limpet covalent compound which was covalently bound to keyhole limpet covalent compound which was cavalently bound to keyhole limpet covalent compound which was [1F10, 4A10, 1C11, 5G4, 23F8, 2D5, 5B6 and 3E8) were producing MADS that were strongly positive against glutatione-mercuric ions but negative against glutathione without mercuric ions. RNA was isolated from hybridoma cells with guanidine isothiocyanate. First strand cDNA synthesis was catalysed by Multy reverse transcriptese. The primers used for cDNA synthesis contine expressed by the hybridoma of interest, or to the Fs and of the C kappa domain. Some of the primers used for cDNA synthesis are shown in AAQ97511-Q97518. The primer used for cDNA synthesis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptide(s) which bind heavy metals, esp. mercury - derived from monoclonal antibodies, used for detecting, removing, adding or neutralising heavy metals
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        for PCR amplification of that variable region, in conjunction with an appropriate V-region primer. In addition, the VH primer AAQ97518 was used to amplify the MAD 2DS and 5B6 heavy chains. The sequences of the PCR amplified nucleotides were determined. These are given in AAQ97498-Q97510 and the deduced AA sequences in AAR79241-R79250 ft AAR78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45 and in the claims are different from the descriptions in the sequence listings are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the murine PIP3 recognizing monoclonal antibody variable region light chain described in the method of the invention.
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antibody polypeptide was also used
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(IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.
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Score 54; DB 18; Length 99; Pred. No. 0.074; 1; Mismatches 0; Indels

93.1%; 88.9%;

99 AA;

Conservative

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Similarity
8; Conserva
                                                                                  1 QHHYGTPYT
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              Sequence
                                    Query Match
                                                 Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-DNA antibody which specifically binds DNA hairpin - useful to develop prods. for diagnosis and treatment of disorders, e.g. glomerulonephritis or systemic lupus erythematosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorder.

Calf thymus DNA was used to immunise a MRL-1pr mouse, spleen cells from which were then fused with Sp2/0 myeloma cells to give hybridomas producing the anti-DNA MAD. 15d8 was found to react strongly with single stranded DNA and poly(dT), and weakly with poly(dG).
                                                                                                                                                                          Light chain; variable region; anti-DNA; monoclonal; antibody; MAb 15d8; hairpin; diagnosis; inflammatory glomerulonephritis; systemic lupus erythematosus; screening; treatment; prevention;
                                                                                                                                                      Anti-DNA antibody 15d8 light chain variable region.
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/label= framework_II
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                                                                                AAW04587 standard; Protein; 99 AA
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/label= CDR_III
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/label= CDR_II
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/label= CDR_I
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                                                                                                                              (first entry)
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            QHHYGTPYT
 QHHYGTPYT
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                                                                                                                              12-AUG-1997
                                                                                                                                                                                                                SLE; disease
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                                                        RESULT 4
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The present sequence is the light chain variable region of the anti-DNA monoclonal antibody (MAb) 9f11, which has a high affinity for single stranded DNA, low or no affinity for double stranded DNA and specifically pinds a DNA hairpin. The MAD can be used diagnose disorders associated with the pathological complexation of DNA, e.g. inflammatory glomerulonephritis and systemic lupus erythematosus. It can also be used to generate reagents to screen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-DNA antibody which specifically binds DNA hairpin - useful to
                                                                                                                                                                    Light chain; variable region; anti-DNA; monoclonal; antibody; MAb 9f11; hairpin; diagnosis; inflammatory glomerulonephritis; systemic lupus erythematosus; screening; treatment; prevention;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        develop prods. for diagnosis and treatment of disorders, e.g. glomerulonephritis or systemic lupus erythematosus
                                                                                                                                             Anti-DNA antibody 9f11 light chain variable region.
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/label= framework_III
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|abel= framework II
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| label= framework_I
                                                                  AAW04596 standard; Protein; 99 AA.
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/label= J_region
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/label= CDR_III
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/label= CDR_II
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                                                                                                                   12-AUG-1997 (first entry)
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 83
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81 QHHYGTPFT
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WPI; 1997-011854/01.
N-PSDB; AAT43743.
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      disorder.

Calf thymus DNA was used to immunise a MRL-1pr mouse, spleen cells from which were then fused with Sp2/0 myeloma cells to give hybridomas producing the anti-DNA MAb. 9f11 was found to react strongly with single stranded DNA and poly(dT), and weakly with
                                                                                                                                                                                                                  Light chain; variable region; anti-DNA; monoclonal; antibody; MAb 15b10; hairpin; diagnosis; inflammatory glomerulonephritis; systemic lupus erythematosus; screening; treatment; prevention; SLE; disease.
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pharmaceutical agents, and treat and/or prevent an above
                                                                         Score 54; DB 18; Length 99;
Pred. No. 0.074;
1; Mismatches 0; Indels
                                                                                                                                                                                                          Anti-DNA antibody 15b10 light chain variable region.
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/label= framework_III
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/label= CDR_II
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/label= CDR_I
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Best Local Similarity 88.9%;
Matches 8; Conservative
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/label= 1
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N-PSDB; AAT43742.
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81 QHHYGTPFT
                                                                                                        1 QHHYGTPYT
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The present sequence is the light chain variable region of the anti-DNA monoclonal antibody (MAb) 15bl0, which has a high affinity for single stranded DNA, low or no affinity for double stranded DNA and specifically binds a DNA hairpin. The MAb can be used diagnose disorders associated with the pathological complexation of DNA, e.g. inflammatory glomerulonephritis and systemic lupus erythematosus. It can also be used to generate reagents to screen
                                                                                                                                                                                                                     disorder.

Calf thymus DNA was used to immunise a MRL-lpr mouse, spleen cells from which were then fused with Sp2/0 myeloma cells to give hybridomas producing the anti-DNA MAD. 15b10 was found to react strongly with single stranded DNA and poly(dT), and weakly with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Light chain; variable region; anti-DNA; monoclonal; antibody; MAD 513; hairpin; diagnosis; inflammatory glomerulonephritis; systemic lupus erythematosus; screening; treatment; prevention; SLE; disease.
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                                                                                                                                                                                               for pharmaceutical agents, and treat and/or prevent an above
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 54; DB 18; Length 99; Pred. No. 0.074;
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/label= framework_III
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/label= framework_II
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/label= framework
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/label= J_region
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/label= CDR_I
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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/label=
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PE38KDEL; plasmid; pUL140; heavy; chain; light; variable region; VH; WL; monoclonal antibody; WAb; PR1; PCR; amplify; PR1-hybridoma RNA; primer; complementarity determining regions; CDR; drug; cytotoxin; prostate cell associated antigen; radioisocope; PCAA; prostate; cells; cancer; diagnosis; benign prostate hyperplasia.
                                                                                                                                                                                                     The present sequence is the light chain variable region of the group 9f11 putative consensus anti-DNA monoclonal antibody (MAb), which has a high affinity for single stranded DNA, low or no affinity for double stranded DNA and specifically binds a DNA hairpin. The MAb can be used diagnose disorders associated with the pathological complexation of DNA, e.g. inflammatory glomerulonephritis and systemic lupus erythematosus. It can also be
                                                                                                                                                                                                                                                                                                                                used to generate reagents to screen for pharmaceutical agents, and treat and/or prevent an above disorder.

He sequence was derived by aligning homologous anti-DNA MAb, whose sequences have been published, as well as several MAb of other specificities obtained from a database search.
                                                                                                                    develop prods. for diagnosis and treatment of disorders, e.g. glomerulonephritis or systemic lupus erythematosus
                                                                                                   Anti-DNA antibody which specifically binds DNA hairpin
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Pred. No. 0.081;
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/label= PR1 Vl
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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              Swanson PC;
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                                                 WPI; 1997-011854/01.
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                                                                    N-PSDB; AAT43808
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              Glick GD,
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                                                                                                              The present sequence is the light chain variable region of the anti-DNA monoclonal antibody (MAb) 5f3, which has a high affinity for single stranded DNA, low or no affinity for double stranded DNA and specifically binds a DNA hairpin. The MAb can be used diagnose
                                                                                                                                                                                                                                                          disorder.

Calf thymas DNA was used to immunise a MRL-lpr mouse, spleen cells from which were then fused with Sp2/0 myeloma cells to give hybridomas producing the anti-DNA MAb.
              useful to
                                                                                                                                                                                    disorders associated with the pathological complexation of DNA, e.g. inflammatory glomerulonephritis and systemic lupus erythematosus. It can also be used to generate reagents to screen for pharmaceutical agents, and treat and/or prevent an above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Light chain, variable region, anti-DNA, monoclonal, antibody, 9f11 group; hairpin, diagnosis, inflammatory glomerulonephritis, systemic lupus erythematosus, screening; treatment; prevention; SLE, disease; consensus; putative.
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         Anti-DNA antibody which specifically binds DNA hairpin - usef develop prods. for diagnosis and treatment of disorders, e.g. glomerulonephritis or systemic lupus erythematosus
                                                                                                                                                                                                                                                                                                                                                                                     Score 54; DB 18; Length 99;
Pred. No. 0.074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-DNA antibody 9f11 group light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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/label= J_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 io..56
/label= CDR_II
                                                                             Example; Fig 8; 102pp; English
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/label= CDR_I
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88.9%;
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/label= f
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/label= f
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/label= (
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81 OHHYGTPFT 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QHHYGTPYT
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                  99 AA;
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                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW07439;
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RESULT 8

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AAW07439

Key

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Gaps

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Length 107; 0; Indels us-10-007-790-10.rag

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pullato and represents the heavy chain and light chain variable regions pullato and represents the heavy chain and light chain variable regions (WH and VL) of the monoclonal antibody (WAb) PR1. The CDNA encoding this sequence was derived by PCR amplification of reverse transcribed PR1-hybridoma RNA using the primer sequences given in AAG64477-81. The VH and VL complementarity determining regions (CDRs) are used in the construction of the MAb of the invention which competes with RN1 for binding to a prostate call associated antigen. The MAb of the invention can be used for targetting a drug, cytotoxin or radioisotope to prostate cells of a patient suffering from prostate cancer. It can individual and for the diagnosis and treatment of other conditions involving abnormal growth of prostate cells, eg. benign prostate in an individual and for the diagnosis and treatment of other conditions involving abnormal growth of prostate cells, eg. benign prostate cells but only weakly with a few other normal human tissues. The effect of therapy on normal prostate cells does not threaten the overall health
                                                                                                                                                                                                                                                          sequence is encoded by the PE38KDEL fragment of the plasmid
                                                                                                Monoclonal antibody specific for prostate cells - used in the diagnosis and treatment of conditions involving abnormal growth of prostate cells, esp prostate cancer.
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0
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                                                                                                                                                                                                       Example 3; Fig 1; 64pp; English
                        WPI; 1994-151334/18.
N-PSDB; AAQ64476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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Best Local Similarity 88.9 Matches 8; Conservative |||||||:| QHHYGTPFT 230 1 QHHYGTPYT 9 222 음

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Gaps

AAU72864 standard; Protein; 256 AA (first entry) P4-15 single chain Fv. 26-FEB-2002 AAU72864; RESULT 10 AAU72864 

Human; NKG2D; NKG2D receptor complex; cancer; infectious disease; tumour; autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary; intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix; prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; Fv sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DAP10; helminth; cytostatic; antimicrobial; immunomodulatory; l1B2D10; 6H7B7; 8G7C10; 6E5A7; 11B2D10; 6H7B7; 8G7C10; 6E5A7; 11B2D10x4-7; 8G7C10x4-7; 6E5A7x4-7; P4-2; P4-3; P4-14; P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; 3B10xP4-3; 3B10xP4-14; p5-3 tetramerisation domain; 3B10xP5-2; 3B10xP5-23.

Homo sapiens

WO200171005-A2

27-SEP-2001

26-MAR-2001; 2001WO-EP03414

24-MAR-2000; 2000EP-0106467

(KUFE/) KUFER P.

Lutterbuese R, Borschert K, Kischel R; Riethmueller G, Hofmeister R; Kufer P, Mayer M,

The invention relates to a multifunctional polypeptide comprising a domain with a binding site that specifically recognises an extracellular group of the NKG2D receptor complex and a second domain which functions as a receptor or ligand. The polypeptide and its associated composition for the treatment of cancer, infections and/or autoimmune conditions. The cancer may be a tumour of the head and neck, stomach, composition for the treatment of cancer, infections and/or autoimmune conditions. The cancer may be a tumour of the head and neck, stomach, composition for interior, errors, prostate, kidney, testis, thyroid, bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma. The infectious diseases can be caused by viruses, bacteria, fungi, protezoa or helminths. The autoimmune diseases include multiple sclerosis, Grave's disease, ankylosing spondylitis, acute anterior uveitis, Goodpasture's syndrome, myssthenia gravis, insulin-dependent Multifunctional polypeptides comprising binding sites that specifically recognise extracellular groups of the NKG2D receptor complex and domains which function as receptors or ligands, useful for treating diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and autoimmune hepatitis. Sequences AAU72820-AAU72875 represent the NKG2D receptor and the polypeptides of the invention. Example 7; Fig 16; 114pp; English cancers and infectious diseases WPI; 2002-055119/07. N-PSDB; AAS97138. 256 AA; Sequence Query Match 

86.2%; Score 50; DB 23; Length 256; 88.9%; Pred. No. 0.96; ive 0; Mismatches 1; Indels Best Local Similarity 88.5 Matches 8; Conservative 226 QHHYGTPLT 234 1 QHHYGTPYT 9 ò

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Gaps

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AAU72873 standard; Protein; 503 AA. RESULT 11 AAU72873 

AAU72873;

(first entry) 26-FEB-2002

3B10xP5-2 bispecific single chain Fv.

Human; NKG2D; NKG2D receptor complex; cancer; infectious disease; tumour; autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary; intrahepatic bille duct; pancreas; lung; larynx; breast; uterus; cervix; prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; Fv; sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DAP10; helminth; cytostatic; antimicrobial; immunomodulatory; 1182D10; 6H7E7; 8G7C10; 6ESA7; 11B2D10; 447; 8G7C10x47; 6ESA7; 11B2D10x47; 6G5A7x47; 8G7C10x47; 6FSA7x47; 6FSA7

WO200171005-A2.

27-SEP-2001.

26-MAR-2001; 2001WO-EP03414.

24-MAR-2000; 2000EP-0106467.

(KUFE/) KUFER P.

Kufer P, Riethmueller G, Lutterbuese R, Borschert K, Kischel R;

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containing cytotoxin for treating cancer, infection or genetic
                                            Disclosure; Figure 12c; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                               Matches
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    ##X#XDDDDDDDDDDDDDXX
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                                                                                                                                                                  The invention relates to a multifunctional polypeptide comprising a domain with a binding site that specifically recognises an extracellular group of the NKG2D receptor complex and a second domain which functions as a receptor or ligand. The polypeptide and its associated polymorleotide are used for the preparation of a pharmaceutical composition for the treatment of cancer, infections and/or autoimmune conditions. The cancer may be a tumour of the head and neck, stomach, oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung, larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid, larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid, larynx, breast, ovary, uterus, cervix, prostate, bacteria, fungi, conditions diseases can be caused by viruses, bacteria, fungi, protozoa or helminths. The autoimmune diseases include multiple cure instructions, Grave's disease, ankylosing spondylitis, acute anterior uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and curoimmune hepatitis. Sequences AAV728020-AAVV2875 represent the NKG2D receptor and the polypeptides of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                     recognise extracellular groups of the NKG2D receptor complex and domains which function as receptors or ligands, useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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Pred. No. 2;
0; Mismatches 1; Indels
                                                                    polypeptides comprising binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW46483 standard; protein; 109 AA.
                                                                                                                                          Example 5; Fig 16; 114pp; English
                                                                                                                  cancers and infectious diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                               86.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Query Match
Best Local Similarity 88.90,
Best Local Similarity
8, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antigen; immuno-conjugate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   473 OHHYGTPLT 481
Hofmeister
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                             WPI; 2002-055119/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QHHYGTPYT
                                                                                                                                                                                                                                                                                                                                                                                                                                   503 AA;
                                            N-PSDB; AAS97147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8019 VK antibody
                                                                      Multifunctional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9803870-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
 Mayer M,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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AAW46483
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This is the amino acid sequence of 8019 VK antibody. The invention relates to the site-specific photo-attachment of a nucleic photo-affinity compound to an antibody which comprises reacting them under conditions that promote attachment of the photoaffinity compound to at least 1 nucleotide binding site in the antibody. Also claimed are: photoaffinity compound-antibody conjugates produced this way, and immuno-conjugates comprising cytotoxic or therapeutic agent site-specifically attached to the photoaffinity compound in the conjugate. When the conjugate is labelled it is used for detection or quantitation of an antigen (Ag) by any standard immunoassay format, while immuno-conjugates are used therapeutically, e.g. in cases of tumours, infections or genetic diseases, or as imaging agents. The conditions, particularly a single 2-5 minute photoactivation results in almost 100% attachment (contrast conditions usually required to attach
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Light chain; variable region; complementarity determining region; CDR 3; anti-Tie2 kinase receptor; monoclonal antibody; 15B8; angiogenetic; vascular-general; proliferative; antiischemic; cerebroprotective; cardiant; agonist; antibody inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY92161-63 are light chain CDR (complementarity determining regions) from a novel murine anti-Tie2 kinase receptor agonist monoclonal antibody 1588. Tie2 is a single-transmembrane, tyrosine kinase receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tie2 receptor agonist antibodies useful for promoting angiogenesis in patients suffering from strokes and myocardial infarctions
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                               Score 49; DB 19; Length 109;
Pred. No. 0.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murine 15B8 light chain variable region CDR 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 14; Page 41; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY92163 standard; Peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Holmes SD, Erickson-miller CL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SMIK ) SMITHKLINE BEECHAM CORP (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                           84.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Conservative
                                                                                                                                                                                                                                                                                                                           molecules to antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QHHYGTPYT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                        109 AA;
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                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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photo-affinity agents to antibodies - useful as immunoassay reagents for detecting antigen, also immuno-therapeutic complex also

Conjugates formed by site-specific attachment of nucleic

Rajogopalan K;

Pavlinkova G,

Kohler H,

BE,

Haley

WPI; 1998-120935/11.

(KENT ) UNIV KENTUCKY RES FOUND

97WO-US12223 96US-0681432

22-JUL-1997; 23-JUL-1996;

29-JAN-1998

Amino acid sequence of anti-p53 antibody light chain clone 163.9.

(first entry)

08-FEB-2001

AAB18865;

AAB18865 standard; Protein; 113 AA

RESULT 1

|||| ||| QHHYSIPYT 97

89

g

p53; antibody; immune response; vaccine; gene therapy; cancer; rheumatoid arthritis; coronary heart disease.

Homo sapiens.

(SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD

Coomber DWJ

Ward RL,

2000-638249/61.

N-PSDB; AAA96142

15-MAR-2000; 2000WO-AU00189

28-SEP-2000

19-MAR-1999;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      light chain, variable region, anti-Tie2 kinase receptor, agonist, monoclonal antibody, 15B8; Angiogenetic, vascular-general; proliferative, antiischemic, cardiant, cerebroprotective, antibody inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 may also
                                                     stroke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This is a murine anti-Tie2 kinase receptor agonist monoclonal antibody 15B8 light chain variable region. Tie2 is a single-transmembrane, tyrosine kinase receptor ('Tie' stands for tyrosine kinase receptor with immunoglobulin and endothelial growth factor (EGF) homology domain(s)). Anti-Tie2 antibodies may be administered to enhance anglogenesis in mammals suffering from ischemic disease, myocardial infarction or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tie2 receptor agonist antibodies useful for promoting angiogenesis in patients suffering from strokes and myocardial infarctions
('Tie' stands for tyrosine kinase receptor with immunoglobulin and endothelial growth factor (EGF) homology domain(s)). Anti-Tie2 antibodies may be administered to enhance angiogenesis in mammals suffering from ischemic disease, myocardial infarction or cerebral st or other vascular diseases such as diabetes. It may also be used to enhance endothelial cell survival and to promote haematopoietic or megakaryocyte cell proliferation (claimed).
                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                              ö
                                                                                                                                                                          79.3%; Score 46; DB 21; Length 9; 77.8%; Pred. No. 7.8e+05;
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                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murine 15B8 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                   AAY92157 standard; Protein; 107 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 10; Page 38; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Erickson-miller CL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM CORP (SMIK ) SMITHKLINE BEECHAM PLC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                          Local Similarity 77.8
hes 7; Conservative
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                                                                                                                                                                                                                                              1 QHHYGTPYT
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                                                                                                                                            9 AA;
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                                                                                                                                            Sequence
                                                                                                                                                                            Query Match
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                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                 RESULT 14
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The present sequence represents the light chain of an antibody reactive against p53. The antibody is obtained from a vertebrate host expressing con immune response against a naturally occurring disease. The antibodiles are useful in pharmaceutical compositions, which additionally contain correlators, drugs, prodrugs, toxins and imaging markers e.g. radioisocropes correlators, drugs, prodrugs, toxins and imaging markers e.g. radioisocropes correlatoring in inducing an immune response against a disease in a vactobrate, for treatment and/or prophylaxis of disease and for detection currebrate, for treatment and/or prophylaxis of disease and for detection correlatorial as for gene therapy and recombinant production of the polypeptides. In particular, the following can be treated cancer, rheumatoid arthritis of and coronary heart disease. Cancers include carcinogenic tumours, tumours, competitudes and neck tumours, hepatic cancer, paracreatic cancer, ovarian cancer, head and neck tumours, hepatic cancer, paracreatic cancer, ovarian cancer, curinary/genital tract cancer, oseophageal cancer, mesenchymal tumours, e.g. B cell lymphoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide fragments, useful in treatment and diagnosis of cancer, rheumatoid arthritis and coronary heart disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 4.3;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW03721 standard; Protein; 128 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 30; Page 140; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75.9%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 75.9
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QOYYGTPYT 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QHHYGTPYT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95
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ID AAW0
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Gaps

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79.3%; Score 46; DB 21; Length 107; 77.8%; Pred. No. 1.8; ive 0; Mismatches 2; Indels

Best Local Similarity 77.8 Matches 7; Conservative

Query Match

QHHYGTPYT

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1 QHHYGTPYT 9

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murine anti-human glycoprotein (gp) 39 monoclonal antibody (MAb) 39-1.106 (a member of the murine kappa V subfamily). The MAb was c prepd. by immunising a 6-8 week old BALBAC mouse with a gp39-CD8 fusion protein, and 3 days later harvesting and fusing spleen and lymph cells to mouse melanoma cells, to produce an anti-human gp39 c MAb producing hybridoma. The MAb may be useful for diagnosing disease states, inhibiting B-cell activation and for treating immunological disorders, e.g. autoimmune disorders, allergic responses, organ rejection and graft versus host disease. It may also be used for imaging cells which express gp39 on their surface, e.g. tumour cells, and to target therapeutic agents to such cells. The MAb inhibits the CD40/gp39 interaction, therefore limiting both prim, and sec. responses to T-cell dependent antigens and Ab prodn. specific to these antigens. A typical compsn. for intramuscular injection pref. contains 50 mg of MAb in 1 ml of sterile buffered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Monoclonal antibodies specific for different epitope(s) on human gp39 - used for inhibiting B cell activation and for the diagnosis of various disorders, e.g. cancer, psoriasis etc..
                                                                                               Light chain; variable region; murine; mouse; anti-human; disease; glycoprotein 39; gp39; monoclonal; antibody; 39-1.106; hybridoma; diagnosis; inhibition; B-cell; activation; treatment; disorder; immune; autoimmune; allergic response; organ rejection; drug; graft versus host; cell imaging; tumour; targetted; delivery;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present sequence is the light chain variable region of the
                                                                                                                                                                                                                                                                                                                                                           /note= "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                          "complementarity determining region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "complementarity determining region 3"
                                                               Anti-human gp39 MAb 39-1.106 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gordon ML;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bajorath J, Gilliland LK,
Hollenbaugh D, Siadak AW;
                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                         /label= sig_peptide
                                                                                                                                                                                                                                                                                                                         /label= mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96WO-US01119.
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                                 (first entry)
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                                   02-APR-1997
                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9623071-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aruffo AA,
Harris LJ,
                                                                                                                                                                                     targeted.
                                                                                                                                                                                                                                                                      Peptide
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                                                                                                                           Mouse monoclonal antibody B72.3; humanised antibody molecule;
TAG-72 antigen; antigen binding site; complementarity determining region;
VL domain; light chain cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A chimeric mouse-human light chain gene was constructed from B72.3 light chain clone (see AAN90672) and an M13-derived vector contg. the human c-kappa gene. Heavy and light chimeric genes as well as mouse heavy and light chain cDNA clones were were the separately into plasmid pEE6. The 4 expression constructs inserted separately into plasmid pEE6. The 4 expression constructs were used singly or in heavy/light chain gene pairs to transfect COS-1 cells. Transfection of COS cells with both the chimeric heavy and light chain genes generated a complete chimeric Ab molecule with TAG-72 antigen binding specificity. Humanising the B72.3 does not adversely affect its binding activity and this produces a humanised antibody molecule (HAM) which is useful in both therapy and diagnosis of certain carcinomas, eg solid tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant humanised antibody specific for TAG-72 - having complementary determining regions of variable domains from mouse antibody and the remainder from human immunoglobulin
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Pred. No. 5.1;
1; Mismatches 1; Indels
                                                                                     Predicted sequence of variable light (VL) region of B72.3 monoclonal antibody (MAb) from cDNA clones pBH41 & pBL52.
                                                                                                                                                                                                                                                                                                                                                                                                                       88WO-GB00731, GB-020833.
                                                                                                                                                                                                                                                                                                  /note="human C region"
                                                                                                                                                                                                                                                      /note="signal peptide"
                                                                                                                                                                                                                         Location/Qualifiers
AAP90835 standard; protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ig 1B; page 1/13; 49pp; English.
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Guest Local Similarity 77.00,
Best Local 7; Conservative
                                                                                                                                                                                                                                                            135
135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CLLT ) CELLTECH LTD.
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                                                        28-JUN-1990
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                             AAP90835;
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                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                    Protein
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Gaps

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75.9%; Score 44; DB 17; Length 128; 77.8%; Pred. No. 4.9; ive 0; Mismatches 2; Indels

Best Local Similarity 77.8 Matches 7; Conservative

128 AA;

Sequence Query Match

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Monoclonal antibodies specific for different epitope(s) on human gp39 - used for inhibiting B cell activation and for the diagnosis of various disorders, e.g. cancer, psoriasis etc..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is the light chain variable region of the humanised murine anti-human glycoprotein (gp) 39 monoclonal antibody (MAD) 39-1.106. The MAD may be useful for diagnosing disease states, inhibiting B-call activation and for treating immunological disorders, e.g. autoimmune disorders, allergic responses, organ rejection and graft versus host disease. It may also be used for imaging cells which express gp39 on their surface, e.g. tumour cells, and to target therapeutic agents to such cells. The MAD inhibits the CD40/gp39 interaction, therefore limiting both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prim. and sec. responses to T-cell dependent antigens and Ab prodn. specific to these antigens. A typical compsn. for intramuscular injection pref. contains 50 mg of MAb in 1 ml of sterile buffered
                                                                                                                                                           Light chain; variable region; muxine; mouse; anti-human; disease; glycoprotein 39; gp39; monoclonal; antibody; 39-1.106; hybridoma; diagnosis; inhibition; Brecll; activation; treatment; disorder; immune; autoimmune; allergic response; organ rejection; drug; graft versus host; cell imaging; tumour; targetted; delivery;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75.9%; Score 44; DB 17; Length 171; ilarity 77.8%; Pred. No. 6.6; Conservative 0; Mismatches 2; Indels
                                                                                                                              Humanised MAb 39-1.106 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bajorath J, Gilliland LK, Gordon ML;
Hollenbaugh D, Siadak AW;
                                                                                                                                                                                                                                                                                                                                              codon TAG'
                                                                                                                                                                                                                                                                                                                                                                                codon TAA'
                                                                                                                                                                                                                                                                                                                                                                                                               codon TAA"
                                                                                                                                                                                                                                                                                                                                              note= "corresponding
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                                AAW03725 standard; Protein; 171 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 13; Fig 16; 167pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BRIM ) BRISTOL-MYERS SQUIBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96WO-US01119.
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                                                                                               (first entry)
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                                                                                                                                                                                                                                            targeted; humanised
                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference 157
                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference 165
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                             Misc-difference 1
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                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JAN-1995;
                                                                                                                                                                                                                                                                                Mus musculus
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                                                                                               02-APR-1997
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Harris LJ,
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                                                                 AAW03725;
RESULT 18
                 4AW037
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The bivalent antigen-binding protein B72.3 Fv (AAR20184) is an example of the antigen-binding proteins of the invention. They comprise a first Fv fragment bound to at least one other Fv fragment by a linker which keeps the Fv fragment apart. The connecting structure of AAR20184 comprises a joining sequence derived from a human 1gG1 domain linked to a complete human 1gG4 hinge region. AAR20185 is the sequence of the shortened hinge version of the B72.3 single chain Fv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 New multivalent antigen-binding proteins - comprise Fv fragment linked to at least 1 other Fv fragment spacer and useful for in-vivo diagnosis or therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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Pred. No. 11;
1; Mismatches 1; Indels
                                                                                                                                                                 Sequence of the shortened hinge version of the B72.3 single chain Fv hinge.
                                                                                                                                                                                                      Fv fragment; in vivo diagnosis; therapy; antibody
                                                                                                                                                                                                                                                                                                                                                                                    Owens RJ, Yarranton GT;
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                                                                                        AAR20185 standard; peptide; 271 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR12235 standard; Protein; 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example; Fig 5; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75.9%;
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                      131 QHHYNTPLT 139
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N-PSDB; AAQ20381.
1 QHHYGTPYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           271 AA;
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                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                         11-JUN-1991;
                                                                                                                                                                                                                                                                                                                                   11-JUN-1990;
                                                                                                                                         15-APR-1992
                                                                                                                                                                                                                                                                                36-DEC-1991
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                                                                                                                                                                                                                                                                                                                                                                                    King DJ,
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                                                                                                                AAR20185
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                                                                          AAR20185
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Gaps

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Recombinant anti-rotavirus antibody; mouse; heavy chain variable region; VL; light chain variable region; VL; pCANTAB SE vector; treatment; probiotic bacteria; antibacteria; antiviral; gastrointestinal tract; immunise; neonate; immunosuppressed; immunodeficient; dI pathogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Composition for supplementing or replacing an immune response against gastrointestinal pathogens in e.g. newborn infants, comprises probiotic microorganisms expressing antibodies specific for the gastrointestinal
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= E tag domain
/note= "Enables immunodetection and immunoaffinity
purification of the recombinant antibody"
                     This is the light (kappa)-chain variable (V) region of a mouse monoclonal antibody (MAb), 2G12, and is specific for an HIV-1 viral antigen. It is used in the construction of a chimeric MAb comprising heavy and light chains having murine V regions and human C regions. The chimeric MAbs are more effective than murine MAb 2G12 since they have an increased compatibility in humans. The heavy and light chain V-regions are joined by manipulating their respective joining (J) regions, to generate restriction enzyme recognition sites. The chimeric MAbs can be treatment. They can also be used in diagnosis of HIV.
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                                                                                                                                                                                                       Score 43; DB 12; Length 127; Pred. No. 7.1; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117...151
/label= Linker_region
152..250
/label= Mouse_Light_chain_variable_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ö,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Mouse_Heavy_chain_variable_region
                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant mouse anti-rotavirus antibody (Clone 11).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                  AAY44972 standard; Protein; 268 AA.
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  Disclosure; fig 8; 107pp; English
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                                                                                                                                                                                                          74.1%;
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Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                     109 QHHYGAPPT 117
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                                                                                                                                                                                                                                                           1 OHHYGTPYT
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                                                                                                                                                                                                                                                                                                                                                                            AAY44972;
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                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                  The mouse VL gene product may be used to produce chimeric mousemann Abman Abs against HIV-1 comprising human ig constant regions and murine variable regions. These novel sequence are useful in treatment, diagnosis and prophylaxis of HIV infections, and may be
                                                                                                                                                                                                                   New chimeric mouse human antibodies - used in treatment, diagnosis and prophylaxis of HIV infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New chimeric mouse-human antibodies - used to detect, kill and remove HIV-1 antigen from sample
                                                                                                                                                                                                                                                                                                                         treatment, diagnosis and prophylaxis of HIV infections, and me
produced by a bacterial, yeast or mammalian expression system.
                                                                                                                                                                                                                                                                                                                                                                                         Length 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Light (kappa) chain variable region of murine 2G12 immuno-
globulin.
                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                      Ghosh-Dastidar P, Robinson RR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric antibodies; immunoconjugates; HIV; AIDS
                                                                                                                                                                                                                                                                                                                                                                                        Score 43; DB 12;
Pred. No. 7.1;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR12357 standard; Protein; 127 AA
                                                                                                                                                                                                                                                         Disclosure, Fig 8; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                    74.18;
                                                                            90WO-US06627.
                                                                                                    89US-0433703
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                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 77.8
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                                                                                                                                                      Better MD, Horwitz AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QHHYGAPPT 117
                                                                                                                                                                               WPI; 1991-178106/24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QHHYGTPYT
                                                                                                                            (XOMA-) XOMA CORP.
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                                                                                                                                                                                           N-PSDB; AAQ12015
                                                                           13-NOV-1990;
                                                                                                   13-NOV-1989;
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                         WO9107494-A.
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                                                  30-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR12357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109
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 Mus sp.
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inserted into pcANTAB SE expression vector (clone II). The vector is used to transform probiotic bacteria like, Lactobacilli for expression and secretion of recombinant anti-rotavirus antibodies. The antibodies have antibacterial and antiviral activity. Antibody-expressing probiotic bacteria can be administered for treatment of gastrointestinal (II) tract infections and to immunise neonates, humans or immunosuppressed/immunodeficient adults acutely exposed to a bolus of GI pathogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of an antibody and/or chemokine construct that binds to a chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chemokine construct; human immunodeficiency virus 1; allergic disease; skin disease; immunological disorder; autoimmune disease; psoriasis; multiple sclerosis; rheumatoid arthritis; inflammatory bowel disease; diabetes; skin inflammation; atopic dermatitis; inflammatory disease; inflammatory renal disease; HIV-1; transplant rejection; mutine; CDR3; light chain variable domain; VL; complementarity determining region 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor, for eliminating cells latently infected with primate
immunodeficiency virus, or treating, preventing and alleviating immune
                                                           present sequence is the recombinant mouse anti-rotavirus antibody comprises of mouse heavy chain (VH) and light chain (VL) variable jions joined by a linker. The recombinant antibody encoding DNA is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murine MC-1 antibody light chain variable domain (VL) CDR3 peptide.
                                                                                                                                                                                                                                                                        21; Length 268;
                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                      Score 43; DB 2
Pred. No. 16;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Page 116, 117pp, English
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                               Disclosure, Fig 1; 48pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE22199 standard; peptide; 9 AA
                                                                                                                                                                                                                                                                        74.18;
77.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-SEP-2001; 2001WO-EP10433
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                                                                                                                                                                                                                                                                                                                                                        231 QHYYGTPRT 239
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                    QHHYGTPYT
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                                                                                                                                                                                                                                          Sequence
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The invention relates to the use of an antibody and/or chemokine construct that binds a chemokine receptor for preparing a pharmaceutical composition for eliminating cells latently infected with a primate immunodeficiency virus (e.g. human immunodeficiency virus (HIV-1). They are used in gene therapy and as vaccines. The antibody and/or chemokine

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of an antibody and/or chemokine construct that binds to a chemokine receptor, for eliminating cells latently infected with primate immunodeficiency virus, or treating, preventing and alleviating immune
           treating, preventing and/or alleviating immunological disorders including autoimmune diseases (e.g. multiple sclerosis, type I diabetes and rheumation arthritis), allergic diseases, skin diseases (e.g. skin inflammation, atopic dermatitis and psoriasis), inflammatory diseases such as inflammatory joint diseases (chronic arthritis), inflammatory renal diseases and inflammatory bowel diseases and graft versus host and transplant rejections. The present sequence is murine MC-1 antibody (CDR3) peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chemokine construct, human immunodeficiency virus 1; allergic disease, skin disease, immunological disorder; autoimmune disease, psoriasis; multiple sclerosis; rheumatooi arthritis; inflammatory bowel disease; diabetes; skin inflammation; atcpic dermatitis; inflammatory disease; inflammatory care inflammatory disease; inflammatory companie inflammatory disease; MV-1; transplant rejection; CCRS; murine; MC-1 antibody; VL; light chain variable domain; chemokine receptor 5.
preparing a pharmaceutical composition for
                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                            Score 42; DB 23; L
Pred. No. 7.8e+05;
0; Mismatches 2;
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                                                                                                                                                                                                                                                72.4%;
77.8%;
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                                                                                                                                                                                                                                              Query Match 72.4
Best Local Similarity 77.6
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                         1 OHHYGTPYT
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                                                                                                                                                                                                           9 AA;
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                                                                                                                                                                                                             Sequence
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inflammation, atopic dermatitis and psoriasis), inflammatory diseases such as inflammatory joint diseases (chronic arthritis), inflammatory renal diseases and inflammatory bowel diseases and graft versus host and transplant rejections. The present sequence is murine MC-1 antibody light chain variable domain (VL)(1). This antibody is specific for human chemokine receptor 5 (CCR5).
                                                                                                                                                                                           Gaps
                                                                                                                                                                                           ö
                                                                                                                                                        Length 92;
                                                                                                                                                                                           2; Indels
                                                                                                                                                        Score 42; DB 23;
Pred. No. 7.5;
                                                                                                                                                                                         0; Mismatches
                                                                                                                                                  72.4%;
                                                                                                                                                                       Local Similarity 77.8
les 7; Conservative
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                                                                                                                                                                                                                           1 QHHYGTPYT
                                                                                                                      92 AA;
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AAE22189 standard; Protein; 107 AA. 83 OHHYDTPRT 81 RESULT 25 AAE22189

(first entry) 25-JUL-2002 AAE22189; 

skin disease; immunological disorder; autolimmune disease; psoriasis; multiple sclerosis; rheumatoid arthritis; inflammatory bowel disease; diabetes; skin inflammation; atopic dermatitis; inflammatory disease; inflammatory renal disease; HIV-1; transplant rejection; CRS; murine; MC-1 antibody; VL; light chain variable domain; chemokine receptor 5. Chemokine construct; human immunodeficiency virus 1; allergic disease; Murine MC-1 antibody light chain variable domain (VL)(1) #1.

WO200220615-A2 sb. Mus

14-MAR-2002.

10-SEP-2001; 2001WO-EP10433

08-SEP-2000; 2000EP-0119694.

(MICR-) MICROMET AG

Mack M, Schloendorff D,

Σ

Spring

WPI; 2002-362240/39. N-PSDB; AAD35248.

Use of an antibody and/or chemokine construct that binds to a chemokine receptor, for eliminating cells latently infected with primate immunodeficiency virus, or treating, preventing and alleviating immune disorders

Example 2; Page 49; 117pp; English.

The invention relates to the use of an antibody and/or chemokine construct that binds a chemokine receptor for preparing a pharmaceutical composition for eliminating cells latently infected with a primate immunodeficiency virus (HIV-1). They are used in gene therapy and as vaccines. The antibody and/or chemokine construct is also used for preparing a pharmaceutical composition for treating, preventing and/or alleviating immunological disorders including autoimmune diseases (e.g. multiple sclerosis, type I diabetes and rheumatoio, ancopic dermatitis and psoriatishs), inflammatory diseases inflammatory joint diseases (chronic arthritis), inflammatory diseases such as inflammatory joint diseases (chronic arthritis), inflammatory inflammatory bowel diseases and transplant rejections. The present sequence is murine MC-1 antibody

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                                                                          Gaps
light chain variable domain (VL)(1). This antibody is specific for human chemokine receptor 5 (CCR5).
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                                                     Length 107
                                                                           Indels
                                                                          2;
                                                      23;
                                                     Score 42; DB 2
Pred. No. 8.8;
0; Mismatches
                                                      72.4%;
77.8%;
                                                                           7; Conservative
                                                                                             1 QHHYGTPYT 9
                                107 AA;
                                                              Similarity
                                                     Query Match
Best Local S
Matches 7
                                  Sequence
  22X28
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QHHYDTPRT 97 89

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RESULT 26 AAE22193

AAE22193 standard; Protein; 495

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AAE22193;

25-JUL-2002 (first entry)

Murine CCR5xCD3 bispecific single chain antibody construct.

Chemokine construct; human immunodeficiency virus 1; allergic disease; skin disease; immunological disorder; autoimmune disease; psoriasis; multiple sclerosis; rheumatoid arthritis; inflammatory bowel disease; diabetes; skin inflammation; atopic dermatitis; inflammatory disease; inflammatory renal disease; HIV-1; transplant rejection; CCRxCD3; antibody; chemokine receptor 5; CD3 antigen; chimeric; murine.

Chimeric - Unidentified Chimeric - Mus

WO200220615-A2

14-MAR-2002

10-SEP-2001; 2001WO-EP10433 

08-SEP-2000; 2000EP-0119694 05-SEP-2001; 2001US-0948004

(MICR-) MICROMET AG

Spring M; Mack M, Schloendorff D,

WPI; 2002-362240/39. N-PSDB; AAD35252.

Use of an antibody and/or chemokine construct that binds to a chemokine receptor, for eliminating cells latently infected with primate immunodeficiency virus, or treating, preventing and alleviating immune disorders

Claim 29; Page 52; 117pp; English.

The invention relates to the use of an antibody and/or chemokine construct that binds a chemokine receptor for preparing a pharmaceutical composition for eliminating cells latently infected with a primate composition for eliminating cells latently infected with a primate composition for eliminating ells human immunodeficiency virus (HIV-1). They are used in gene therapy and as vaccines. The antibody and/or chemokine construct is also used for preparing a pharmaceutical composition for treating, preventing and/or alleviating immunological disorders including autoimmune diseases (e.g. multiple sclerosis, type I diabetes and rheumatoid arthritis), allergic diseases, skin diseases (e.g. skin inflammatory diseases (chronic arthritis), inflammatory diseases such as inflammatory bowel diseases and graft versus host and transplant rejections. The present sequence is CCRSCXCD3 bispecific and transplant rejections. The present sequence is CCRSCXCD3 bispecific single chain matibody construct. This antibody construct comprises light chain variable domain (VL) and heavy chain variable (VH) domains of murine MC-1 antibody specific for human chemokine receptor 5 (CCRS)

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Chimeric; antibody; human parathormone related peptide; hPTRP; mouse; L chain; H chain; hypercalcaemia; cancer; malignant lymphoma; CDR; hypophosphaemia; pathogen; vitamin D resistance; V region; C region; humanised.
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                                                                                                                                                                                                                                                      Chimeric L chain V region CDR-3 for an antibody against hPTRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 9; Page 124; 182pp; Japanese.
                                                                                                                 AAW57579 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sato K, Wakahara Y, Yabuta N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97JP-0214168
96JP-0255196
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                                                                                                                                                                                                            03-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
Chimeric - Mus sp.
Chimeric - Homo sapiens.
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QQHYSTPFT
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les 6; Conser
1 QOHYSTPFT
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26-SEP-1996;
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                                                                                                                                                                AAW57579;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A humanised anti-HMI.24 antibody has been developed which comprises human L and H chain C regions, and L and/or H chain V regions containing material originating in mouse anti-HMI.24 antibody. The V regions contain framework (FR) regions of human origin and complimentarity determining regions (CDR) of mouse origin, leading to a reshaped humanised antibody. The C regions are human Ck (L-chain) and human G agmam (specially C gamma 1) (H-chain). The FR regions of the L chain V region are derived from human subtype HSG1 (e.g. from human antibody RE1) and the FR regions of the H chain V region are derived from human antibody HG3 and FR4 from human antibody HG3 in The present sequence represents mouse L chain V region CDR 3 from the present invention. The antibodies are used for the treatment of myeloma, especially by injection, intravenously,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               intramuscularly or subcutaneously. The antibodies are used at 0.01-1000 (especially 5-100) mg/kg body weight. The humanised antibody has low antigenicity and is therefore effective therapeutically in humans.
and VH and VL domains of an antibody specific for a CD3 antigen joined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse, human, humanised, anti-HM1.24 antibody; myeloma, FR, CDR, framework region, complimentarity determining region, antigenicity.
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                                                                                                              Length 495;
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69.0%; Score 40; DB 19; Length 9;
Best Local Similarity 66.7%; Pred. No. 7.8e+05;
Matches 6; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Humanised anti-HM1.24 antibody - for treatment of myeloma
                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tsuchiya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse anti-HM1.24 antibody L chain V region CDR 3.
                                                                                                                   23;
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                                                                                                                   DB
                                                                                                                                         44;
                                                                                                                                                                0; Mismatches
                                                                                                                 Score 42;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ohtomo T,
                                                                                                                                                                                                                                                                                                                                                                               AAW62191 standard; peptide; 9 AA
                                                                                                            72.4%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96JP-0264756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CHUS ) CHUGAI SEIYAKU KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Koishihara Y, Kosaka M,
                                                                                                                                       Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                           QHHYDTPRT 97
                                                                                                                                                                                                              1 QHHYGTPYT 9
                   by a peptide linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-286421/25.
                                                                    495 AA;
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                                                                       Sequence
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                                                                                                                   Query Match
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New antibodies have been developed which are specific for human parathormone related peptides (hPTRP). The antibodies comprise chimeric Land/or H chains, where the C region is of human and L region of mouse, origin. The present sequence represents a specifically claimed region of an antibody of the invention. Host cells, transformed with vectors containing DNA encoding antibodies of the invention, can be used to produce the antibodies. The antibodies may be used to treat hypercalcaemia, especially that due to a malignancy, e.g. cancers of pancreas, lung, throat, larynx, tongue, gum, oesophagus, stomach, liver, breast, kidney, bladder, womb or prostate or malignant lymphoma. They may also be used for treatment of hypophosphaemia such as that due to pathogens or to vitamin D resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40; DB 19; L
Pred. No. 7.8e+05;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY02549 standard; Peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69.0%;
ilarity 66.7%;
Conservative
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ID AAY0
XX
AC AAY0
XX
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1 QHHYGTPYT 9

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Hypercalcemic crisis; parathyroid hormone related peptide; PTHrP; tumour.
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                                                                                                                                                                                                                                   The present invention describes compositions for the treatment of cachexia containing a substance which inhibits the binding of a parathyroid hormone related peptide (PTHTP) to its receptor, as an active component. This substance may be an antagonist to the receptor, recognising PTHTP. The antibody is preferably humanised or chimeric. The present invention also describes a humanised antibody prepared by hybridoma 23-57-137-1 (FREM BP-5631). The composition is used for the treatment of cachexia arising in connection with diseases such as cancer, thereby improving the quality of life of the patient. The present sequence represents mouse humanised antibody light chain CDS3 from #23-57-137-1 from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treatment of hypercalcemic crisis with a substance inhibiting binding of parathyroid hormone related peptide to its receptor
                                                                                                                   Inhibitors of binding of parathyroid hormone related peptide to its receptor - useful for, e.g. treatment of cachexia arising from cancer or other diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 40, DB 20; Length 9;
Pred. No. 7.8e+05;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibody H chain V region CDR3 peptide seq ID No: 61.
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                                                                                                                                                                                                    Example 2; Page 85; 125pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY77517 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 69.0%;
Similarity 66.7%;
6; Conservative
                                           Tunenari
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    (CHUS ) CHUGAI SEIYAKU KK.
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                                                                                WPI; 1999-070101/06.
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QHHYGTPYT
                                           Sato K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
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                                         Ishii K,
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                                                                            Reconstituted human antibody; peptide antigen HM1.24; framework region; complementary determining region; CDR; anti-HM1.24 antibody; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The specification describes a reconstituted human antibody recognizing the peptide antigen HM1.24. This human antibody contains natural human framework regions modified by amino acid substitutions to provide homogeneity with a previously designed framework region (which may arise from a human or non-human source); and complementary determining regions (CDR) derived from a non-human anti-HM1.24 antibody. The reconstituted antibody is useful in the treatment of diseases in which the surface antigen HM1.24 is implicated such as myeloma. The present sequence is used in the creation of the antibodies of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; parathyroid hormone related protein; PTHrP; cachexia; cancer; inhibitor; humanised.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reconstituted human antibody useful in the treatment of myeloma
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                                     Artificial CDR(3) of L chain V region of antiHM1.24 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69.0%; Score 40; DB 20; Length 9; 66.7%; Pred. No. 7.8e+05; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 83; 256pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW89631 standard; peptide; 9 AA.
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97JP-0125505.
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(first entry)
                                                                                                                                                                                                                                                                                                                                      (CHUS ) CHUGAI SEIYAKU KK
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1 QOHYSTPFT
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15-MAY-1997;
  16-JUL-1999
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Synthetic.
                                                                                                                                      Synthetic.
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RESULT 30 AAW89631

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RESULT 32 AAG67115

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Matches

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Parathyroid hormone-related peptide, PTHrP; antagonist, antibody, calcium regulation disorder, serum calcium concentration, light chain, humoral hypercalcaemia of malignancy, cytostatic, analgesic, CDR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The specification describes a treatment for dental diseases. The treatment comprises a substance that inhibits binding between parathyroid hormone-associated peptide and its receptor. The present sequence represents a human peptide, which is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parathyroid hormone-associated peptide binding inhibitors useful
                                                                                                                                                                                        Parathyroid hormone-associated peptide; PTHrP; dental disease.
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                                                                                                                                               Amino acid sequence of a human peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 116; 140pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-PTHrP Ab VL CDR3, SEQ ID NO:61.
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                     AAG63397 standard; peptide; 9 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treating dental disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kato A, Suzuki M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                      15-OCT-2001
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                                                                AAG63397;
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    AAG63397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The specification describes a tissue decomposition inhibitor, which comprises a substance that inhibits peptides associated with parathyroid hormone (PTH) from binding with their receptor. The method is used to inhibit tissue decomposition caused by cancer cachexia, septicemia, heavy external injury or muscular dystrophy, and for treating patients with elevated cytokine (Interleukin-6, Granulocyte colony stimulating factor, Interleukin-11 and Leukemia inhibitory factor) levels. It may also be used for preventing weight loss caused by cancer cachexia. The present sequence represents a peptide, which is used in the course of the invention.
the treatment of hypercalcemic crisis, such as that associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tissue decomposition inhibitor; parathyroid hormone; cancer cachexia; septicomia; injury; injury; muscular dystrophy; cytokine; interleukin-6; granulocyte colony stimulating factor; interleukin-11; leukemia inhibitory factor; weight loss.
                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tissue decomposition inhibitor that prevents parathyroid hormone associated proteins from binding to its receptor \,
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Pred. No. 7.8e+05;
1; Mismatches 2; Indels
                                                                                                             7.8e+05;
                                                                                                         DB 21;
                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sato K;
                                                                                                      Score 40;
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amino acid sequence of a human peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 109; 132pp; Japanese.
                                                                                                                                                                                                                                                                                                                                 AAG67115 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Onuma E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69.0%;
                                                                                                    69.0%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-AUG-2000; 2000WO-JP05886
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Best Local Similarity 66.79,
G; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CHUS ) CHUGAI SEIYAKU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tsunenari T,
                                                                                                                                                                                        1 QHHYGTPYT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-550131/61
                         a malignant tumour.
                                                                                                                                                                                                               | || ||:|
1 QOHYSTPFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | || || || || OOHYSTPFT
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                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 AA;
                                                                9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200164249-A1.
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                                                                                                                                                                                                                                                                                                                                                                            AAG67115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saito H,
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RESULT 33

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Gaps

The present invention describes an agent (I) for ameliorating low

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                                                                                                                                                                                                      recognises parathyzoid hormone-related peptide (PTHTP) - see AAG64793.

The composition consists of a solution of the antibody in a buffer of pH and their salts. The composition has increased storage stability, especially at elevated temperatures. The composition antagonises the action of PTHTP, and may be used in the treatment of diseases involving disturbances of calcium regulation (high or low serum calcium concentration) such as humoral hypercalcaemia of malignancy and as an analgesic. The present sequence represents one of the light chain complementarity determining regions (CDR) of an anti-PTHTP antibody.
                                                                                                   Composition for treating diseases of calcium regulation and for use as an analgesic, comprises an antibody recognizing parathyroid hormone
                                                                                                                                                                                           invention relates to a stabilised composition of an antibody which
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                        Score 40; DB 22; Length 9;
                                                                                                                                                             Examples; Page 107; 128pp; Japanese.
                                              Koga A;
                                                                                                                                                                                                                                                                                                                                                                                                       69.0%;
                                           Yamazaki T, Hayasaka A,
               CHUGAI SEIYAKU
                                                                        WPI; 2001-425590/45
                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                              related peptide
                                                                                                                                                                                                                                                                                                                                                                           9 AA;
                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Pred. No. 7.8e+05;
1; Mismatches 2; Indels
              6; Conservative
                                          1 OHHYGTPYT 9
                                                                    1 QQHYSTPFT 9
              Matches
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AAB76893 standard; Peptide; 9 AA. (first entry) 12-APR-2001 AAB76893; 

Human PTHrP mouse MAb L chain V region CDR3 SEQ ID NO:61.

Human; mouse; parathyroid hormone-related peptide; PTHrP; vasopressin; monoclonal antibody; antidiarrheic; antiemetic; antidiabetic; antipyretic; cancer; dehydration; excessive urination; thirst; vomiting; diarrhoea; fever; perspiration; diabetes.

Homo sapiens

WO200102010-A1.

11-JAN-2001

03-JUL-2000; 2000WO-JP04413.

02-JUL-1999;

(CHUS ) CHUGAI SEIYAKU KK

Ogata E,

Inhibitor of parathyroid hormone related peptide binding to its receptor can ameliorate symptoms caused by a decrease in vasopressin WPI; 2001-112507/12.

Azuma Y;

Onuma E, Tsunenari T, Saito H,

Example 2; Page 92; 114pp; Japanese

receptor can level due to

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; mouse; hypercalcaemia; parathyroid hormone; PTH; PTHrP; parathyroid hormone related peptide; analgesic; immunosuppressive; nontropic, neuroprotective; antiinflammatory; cytostatic; antihyroid; eating-disorder; cardiovascular; pain; immune suppression; appetite; digestive system; protein metabolism; immune suppression; appetite; blood chemistry; thyroid function; electrolyte balance; neurological; central nervous system disorder; sleep disturbance; brain function; brain circulation; autonomic nervous system; blood poisoning; dropsy; inflammation; blood disease; calcium disturbance; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes an agent (1) for the treatment and prevention of diseases other than hypercadcaemia associated with parathyroid hormone (PTH) or parathyroid hormone related peptide (PTHrP). (1) contains as an active component a substance which promotes or hibhbits the binding of ligands to PTH receptor or PTHFP receptor, or is an agonist to antagonist to these receptors. (1) have analgesic, immunosuppressive, nootropic, neuroprotective, antiinflammatchy,
vasopressin levels, and symptoms caused by this depression, containing as an active component a substance which inhibits the binding of parathyroid hormone related peptide (FTHFP) to its receptor. (I) has antidiarheic, antiemetic, antidiabetic and antipyretic activities. (I) can be used for the amelioration of symptoms caused by decrease in vasopressin levels, such as that due to cancer are treated using the agent. These symptoms include dehydration, excessive urination, thirst, vomiting, diarrhoea, fever, perspiration and diabetes. AAF69085 to AAF69140 and AAB7687 to AAB76897 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Agents modifying the binding of ligands to parathyroid hormone recepto: or parathyroid hormone related peptide receptor for treatment of disorders associated with parathyroid hormone other than hypercalcemia
                                                                                                                                                                                                                                                                                                            Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human PTHrP mouse MAb L chain V region CDR3 SEQ ID NO:61.
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                                                                                                                                                                                                                                                                                                       69.0%; Score 40; DB 22; Lularity 66.7%; Pred. No. 7.8e+05; Conservative 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tsunenari T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example; Page 103; 130pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB76912 standard; Peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                  1 QHHYGTPYT
                                                                                                                                                                                                                                                              9 AA;
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                                                                                                                                                                                                                                                              Sequence
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cytostatic, antithyroid, eating-disorders and cardiovascular activities. It is used for treatment and prevention of disorders associated with PTH disgestive spatem, praint immune suppression; disturbances of the appetite, blood chemistry, thyroid function, and electrolyte balance; central nervous system disorders such as aleep disturbance, neurological disturbances, brain function disturbance, brain circulation disturbance and autonomic nervous system disturbance, and disorders caused by PTH or PTHP associated cytokine cascade including blood poisoning, dropsy, inflammation, blood disease, calcium disturbance and autoimmune disease. Treatment and prevention of disorders other than hypercalcaemia which malignant tumours, and thereby ameliorating the quality of life of patients and sherbyly ameliorating the quality of life of these patients. AAPPG914 to AAPPG916 and AAPPG989 to AAPPG916 each with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Agents inhibiting binding of parathyroid hormone related peptide to its receptor for treatment of drug-resistant hyperglycemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes an agent (I) for the treatment of drug-resistant hyperglycaemia. (I) contains as an active component a substance which inhibits the binding of parathyroid hormone related peptide (FTHIP) to its receptor. (I) is a calcium-antagonist. (I) can be used for treatment of drug-resistant hyperglycaemia e.g. associated with cancer. The hyperglycaemia is resistant to treatment with other drugs including bone resorption inhibitors (such as bisphosphonate or calcitonin), calcium elimination promoters and intestinal calcium absorption inhibitors. AAF69197 to AAP69252 and AAB76917 to AAB76935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               parathyroid hormone related peptide; gastrointestinal; cancer; central nervous system; calcium-antagonist; bone resorption inhibitor; bisphosphonate; calcitonin; calcium elimination promoter; intestinal calcium absorption inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mouse; drug-resistant hyperglycaemia; PTHrP; cardiovascular;
                                                                                                                                                                                                                                                                                                                                                                                               .
                                                                                                                                                                                                                                                                            sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                     Score 40; DB 22; Length 9;
Pred. No. 7.8e+05;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human PTHrP mouse MAb L chain V region CDR3 SEQ ID NO:61.
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hes 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                  OHHYGTPYT
                                                                                                                                                                                                                                                                                                                     9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB76931;
                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Agents for ameliorating symptoms caused by joint diseases relating to PTH or PTHrP e.g. chronic rheumatoid arthritis, containing inhibitors on receptor binding of parathyroid hormone-related peptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                      Joint disease; PTH; PTHrP; parathyroid hormone-related peptide; parathyroid hormone; osteopathic; rheumatoid arthritis; arthritis.
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represent sequences used in the exemplification of the present
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                                                                                                    Indels
                                                                      Score 40; DB 22; L. Pred. No. 7.8e+05; 1; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                          Human joint disease related peptide SEQ ID NO 61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 92; 112pp; Japanese.
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                                                                                                                                                                                                                                      ABB95191 standard; Peptide; 9 AA.
                                                                         69.0%;
66.7%;
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                                                                                                       6; Conservative
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QQHYSTPFT
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Best Local Similarity
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                                             9 AA;
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                   invention
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AAW00832
ID AAW00
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ABB95191
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96WO-JP03089.

01-MAY-1997. 24-OCT-1996;

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Mus sp.

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                                                                                                                                                                                                                                                                                                                                                   useful
                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is the light chain variable region of the anti-human Fas ligand monoclonal antibody (MAD) NOK-5. NOK-5 is produced by the hybridoma NOK-5 (FERM BP-5048), which was prepared by immunising mice with transformed human Fas ligand expressing COS cells, and fusing spleen cells isolated from the mice with myeloma P3x6A948.653 (ATCC CRL-1580) cells. The MAD recognises the human Fas ligand on the cell surface or in solution, and can be used to inhibit the apoptosis inducing cell surface Fas ligand/Fas reaction. The MAD can also be used for a Fas ligand assay in phiological samples (e.g. human blood), especially for disease diagnosis, e.g. hepatitis, infectious mononucleosis and systemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Light chain; variable region; mouse; murine; human; Fas ligand; FasL; monoclonal antibody; MAb; hybridoma; treatment; hepatitis; hepatitis B virus; HBV; hepatitis C virus; HCV; apoptosis; liver cell; glutamate oxaloacetate; pyruvate transaminase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                               Monoclonal antibody specifically recognising the Fas ligand - for the detection of Fas ligands either on cell surface or in
                                             Variable light chain of anti-human Fas ligand antibody NOK-5.
                                                                    Variable region; light chain; human; Fas ligand; monoclonal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-human FasL antibody (NOK5) light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40; DB 17; Length 105;
Pred. No. 19;
                                                                               antibody; NOK-5; hybridoma; inhibition; apoptosis; assay; diagnosis; disease; hepatitis; infectious mononucleosis; systemic lupus erythematosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                      Okumura K, Yagita H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               Claim 28; Page 91; 133pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW19018 standard; Protein; 105 AA.
                                                                                                                                                                                                                                                             (SUME ) SUMITOMO ELECTRIC IND CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69.0%;
                                                                                                                                                                                                                           95JP-0303492.
95JP-0087420.
                                                                                                                                                                                                     96WO-JP00734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 66.
                                                                                                                                                                                                                                                                                      Kayagaki N, Nakata M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89 OCHYSSPYT 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QHHYGTPYT 9
                                                                                                                                                                                                                                                                                                             WPI; 1996-443140/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lupus erythematosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105 AA;
                                                                                                                                                                                                                                                                                                                       N-PSDB; AAT39558
                      29-MAY-1997
                                                                                                                               Mus musculus
                                                                                                                                                      WO9629350-A1
                                                                                                                                                                                                    21-MAR-1996;
                                                                                                                                                                                                                          27-OCT-1995;
20-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
AAW00832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW19018;
                                                                                                                                                                                                                                                                                                                                                                        solution
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The present sequence is the light chain variable region of the murine anti-human Fas ligand (FasL) monoclonal antibody (MAD) NOK5, which is expressed by the hybridoma NOK5 (FERM BP-5044). The MAD can be used in the preparation of a composition for the effective carls caused by hepatitis, including hepatitis in liver calls caused by the binding of FasL to Fas expressing liver in liver calls caused by the binding of FasL to Fas expressing liver calls, and improves liver function by improving blood glutamate calls, and improves liver function by improving blood glutamate calls from mice immunised with FasL expressing COS calls were fused with mouse myeloma cells to produce hybridomas. The hybridomas were screened for anti-FasL activity, and the active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                  Anti-human Fas Ligand antibody to treat hepatitis - controls apoptosis in liver cells and improves liver function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40; DB 18; Length 105;
Pred. No. 19;
1; Mismatches 2; Indels
                                                           Seino K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       completed: July 18, 2003, 15:06:45
                                                           Okumura K,
(SUME ) SUMITOMO ELECTRIC IND CO.
                                                                                                                                                                                                                                                                                        Claim 6; Page 41; 51pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                        Kayagaki N, Nakata M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clones NOK1-5 isolated
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                                                                                                                 1997-258767/23.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Job time : 31.42 secs
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Sequence Sequence

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ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
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CORGANISM: Mus musculus
US-09-257-069-10
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Best Local Similarity
Matches 9; Conserv
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55402
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Sequence 34, Appl
Sequence 35, Appl
Sequence 70, Appl
Sequence 71, Appl
Sequence 72, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
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Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 27, Appli
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Sequence 24, Appl
Sequence 4, Appli
                                                                                                                      July 18, 2003, 15:03:46; Search time 10.44 Seconds (without alignments) 25.365 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 1, 1
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Patent No. 5
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/ReCOMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-888-366-24
US-08-881-037-32
US-08-881-037-34
US-08-881-037-34
US-08-881-037-34
US-08-881-037-34
US-08-881-037-72
US-08-881-037-72
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US-08-881-037-72
US-08-881-037-72
US-08-881-037-72
US-08-379-057-28
US-08-379-057-28
US-08-379-057-28
US-08-378-057-28
US-08-378-057-28
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US-08-378-057-28
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US-08-477-347-11
US-08-397-411-5
                                                                                                                                                                                                                                                                                                                                 262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                          seq length: 0
seq length: 2000000000
                                                                                                                                                                                             US-10-007-790-10
58
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Match Length
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Maximum DB
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APPLICANT: Lopez, Osvaldo
APPLICANT: Wylie, Dwane E.
APPLICANT: Wylie, Dwane E.
APPLICANT: Wagner, Fred W.
TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore
CORRESPONDENCES: 39
CORRESPONDENCE ADDRESS:
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                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application US/09257069
Patent No. 6348580
GENERAL INFORMATION:
TRIB OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE:
GURRENT APPLICATION NUMBER: US/09/257,069
CURRENT APPLICATION NUMBER: US/09/257,069
FILE REFERENCE:
PRIOR APPLICATION NUMBER: US/09/257,069
FRIOR APPLICATION NUMBER: US/09/07
FRIOR SEC ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUDRESSEE: Merchant & Gould STREET: 90 South 7th Street, 3100 No. 5972656west Ctr. CITY: Minneapolis STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 58; DB 4; Length 9; 100.0%; Pred. No. 2e+05;
US-08-564-164A-4
US-08-765-783A-83
US-09-416-557-83
US-08-765-783A-73
US-08-765-783A-73
US-08-921-100-73
US-08-921-100-73
US-08-921-100-73
US-08-902-201-73
US-08-902-201-73
US-08-902-201-73
US-08-902-201-73
US-08-902-201-73
US-08-902-201-73
US-08-902-201-73
US-08-902-201-73
US-08-902-201-73
US-08-902-201-77
US-08-902-201-77
US-08-902-102-73
US-08-902-102-73
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Patent No. 5972656
GENERAL INFORMATION:
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1 QHHYGTPYT 9
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US-08-881-037-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Medical & Biological Laboratories Co., Ltd.
TITLE OF INVENTION: Monoclonal Antibody Specific for
TITLE OF INVENTION: Phosphatidylinositol-3,4,5-Triphosphate
FILE REFERENCE: M3-008-US
CURRENT APPLICATION NUMBER: US/09/257,069
CURRENT FILING DATE: 1999-02-24
PRIOR PILING DATE: 1998-09-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 107;
0.008;
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                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 58; DB 2;
Pred. No. 0.008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                      NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.39USC1
TELECOMNUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/187,407
FILING DATE: 27-27AN-1994
FILING PAPLICATION DATA:
APPLICATION NUMBER: US 07/990,542
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/493,299
FILING DATE: 14-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/493,299
FILING DATE: 14-MAR-1990
FILING DATE: 14-MAR-1990
ATTORNEY AGENT INFORMATION:
APPLICATION NUMBER: US 07/324,392
FILING DATE: 14-MAR-1999
                                                       APPLICATION NUMBER: US/08/888,366
FILING DATE: 03-JUL-1997
CLASSIFICATION: 435
PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09257069
Patent No. 6348580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 107
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: protein US-08-888-366-24
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US-09-257-069-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89 QHHYGTPYT 97
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                                                                              FILING DATE: 03 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
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RESULT 4

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Gaps
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Pred. No. 0.034;
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                                                                                                                                                                                                                                                                                                          SOFTWARE: PC-DOS/MS-DOS
SUFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NOMBER: US/08/881,037
FILING DATE: 23-UNM-1997
PRIOR APPLICATION: 530
        GENERAL INFORMATION:
APPLICANT: Galck, Gary D.
APPLICANT: Galck, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 33, Application US/08881037
Patent No. 6080588
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, Antoinette F.
REGISTATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 20344211071
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
Sequence 32, Application US/08881037 Patent No. 6080588
                                                                                                                                                                                                                                                                         ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.1%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX:
information for SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (650) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 88.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
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Gaps
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Pred. No. 0.034;
1; Mismatches 0; Indels
                                                                                                                              Score 54; DB 3; Length 99;
Pred. No. 0.034;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/081,037

FILING DATE: 23-JUN 1997

CLASSIFICATION NUMBER: US/08/443,540

PILING APPLICATION DATA:

APPLICATION NUMBER: US 08/443,540

FILING DATE: 18-MAY-1995

CLASSIFICATION: 530

ATTORNEY/AGENT INPORMATION:

NAME: Konski, Antoinette F.

REGISTRATION UNMBER: 34,202

REFERENCE/DOCKET NUMBER: 203442110710

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Glick, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Poerster
STRRET: 755 Page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                          Sequence 35, Application US/08881037 Patent No. 6080588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 69, Application US/08881037 Patent No. 6080588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.1%;
88.9%;
                                                                                                                                93.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 aming acids
                                                                                                                                Query Match
Best Local Similarity 88.99
Matches 8; Conservative
          99 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                 SS: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                               81 QHHYGTPFT 89
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                                ; TYPE: amino acid
; STRANDEDNESS: sir;
; TOPOLOGY: linear
US-08-881-037-34
                                                                                                                                                                                                                 1 QHHYGTPYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY:
US-08-881-037-35
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US-08-881-037-69
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          LENGIH:
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037
FILING DATE: 23-JUN-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
ATTONENY/AGENT INFORMATION:
NAME: ROGIST, AALCOINETE F.
REGISTRATION NUMBER: 34,202
REFRENCE/DOCKET NUMBER: 34,202
REFRENCE/OCKET NUMBER: 34,202
REJERRANION: (650) 813-5600
TELEPHONE: (650) 813-5600
TELEPHONE: (650) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037 FILING DATE: 23-JUN-1997 CLASSIFICATION: 530 PRIOR APPLICATION DATA:
APPLICATION DATA: PROME SPILICATION NUMBER: US 08/443,540 FILING DATE: 18-MAY-1995 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 34, Application US/08881037
Patent No. 6080588
GENERAL INFORMATION:
APPLICANT: Glick, Gary D.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Poerster
STREET: 755 Page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 54; DB 3;
Pred. No. 0.034;
1; Mismatches
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NAME: KONSKI, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442110710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                            33:
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                                                                                                                                                                                                                                                                                                                        TELEX:
INFORMATION FOR SEQ ID NO: 33
SEQUENCE CHARACTERRISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QHHYGTPYT 9
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US-08-881-037-34
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Score 54; DB 3; Length 107;
Pred. No. 0.036;
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MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Elm Pr Compatible
OPERATIOR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037
FILING DATE: 23-JUN-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION S30
ATTORNEY/AGENT INFORMATION:
NAME: KORSK, ANTOINETE P.
REGISTRATION NUMBER: 203442110710
TELECOMMUNICATION NUMBER: 203442110710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 71, Application US/08881037
Patent No. 6080588
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: MOTISON & FOOTSTER
                    CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
ATYONERY/ABENT INFORMATION:
NAME: KONSKi, Ancinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442110710
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (650) 813-5600
TELEFAX: (650) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
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88.9%;
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TELEFAX: (650) 494-0792
                                                                                                                                                                                                                                                                                            TELEX:
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 93.1
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89 QHHYGTPFT 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QHHYGTPYT 9
                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94304-1018
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                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
US-08-881-037-71
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                                                                                                                                                                                                                  CUMPUTER READABLE FORM:

MEDITUM TYPE: FORM:

MEDITUM TYPE: FORM:

OMPUTER: IBM PC compatible

OMPUTER: IBM PC compatible

OMPUTER: IBM PC compatible

OMPUTER: IBM PC compatible

OFFRATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/881,037

FILING DATE: 23-UN-1997

CLASSIFICATION S 30

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/443,540

ATCOMENTY AGENT INFORMATION:

NAME: ROGHEN: Antoinette F.

REGISTRATION NUMBER: 34,202

RESERRORE/DOCKET NUMBER: 34,202

REFERENCE/DOCKET NUMBER: 203442110710

TELECOMMUNICATION INFORMATION:

TELEFRAX: (650) 813-5600

TELEFRAX: (650) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/881,037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 70, Application US/08881037
Patent No. 6080588
GENERAL INFORMATION:
APPLICANT: Glick, Gary D.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: MONTISON & FOORSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
GENERAL INFORMATION:
APPLICANT: Glick, Cary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: MOTISON & Poerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 54;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 93.1
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |||||||||||||
89 OHHYGTPFT 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear
US-08-881-037-69
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Sequence 2, Application PC/TUS9109166
GENERAL INFORMATION:
APPLICANT: Pastan, Ira H.
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 243;
                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/958,140
FILING DATE: 19921008
CLASSIFICATION: 436
ATTONEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 15280-77
TELEPHONE: (206) 467-9600
TELEPHONE: (206) 467-9600
TELEPAS: (415) 543-5043
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/09166
                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: One Market Plaza, Steuart Street Tower CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 54; DB 1;
Pred. No. 0.084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                            COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY,
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPatible
COMPUTER: IBM PC COMPatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,90
REFERENCE/DOCKET NUMBER: 152
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31,990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 243 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 543-5043 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 88.9
Matches 8; Conservative
    NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    222 QHHYGTPFT 230
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CLASSIFICATION:
                                                                                                   CA.
USA
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                                                                                                         Gaps
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TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO PROSTATE CELLS
                                                            93.1%; Score 54; DB 3; Length 107; 88.9%; Pred. No. 0.036; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3; Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTE: PALS. L.C. COMPUTE: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATION:
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037
FILING DATE: 23-UUN-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                              Sequence 72, Application US/08881037
Fatent No. 6080588
GENERAL INFORMATION:
APPLICANT: Glick, Gary D.
TITLE OF INVENTION:
TITLE OF INVENTION: DNA BINDING ANTIBODIES
CORRESPONDENCES: 113
CORRESPONDENCES: ADDRESSE:
ADDRESSES:
STREET: 755 Page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 23-JUN-1977
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Konski, Antoinette F.
REGISTRATION NUMBER: 34,202
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 34,202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.1%; Score 54;
88.9%; Pred. No.
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; Sequence 2, Application US/07958140
; Patent No. 5489525
; GENERAL INFORMATION:
APPLICANT: Pastan, Ira H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                          Query Match
Best Local Similarity 88.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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Best Local Similarity
                                                                                                                                                                                   89 OHHYGTPFT 97
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                                                                                                                                            1 QHHYGTPYT 9
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US-08-881-037-72
; TOPOLOGY: linear
US-08-881-037-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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0; Mismatches
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LOCATION: (1)...(9)
OTHER INFORMATION: 1588 light chain CDR 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 77.88
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 79.3
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89 QHHYSIPYT 97
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                   US-09-406-532-10
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US-08-379-057-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE OR NUCLEOSIDE PHOTOAFFINITY
COMPOUND MODIFIED ANTIBODIES, METHODS FOR THEIR
MANUFACTURE AND USE THEREOF AS DIAGNOSTICS AND
THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
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                                                                                                               DB 5; Length 243;
                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARES PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/681,432
FILING DATE: 23-JUL-1996
CLASSIFICATION 1530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/822
FILING DATE: 11-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 12,028750-132.
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: HALEY, BOYG E.
APPLICANT: KOHLER, Heinz
APPLICANT: KOHLER, Heinz
APPLICANT: KOHLER, Heinz
APPLICANT: RAJAGOPALAN, Krishnan
APPLICANT: PAULINKONA, Gabriela
TITLE OF INVENTION: UUCLEOTIDE OR NUCLEOSIDE
TITLE OF INVENTION: COMPOUND MODIFIED ANTIBOD
TITLE OF INVENTION: THERAPEUTICS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSED: BURN, DOANE, SWECKER & MATHIS
STREET: P.O. BOX 1404
CITY: Alexandria
                                                                                                             Score 54; DB 5;
Pred: No. 0.084;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08681432
Patent No. 5800991
GENERAL INFORMATION:
                                                                                                             93.1%;
88.9%;
LENGTH: 243 amino acids
FYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-09166-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
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RY: United States
22313-1404
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                           Query Match
Best Local Similarity 88.5
Matches 8; Conservative
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                                                                                                                                                                                                                              222 QHHYGTPFT 230
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89 QHHFGTPWT 97
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 46; DB 4; Length 9; Pred. No. 2e+05;
Sequence 10, Application US/09406532A

Sequence 10, Application US/09406532A

GENERAL INFORMATION:
APPLICANT: Connie L. Erickson-Miller
APPLICANT: Stephen D. Holmes
APPLICANT: James D. Winkler
TITLE OF INVENTION: TIEZ Agonist Antibodies
FILE REFERENCE: P50843
CURRENT APPLICATION NUMBER: US/09/406,532A
CURRENT FILING DATE: 1999-09-27
PRIOR APPLICATION NUMBER: 60/102,098
PRIOR FILING DATE: 1998-09-28
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09406532A

Sequence 4, Application US/09406532A

Sequence 4, Application US/09406532A

GENERAL INFORMATION:

APPLICANT: Connie L. Erickson-Miller

APPLICANT: Stephen D. Holmes

APPLICANT: James D. Winkler

TITLE OF INVENTION: TIE2 Agonist Antibodies

FILE REFERENCE: P50643

CURRENT APPLICATION NUMBER: US/09/406,532A

CURRENT APPLICATION NUMBER: 05/102,098

PRIOR FILING DATE: 1998-09-28

NUMBER OF SEQ ID NOS: 21

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 4

LENGTH: 107
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Patent No. 5876950
GENERAL INFORMATION:
APPLICANT: Sladak, Anthony W.
APPLICANT: Hollenbaugh, Diane L.
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APPLICANT: Siddk, Anthony W.
APPLICANT: Hollenbaugh, Diane L.
APPLICANT: Gillland, Lisa K.
APPLICANT: Gillland, Lisa K.
APPLICANT: Gordon, Marcia L.
APPLICANT: Bajorath, Jurgen
APPLICANT: Aruffo, Alejandro A.
TITLE OF INVENTION: Monoclonal Antibodies Specific For
TITLE OF INVENTION: Different Epitopes of Human gp39 and Methods For Their Use
TITLE OF SEQUENCES: 57
CORRESPONDENCES: ADDRESS:
ADDRESSE: Bristol-Myers Squibb Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                          COPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,057
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: POOT, BILLAIN W.
REGISTRATION NUMBER: 32,928
REGISTRATION NUMBER: 32,928
REGISTRATION NUMBER: ON0133-
TELECOMMULICATION:
TELEPHONE: (206) 727-3670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM FC compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 26-JAN.1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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Patent No. 5876950
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NAME: POOT, BYIAN W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: 000
TELECOMMUNICATION INFORMATION:
         IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 3005 First Avenue CITY: Seattle STATE: Washington COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (206) 727-3670
                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (206) 727-3601
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 108 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (206) 727-3601
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89 QHHYNTPLT 97
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APPLICANT: Siadak, Anthony W.
APPLICANT: Hollenbaugh, Diane L.
APPLICANT: Hollenbaugh, Diane L.
APPLICANT: Gordon, Marcia L.
APPLICANT: Gordon, Marcia L.
APPLICANT: Bajorath, Jurgen
APPLICANT: Aruffo, Alejandron A.
TITLE OF INVENTION: Different Epitopes of Human gp39 and Methods For Their Use
                                                       APPLICANT: Bajorath, Jurgen
APPLICANT: Antifo, Alejandro A.
TITLE OF INVENTION: Monoclonal Antibodies Specific For
TITLE OF INVENTION: Different Epitopes of Human gp39 and Methods For Their Use
TITLE OF INVENTION: In Diagnosis and Therapy
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                      CUMPLAIR CONTROLL CONTROLL COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SUSTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,057
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: POOC, Brian W.
REGISTRATION NUMBER: 0N0133-
TELEPHONE: (206) 727-3601
TELEPHONE: (206) 727-3601
TELEPHONE: (206) 727-3601
TELEPHONE: (206) 727-3601
TELEPHONE: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER: COMPANDER:
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                                                                                                                                                                                                                                                                                   E: Bristol-Myers Squibb Company 3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Bristol-Myers Squibb Company
3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 28, Application US/08379057
Patent No. 5876950
Gilliland, Lisa K.
Gordon, Marcia L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.9%;
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ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 108 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 75.9
Best Local Similarity 77.8
Matches 7; Conservative
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internal
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                                                                                                                                                                                                                                                                                                                              CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89 OHHYNTPLT 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QHHYGTPYT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inear
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FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-379-057-27
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US-08-379-057-28
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Сp

128 amino acids

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Pred. No. 4.1;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20, Application US/08378939
Patent No. 5876961
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
                                                                                                         REPERENCE/DOCKET NUMBER: 33,715
TELECOMMINICATION INFORMATION:
TELEPHONR.
                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
UMBER: PCT/GB91/00935
11-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                 GB 9012995.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REPRENCE/DOCKET NUMBER: 1808
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6040
TELEFAX: (202) 783-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: ROTHWELL, FIGG,
555 THIRTEENTH ST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                     Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative
                                                                  FILING DATE: 11-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: ISACSON, John P.
REGISTRATION NUMBER: 33,
                                                                                                                                                                           TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 4 SEQUENCE CHARACTERISTICS: LENGTH: 271 amin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 108 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-08-400-115-4
                FILING DATE: 11-JUN-: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: protein US-08-378-939-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 QHFWGTPYT 119
                                                   APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 OHHYGTPYT 9
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RY: U.S.
20004
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TITLE OF INVENTION: RECOMBINANT ANTIBODIES AND METHODS FOR ; THEIR PRODUCTION IN WHICH SURFACE RESIDUES ARE ALTERED TO SUST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75.9%; Score 44; DB 6; Length 135; 77.8%; Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                            2; Indels
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CURRENT APPLICATION DATA.
PELLICATION NUMBER: US/08/400,115
FILING DATE: 06-MAR-1995
                                                                                                     Query Match 75.9%; Score 44; DB 2; Best Local Similarity 77.8%; Pred. No. 1.9; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 06-WAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,136
FILING DATE: 27-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/842,193
FILING DATE: 17-WAR-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/353,634
FILING DATE: 05-SEP-1988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5864019
GENERAL INFORMATION:
              TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 OHFWGTPYT 117
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Best Local Similarity
 amino acid
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5219996-19
                                                                      US-08-379-057-12
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;Patent No.
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Gaps

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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gingrich, Roger
APPLICANT: Link, Brian
APPLICANT: Tso, J. Yun
ITILE OF INVENTION: Bispecific Antibody Effective to Treat
TITLE OF INVENTION: B-Cell Lymphoma and Cell Line
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.0%; Score 40; DB 3; Length 107; 75.0%; Pred. No. 7.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALUKESSEE: Townsend and Townsend and Crew STRET: One Market Plaza, Steuart Tower, Suite 2000 STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,411
FILING DATE: 01-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/859,583
FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: SMICH, MILIAM M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-004901
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PatentIn Release #1.0, Version #1.25
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01-MAR-1995
                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESS:
Left Townsend and Tovest One Market Plaza, St.: San Francisco
California
V: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 75.0
Matches 6; Conservative
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                NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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STRANDEDNESS: si
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                                                                                                                                                     ZIP: 94105
                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-397-411-2
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Patent No. 6129914
GENERAL INFORMATION:
APPLICANT: Weiner, George
APPLICANT: Link, Brian
APPLICANT: TSo, J. Yun
TITLE OF INVENTION: Bispecific Antibody Effective to Treat
TITLE OF INVENTION: B-Cell Lymphoma and Cell Line:
              74.1%; Score 43; DB 2; Length 108; 77.8%; Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3; Length 105;
                                                                                                                                                                                                          US-09-065-059-17

Sequence 17, Application US/09065059

Patent No. 6068841

GENERAL INFORMATION:
APPLICANT: SEINO, Ken-ichiro
APPLICANT: YAGITA, Hideo
APPLICANT: YAGITA, Hideo
APPLICANT: NAKATA, Motomi
TITLE OF INVENTION: THERAPEUTIC AGENT FOR HEPATITIS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCDermott, Will & Emery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: ....
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,059
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Bucca Ph.D., Daniel
REGISTRAION NUMBER: P-42,368
REFERENCE/DOCKET NUMBER: P-42,368
REFERENCE/DOCKET NUMBER: 50356-151
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69.0%; Score 40; DB 66.7%; Pred. No. 7; Live 1; Mismatches
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99 Canal Center Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 105 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-065-059-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89 QQHYSSPYT 97
                                                                                                                                89 OHNYGTPLT 97
                                                                                          1 QHHYGTPYT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Alexandria
STATE: Virginia
COUNTRY: USA
          Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
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APPLICANT: Gingrich, Roger
APPLICANT: Gingrich, Roger
APPLICANT: Link, Brian
APPLICANT: Link, Brian
APPLICANT: Link, Brian
APPLICANT: Link, Brian
APPLICANT: Link, Brian
TITLE OF INVENTION: Bispecific Antibody Effective to Treat
TITLE OF INVENTION: B-Cell Lymphoma and Cell Line
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STRRET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STRYE: California
COUNTRY: USA
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                                                                                DB 4; Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                  Score 40; DB 4
Pred. No. 7.9;
L; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION UDMER: US 07/859,583
APTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-004'
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,411
FILING DATE: 01 MAR-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 28
US-08-881-037-68
; Sequence 68, Application US/08881037
; Patent No. 6080588
                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/08397411
Patent No. 6129914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69.0%;
illarity 75.0%;
Conservative
                                                                                  Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 214 amino acids
TYPE: amino acid .
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
  ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-477-347-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                          | || ||:|
87 QQHYSTPFT 95
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                  1 QHHYGTPYT
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APPLICATION NUMBER: US/08/477,347
                                                                                                                                                                                                                                                                                                                                                                                            Score 40; DB 3
Pred. No. 7.1;
0; Mismatches
                                                                                  NAME: Smith, william M.
REGISTRATION NUMBER: 30,223
REPERENCE/DOCKET NUMBER: 011823-004901
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/859,583
FILING DATE: 27-MAX-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: WALLACH, David
APPLICANT: BIGDA, Jacek
APPLICANT: BELEETKY, Igor
APPLICANT: METT, Igor
APPLICANT: METT, Igor
TITLE OF INVENTION: TNF LIGANDS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWNY ****
STRRFF***
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSEE: BROWDY AND NEIMARK
F: 419 Seventh Street, N.W.
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 106271
FILING DATE: 08-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: TOWNSEND, G. KEVIN
REGISTRATION NUMBER: 34,033
REPRENCE/DOCKET NUMBER: WALLACT
TELECHHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-477-347-11
Sequence 11, Application US/08477347
Patent No. 622446
GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: BIGDA, Jacek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/115,685
                                                                                                                                                                           TELEFAX: 415-326-44.2
TELEFAX: 415-326-24.2
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 248633
INFORMATION FOR SEQ ID NO: 11:
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75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-397-411-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89 QHHYGNSY 96
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 6; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Matsumoto, Yoshihiro
APPLICANT: Yamada, Yoshiki
APPLICANT: Sato, Koh
APPLICANT: Tsuchiya, Masayuki
APPLICANT: Yamazaki, Tatsumi
TITLE OF INVENTION: Reshaped Human Antibody to
TITLE OF INVENTION: Interleukin-8
NUMBER OF SEQUENCES: 105
CORRESPEDNDECE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW, suite 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATER: BENEVEL
OPERATING SYSTEM: DOS
SOFTWARE: FastESG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,783A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                    PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR94/00714
PILING DATE: 15-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93/07241
APPLICATION NUMBER: FR 93/07241
ATTORNEY/AGENT INFORMATION:
NAME: Savitzky, Martin F.
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: S193030-US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35029-20001.20
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APPLICANT: Matsumoto, Yoshihiro
APPLICANT: Yamada, Yoshiki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 350,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEPHONE: 202-822-0168
                                                                                                                                                                                                                                                                                         TELEPHONE: (610)454-3816
TELEFAX: (610)454-3808
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 264 amino acids
TYPE: amino acids
                   FILING DATE: 28-DEC-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        232 HFYGTPY 238
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US-08-765-783A-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-564-164A-4
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STATE:
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APPLICANT: Schweighoffer, Fabien
APPLICANT: Tocque, Bruno
TITLE OF INVENTION: Intracellular Binding Proteins and Use
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 94;
                                                                                                                                                                                                                     COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDLIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BATENIN Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/881,037
FILING DATE: 23-JUN-1997
CLASSIFICATION NATA:
APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
             APPLICANT: Glick, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
CORRESPONDENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Konski, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442110710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08564164A
Patent No. 6159947
                                                                                                                         ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 94 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 67.2
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 19426-0107
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89 QHHYGT 94
GENERAL INFORMATION:
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TOPOLOGY:
US-08-881-037-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 29
US-08-564-164A-4
                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                        STATE:
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65.5%; Score 38; DB 2; Length 126; 66.7%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                           E: MORRISON & FOERSTER
2000 Pennsylvania Avenue, NW, suite 5500
                                                                                                                                                                             APPLICANT: Matsushima, Kouji
APPLICANT: Matsumoto, Yoshihiro
APPLICANT: Yamada, Yoshiki
APPLICANT: Stuchiya, Masayuki
APPLICANT: Tsuchiya, Masayuki
APPLICANT: Yamazaki, Tatsumi
TITLE OF INVENTION: Reshaped Human Antibody to
TITLE OF INVENTION: Interleukin-8
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTESED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,783A
FILING DATE: 07-MAR-1997
CLASSIPICATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 77, Application US/08765783A
Patent No. 5994524
GENERAL INFORMATION:
APPLICANT: Mateushima, Kouji
                                                                                                           Sequence 73, Application US/08765783A Patent No. 5994524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 350,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEPHONE: 202-887-1501
TELEFAX: 202-822-0168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Signal Sequence
LOCATION: 1...19
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 126 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 OHHFGFPRT 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington
                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 33
US-08-765-783A-77
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                                                                                                                                                                                                                                                     2; Indels
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                                                                                                                                                                                                       DB 2; Length 9;
2e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000 Pennsylvania Avenue, NW, suite 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Matsuchima, Kouji
APPLICANT: Matsucoto, Yoshihiro
APPLICANT: Yamada, Yoshiki
APPLICANT: Sato, Koh
APPLICANT: Tsuchiya, Masayuki
APPLICANT: Yamazaki, Tatsumi
TITLE OF INVENTION: Reshaped Human Antibody to
TITLE OF INVENTION: Interleukin-8
NUMBER OF SEQUENCES: 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
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COMPUTER: Diskette
COMPUTER: Diskette
FILING DATE: 12-October-1999
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Pred. No. 2e+05;
1; Mismatches
                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                       65.5%; Score 38;
66.7%; Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/765,783
FTLING DATE: 7-MATCH-1997
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 35029-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 83, Application US/09416557
Patent No. 6245894
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEFAX: 202-822-0168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                       Query Match
Best Local Similarity 66.7
Matches 6; Conservative
TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 9 amino acids
                                                                                        ; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-765-783A-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON
                                                                                                                                                                                                                                                                                               1 QHHYGTPYT 9
                                                                                                                                                                                                                                                                                                                            |||:| | |
QHHFGFPRT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QHHYGTPYT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS-09-416-557-83
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Pred. No. 18;
1; Mismatches 2; Indels
                                                                     ZUP: 20006-1888

ZIP: 20006-1888

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/921,100
FILING DATE: 29-AUG-1997
CLASSIFICATION NUMBER: US 08/437,323
FILING DATE: 09-MAY-1995
ATTOR APPLICATION NUMBER: US 08/437,323
FILING DATE: 09-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: WURSAHIGE, KATE H.
REGISTRATION NUMBER: 15580-0001.02
REFERENCE/DOCKET NUMBER: 15580-0001.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MATSUSHIMA, KOUJI
APPLICANT: MATSUMOTO, YOSHIHIRO
APPLICANT: YAMADA, YOSHIKI
APPLICANT: SATO, KOH
APPLICANT: TSUCHIYA, MASSAYUKI
APPLICANT: YAMAZAKI, TATUMI
TITLE OF INVENTION: HUMANIZED ANTI-ILB ANTIBODY
NUMBER OF SEQUENCES: 77
    2000 Pennsylvania Ave. NW, Suite 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. NW, Suite 5500
-CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/921,100
FILING DATE: 29-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/437,323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 77, Application US/08921100 Patent No. 6024956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 126 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (202) 887-076
TELEX: 90-4030
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 66.7
Matches 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein US-08-921-100-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 QHHFGFPRT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QHHYGTPYT 9
                         Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                            COUNTRY: USA
ZIP: 20006-1888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                      APPLICANT: Tsuchiya, Masayuki
APPLICANT: Yamazaki, Tatsumi
TITLE OF INVENTION: Reshaped Human Antibody to
TITLE OF INVENTION: Interleukin-8
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW, suite 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PERENT NO. 6024956
GENERAL INFORMATION:
APPLICANT: MATSUSHIMA, KOUJI
APPLICANT: YAMADA, YOSHIHIRO
APPLICANT: YAMADA, YOSHIKI
APPLICANT: SATO, KOH
APPLICANT: TSUCHIYA, MASSAYUKI
APPLICANT: TSUCHIYA, MASSAYUKI
APPLICANT: YAMAZAKI, TATUMI
TITLE OP INVENTION: HUMANIZED ANTI-IL8 ANTIBODY
                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,783A
FILING DATE: 07-MAR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65.5%; Score 38; 66.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 73, Application US/08921100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: MATEALIGE, KAZE H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 3502:
TELECOMMUNICATION INFORMATION:
TELECHONE: 202-887-1500
TELEPAK: 202-822-0168
Matsumoto, Yoshihiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Signal Sequence

LOCATION:

CTHER INFORMATION:

US-08-765-783A-77
                     Yoshiki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 QHHFGFPRT 116
                                           Sato, Koh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 OHHYGTPYT 9
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STRANDEDNESS: sir
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Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-921-100-73
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                         Score 38; DB 3; Length 126;
Pred. No. 18;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                               APPLICANT: MATSUSHIMA, KOUJI
APPLICANT: MATSUMOTO, YOSHIHIRO
APPLICANT: YAMADA, YOSHIKI
APPLICANT: SATO, KOH
APPLICANT: TSUCHIYA, MASSAYUKI
APPLICANT: YAMAZAKI, TATUMI
TITLE OF INVENTION: HUMANIZED ANTI-ILB ANTIBODY
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,142
FILING DATE: 20-JUN-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           r: 2000 Pennsylvania Ave. NW, Suite 5500
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 20-JUN-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/345,145
FILING DATE: 28-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-902-201-73; Sequence 73, Application US/08902201; Patent No. 6068840 GENERAL INFORMATION: APPLICANT: MATSUSHIMA, KOUJI
                                                                                                                                                                                                                                                      sequence 77, Application US/08880142
Patent No. 6048972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 15:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : (202) 887-1500
(202) 887-0763
                         Similarity 66.7%;
6; Conservative
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amino acid
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                                                                                                                                             |||:| | |
108 QHHFGFPRT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 OHHFGFPRT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QHHYGTPYT 9
                      Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 20006-1888
                                                                                                                    1 QHHYGTPYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-880-142-77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
CITY: Wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
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Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: DC
CUUNTRY: USA
ZIP: Z0006-1888
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,142
FILING DATE: 20-JUN-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/345,145
FILING DATE: 28-NOV-1994
ATTONEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
TELEFRAX: (202) 887-1500
TELEFRAX: (202) 887-1500
TELEFRAX: (202) 887-1500
TELEFRAX: (202) 887-1600
TELEFRAX: (202) 887-1600
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TELEFRAX: (202) 887-1600
TELEFRAX: (202) 887-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: SATO, KOH
APPLICANT: SATO, KOH
APPLICANT: TSUCHTYA, MASSAYUKI
APPLICANT: YAMAZAKI, TATUMI
TITLE OF INVENTION: HUMANIZED ANTI-IL8 ANTIBODY
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSE: MORPICOT:
STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    iSEE: MORRISON & FOERSTER
7: 2000 Pennsylvania Ave. NW, Suite 5500
Waghington
FILING DATE: 09-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 15580-0001.02
TELECOMMUNICATION INFORMATION:
TELEPHANE: (202) 887-1500
TELEFAX: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 73, Application US/08880142
Patent No. 6048972
GENERAL INFORMATION:
APPLICANT: MATSUSHIMA, KOUJI
APPLICANT: NATSUMOTO, YOSHIHIRO
APPLICANT: YAMADA, YOSHIKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1: 126 amino acids
amino acid
                                                                                                                                                                                                                                                         : 126 amino acids
amino acid
                                                                                                                                                               TELEFAX: (202) 887-076.
TELEX: 90-4030
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARATTERISTICS:
LENGTH: 126 amino acid.
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-08-880-142-73
                                                                                                                                                                                                                                                                                             TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-921-100-77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 QHHFGFPRT 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
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                     CORRAGING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/902,201
FILING DATE: 29-JUL-1997
CLASSIFICATION: 424
PRICH APPLICATION DATA:
PRICH APPLICATION NUMBER: US 08/437,328
FILING DATE: 09-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 15580-0001.01
TELEFAX: (202) 887-1500
TELEFAX: (202) 887-1500
TELEFAX: (202) 887-1500
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TELEFAX: (202) 887-0763
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TELEFAX: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 2000 Pennsylvania Avenue, NW, suite 5500 CITY: Washington STATE: DC COUNTY: USA ZIP: 20006-1888 ZIP: 20006-1888 COMPUTER READABLE FORM: WEDIUM TYPE: Diskette COMPUTER: IBM Compatible COMPUTER: Diskette COMPUTER: Diskette COMPUTER: Diskette COMPUTER: Diskette COMPUTER: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Matsushima, Kouji
APPLICANT: Matsushima, Kouji
APPLICANT: Matsushoto, Yoshihiro
APPLICANT: Yamada, Yoshiki
APPLICANT: Sato, Koh
APPLICANT: Tsuchiya, Masayuki
APPLICANT: Tsuchiya, Masayuki
APPLICANT: Tsuchiya, Masayuki
TITLE OF INVENTION: Reshaped Human Antibody to
TITLE OF INVENTION: Interleukin-8
CORRESONDENCE ADDRESS: 105
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/416,557
FILING DATE: 12-October-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35029-20001.10
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Patent No. 6245894
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08/765,783
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 7-March-1997
ATTORNEY/AGENT INFORMATION:
NAWE: MIXEMISC, & Race H
RECISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 35028
        IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
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66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-08-902-201-77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108 QHHFGFPRT 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/902,201
FILING DATE: 29-JUL-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/437,328
FILING DATE: 09-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 15580-0001.01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MATSUSHIMA, KOUJI
APPLICANT: MATSUSHIMA, KOUJI
APPLICANT: YAMADA, YOSHHIKO
APPLICANT: SATO, KOH
APPLICANT: TSUCHIYA, MASSAYUKI
APPLICANT: TSUCHIYA, MASSAYUKI
APPLICANT: TSUCHIYA, MASSAYUKI
TITLE OF INVENTION: HUMANIZED ANTI-ILB ANTIBODY
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
STREFF: MORRISCY:
                                                                                                                                                                                                       SEE: MORRISON & FOERSTER
1: 2000 Pennsylvania Ave. NW, Suite 5500
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSEE: MORRISON & FOERSTER
[: 2000 Pennsylvania Ave. NW, Suite 5500
Washington
                                                                      APPLICANT: TSUCHIYA, MASSAYUKI
APPLICANT: YAMAZAKI, TATUMI
TITLE O INVENTION: HUMANIZED ANTI-IL8 ANTIBODY
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.5%; Score 38; 66.7%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                 ZIP: 2006-1888
COMPUTER READABLE FORM:
MBDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 77, Application US/08902201
Patent No. 6068840
GENERAL INFORMATION:
MATSUMOTO, YOSHIHIRO
                                                SATO, KOH
TSUCHIYA, MASSAYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                          YOSHIKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 126 amino acids
amino acid
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108 QHHFGFPRT 116
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Best Local Similarity
Matches 6; Conserv
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US-08-902-201-77
                                                                                                                                                                                                                                                                                     STATE: DO
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Gaps

Search completed: July 18, 2003, 15:11:51 Job time : 10.44 secs

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61, Appl
5, Appli
7, Appli
5, Appli
61, Appl
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                                                                                                                                                                              July 18, 2003, 15:09:56; Search time 23.22 Seconds (without alignments) 46.031 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Seq
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| cgn2 6/ptodata/1/pubpaa/PCT NEW PUB.pep:*
| cgn2 6/ptodata/1/pubpaa/PCT NEW PUB.pep:*
| cgn2 6/ptodata/1/pubpaa/PCT NEW PUB.pep:*
| cgn2 6/ptodata/1/pubpaa/NS06 NEW PUB.pep:*
| cgn2 6/ptodata/1/pubpaa/NS06 NEW PUB.pep:*
| cgn2 6/ptodata/1/pubpaa/NSOF PUBCOMB.pep:*
| cgn2 6/ptodata/1/pubpaa/NSOF PUBCOMB.pep:*
| cgn2 6/ptodata/1/pubpaa/USOF PUBCOMB.pep:*
| cgn2 6/ptodata/1/pubpaa/USOF NEW PUB.pep:*
| cgn2 6/ptodata/1/pubpaa/USOF PUBCOMB.pep:*
| cgn2 6/ptodata/1/pubpaa/USOF NEW PUB.pep:*
| cgn2 6/ptodata/1/pubpaa/USOF PUBCOMB.pep:*
| cgn2 6/ptodata/1/pubpaa/USOF PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-509-098-130
US-09-509-098-134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   451899 seqs, 118759770 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                      - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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58
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Match Length
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993.1
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
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Maximum DB s
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17 40 69.0 119 11 US-09-800-908-11 Sequence 11, Appl 19 40 69.0 126 10 US-09-760-723-6 Sequence 6, Appli 20 40 69.0 126 12 US-09-269-921-106 Sequence 10, Appl 21 US-09-269-921-106 Sequence 10, Appl 22 40 69.0 126 12 US-09-269-921-107 Sequence 10, Appl 23 40 69.0 126 12 US-09-509-088-12 Sequence 10, Appl 24 69.0 126 12 US-09-509-088-12 Sequence 10, Appl 24 69.0 126 14 US-10-218-253-107 Sequence 10, Appl 26 12 US-09-509-088-12 Sequence 10, Appl 26 12 US-09-509-088-12 Sequence 10, Appl 27 12 US-09-509-088-2 Sequence 10, Appl 28 12 US-09-209-208-2 Sequence 10, Appl 28 12 US-09-209-208-2 Sequence 10, Appl 28 12 US-09-209-208-2 Sequence 10, Appl 29 40 69.0 131 12 US-09-269-921-104 Sequence 10, Appl 29 40 69.0 131 12 US-09-269-921-104 Sequence 10, Appl 29 40 69.0 131 12 US-09-269-921-104 Sequence 10, Appl 39 67.2 175 15 US-09-209-2 Sequence 2, Appl 39 65.5 12 U US-09-730-87-73 Sequence 2, Appl 39 65.5 126 10 US-09-730-87-73 Sequence 2, Appl 39 65.5 126 10 US-09-730-87-73 Sequence 2, Appl 39 65.5 126 10 US-09-730-87-73 Sequence 2, Appl 39 65.5 126 10 US-09-989-896-8 Sequence 2, Appl 39 65.1 12 US-09-899-896-8 Sequence 2, Appl 41 35 62.1 12 US-09-899-896-8 Sequence 2, Appl 41 36 62.1 12 US-09-899-896-8 Sequence 2, Appl 41 35 62.1 12 US-09-899-896-8 Sequence 2, Appl 41 35 62.1 12 US-09-899-896-8 Sequence 2, Appl 41 35 62.1 12 US-09-899-896-8 Sequence 2, Appl 41 35 62.1 12 US-09-899-896-8 Sequence 2, Appl 41 35 62.1 12 US-09-899-896-8 Sequence 11, Appl 42 56 63 11 US-09-899-896-8 Sequence 11, Appl 44 35 60.3 21 US-09-899-896-8 Sequence 11, Appl 42 56 63 21 US-09-899-896-8 Sequence 11, Appl 42 56 69.3 21 US-09-899-896-8 Sequence 11, Appl 42 56 69.3 21 US-09-899-896-8 Sequence 11, Appl 42 56 69.3 21 US-09-899-896-8 Sequence 11, Appl 42 56 69.3 21 US-09-899-896-8 Se
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## ALIGNMENTS

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Sequence 15, Application US/10096246
Publication No. US20030100060A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Fulton, R E
APPLICANT: Alvi, Azhar E
APPLICANT: Alvi, Azhar E
APPLICANT: Nagata, Lealie
TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mor
TITLE OF INVENTION: ScFv Antibody Against Venzuelan Equine Encephalitis Virus (Vee)
TITLE OF INVENTION: 0007
CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE PATENTIN VERSION: 3.1
SEQ ID NO 15
LENGTH: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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US-10-096-246-19
Sequence 19, Application US/10096246
Publication No. US20030100060A1
SENERAL INFORMATION:
APPLICANT: The Minister of National Defence, Government of Canada
APPLICANT: Fulton, R E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.1%; Score 54; DB 15; Length 106; 88.9%; Pred. No. 0.093;
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0
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                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Mouse hybridoma cell line 1A4A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97
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Matches 8; Conserv
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US-10-096-246-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Gaps

.; 0

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APPLICANT: Lal, Preeti
APPLICANT: Lal, Dennifer L.
Corley, Meil C.
Guegler, Karl J.
Baugh, Mariah
Sather, Suaan
Shah, Purvi
TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS
NUMBER OF SEQUENCES: 154
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
                                                                          Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: 1BM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/799,777
FILING DATE: 06-Mar-2001
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 75.9%; Score 44; DB 10; Length 235; Best Local Similarity 87.5%; Pred. No: 8.1; Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                      Indels
                                                                       Score 44; DB 15;
Pred. No. 3.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36, 749
REFERENCE/DOCKET NUMBER: PF-0459 US
                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/002,485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ ID NO: 43 :
; ORGANISM: Mouse hybridoma cell line 1A4Al
US-10-096-246-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (650) 855-0555
                                                                                                                                                                                                                                                                                                                                    Sequence 43, Application US/09799777
Patent No. US20020091244A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 235 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                     Query Match 75.9%;
Best Local Similarity 77.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIBRARY: BRSTNOT04
CLONE: 1969426
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                                                                                                                                                                                                                     89 OHFWGTPYT 97
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APPLICANT: The Minister of National Defence, Government of Canada
APPLICANT: Pulton, R E
APPLICANT: Alvi, Azhar E
APPLICANT: Nagata, Lesie
TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of MC
TITLE OF INVENTION: ScFV Antibody Against Venzuelan Equine Encephalitis Virus (Vee)
FILE REFERENCE: NEL-0007
CURRENT APPLICATION NUMBER: US/10/096,246
CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin version 3.1
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: The Minister of National Defence, Government of Canada
APPLICANT: The Minister of National Defence, Government of Canada
APPLICANT: Fulton, R E
APPLICANT: Alvi, Azhar E
APPLICANT: Negata, Leslie
TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of MC
TITLE OF INVENTION: ScFv Antibody Against Venzuelan Equine Encephalitis Virus (Vee)
TITLE OF INVENTION: NUMBER: US/10/096,246
CURRENT APPLICATION NUMBER: US/10/096,246
CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
  APPLICANT: Nagata, Leslie
TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of MC
TITLE OF INVENTION: SCFV Antibody Against Venzuelan Equine Encephalitis Virus (Vee)
FILE REFERENCE: NEL-0007
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Pred. No. 1.2;
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Pred. No. 0.094;
1; Mismatches 0; Indels
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; ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-096-246-18
                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Mouse hybridoma cell line 1A4A1
                                                                                      CURRENT APPLICATION NUMBER: US/10/096,246
CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin version 3.1
SEQ ID NO 19
LENGTH: 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-096-246-18
; Sequence 18, Application US/10096246
; Publication No. US20030100060A1
; GENERAL INFORMATION:
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; Sequence 14, Application US/10096246
; Publication No. US20030100060A1
; GENERAL INFORMATION:
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88.9%;
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity
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RESULT 8
US-09-423-800-61
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APPLICANT: OLIVE, DANALED
APPLICANT: DAN, BERNARD
TITLE OF INVENTION: CDR-H1-DERIVED PETIDE CB11, PHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: MAMMALS
TITLE OF INVENTION: MAMMALS
FILE REFERENCE: 1129-R-02
CURRENT APPLICATION NUMBER: 0/10/322,142
CURRENT PETING DATE: 2003-02-21
PRIOR FILING DATE: 2001-12-18
PRIOR FILING DATE: 2001-12-18
PRIOR FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 32
SOFTHARE: PATENTIN VET: 2.1
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CURRENT APPLICATION NUMBER: 60/341,349
PRIOR APPLICATION NUMBER: 60/341,349
PRIOR APPLICATION NUMBER: 60/341,349
PRIOR APPLICATION NUMBER: 60/374,754
PROR FILING DATE: 2001-12-18
PROR FILING DATE: 2002-04-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 74.1%; Score 43; DB 15; Length 12; Best Local Similarity 77.8%; Pred. No. 0.7; Matches 7; Conservative 0; Mismatches 2; Indels
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APPLICANT: BRIANT-LONGUET, LAURENCE
APPLICANT: CENUTII, MARTINE
APPLICANT: CHARDES, THIERRY
APPLICANT: DEVAUCHELLE, GERARD
APPLICANT: DEVAUX, CHRISTIAN
APPLICANT: GRANIER, CLAUDE
APPLICANT: MAWAS, CLAUDE
APPLICANT: OLIVE, DANIEL
                                                                         BES, CEDRIC
BRIANT-LONGUET, LAURENCE
CENUTI, MARTINE
CHARDES, THIERRY
DEVAUCHELLE, GERARD
DEVAUX, CHRISTIAN
GRANIER, CLAUDE
MAMAS, CLAUDE
MAMAS, CLAUDE
OLIVE, DANIEL
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Publication No. US20030113322A1
GENERAL INFORMATION:
Sequence 9, Application US/10322142
Publication No. US20030113322A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial Sequence
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 32
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LENGTH: 12
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APPLICANT:
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Gaps
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic VL
; OTHER INFORMATION: domain of the anti-CD4 mAb 13B82
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Pred. No. 5.6;
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APPLICANT: Ohtomo, Toshiniko
APPLICANT: Ohtomo, Toshiniko
APPLICANT: Tsuchiya, Masayuki
APPLICANT: Tsuchiya, Masayuki
APPLICANT: Yoshinara, Yasushi
APPLICANT: Koishinara, Yasushi
APPLICANT: Koishinara, Yasuso
TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY
TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY
CURRENT APPLICATION NUMBER: US/09/269,921
CURRENT FILING DATE: 1999-4-01
EARLIER PILING DATE: 1999-10-03
EARLIER FILING DATE: 1999-10-03
EARLIER FILING DATE: 1999-10-04
NUMBER OF SEQ ID NOS: 137
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Pred. No. 4e+05;
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Fatent No. US20020165363A1
GENERAL INFORMATION:
APPLICANT: SATO, KOH
APPLICANT: TSUNENARI TOSHIAKI
APPLICANT: TSUNENARI TOSHIAKI
APPLICANT: TSHI, KMIE
ITLE OF INVENTION: CACHEXIA REMEDY
FILE REFERENCE: 0485-0036
CURRENT APPLICATION NUMBER: US/09/423,800
CURRENT FILING DATE: 1999-01-12
PRIOR FILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-05-15
PRIOR FILING DATE: 1997-05-15
PRIOR FILING DATE: 1997-07-18
PRIOR FILING DATE: 1997-07-18
SOFTWARE: PATOLICATION NUMBER: JP 194445/1997
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PATOLICATION NUMBER: JP 15505/1997
SOFTWARE: PATOLICATION NUMBER: JP 19505/1997
                                                                                                                                                                                                                                                                                            0; Mismatches
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Publication No. US20030045691A1
GENERAL INFORMATION:
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Best Local Similarity 77.8%;
Matches 7; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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US-09-423-800-61
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SEQ ID NO 5
LENGTH: 9
TYPE: PRT
ORGANISM: murine
PEATURE:
OTHER INFORMATION: Amino acid sequence of CDR(3) of L chain V region of OTHER INFORMATION: mouse anti-HM 1.24 antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-018-61
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Matches 6; Conserv
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                                                                                                                                                                   US-10-218-253-5
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                                                                                            OTHER INFORMATION: Amino acid sequence of CDR(3) of L chain V region of CTHER INFORMATION: mouse anti-HM 1.24 antibody US-09-269-921-5
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APPLICANT: Koishihara, Yasushi
APPLICANT: Koishihara, Yasushi
APPLICANT: Koishihara, Yasushi
TITLE OF INVENITON: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY
FILE REPRENCE: 350.29-20.007.00
CURRENT APPLICATION NUMBER: US/10/218,253
CURRENT FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: PCT/JP97/03553
PRIOR PILING DATE: 1997-10-03
PRIOR FILING DATE: 1997-10-03
PRIOR FILING DATE: 1996-10-04
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Pred. No. 4e+05;
1; Mismatches 2; Indels
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Pred. No. 4e+05;
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Publication No. US20030103970A1
GENERAL INFORMATION
APPLICANT: TSUCHIYA, MASAYUKI
TITLE OF INVENTION: NATURAL HUMANIZED ANTIBODY
FILE REPERENCE: 033466/0274
CURRENT APPLICATION NUMBER: US/09/509,098
CURRENT FILING DATE: 2000-03-22
FRIOR APPLICATION NUMBER: PCT/JP98/04469
FRIOR APPLICATION NUMBER: DCT/JP98/0469
FRIOR FILING DATE: 1999-10-02
FRIOR FILING DATE: 1999-10-03
FRIOR FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 203
SOFTWARE: PATCHING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 203
SOFTWARE: PATCHING DATE: 1997-10-03
SOFTWARE: PATCHING DATE: 1997-10-03
SOFTWARE: PATCHING DATE: 1997-10-03
SOFTWARE: PATCHING DATE: 1997-10-03
SOFTWARE: PATCHING DATE: 1997-10-03
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Publication No. US20030129185A1
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66.7%;
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ORGANISM: Artificial Sequence
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APPLICANT: Ono, Koichiro
APPLICANT: Ohtomo, Toshihiko
APPLICANT: Tsuchiya, Masayuki
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SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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                                              ORGANISM: murine
                             TYPE: PRT
                                                                           FEATURE:
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W3-10-169-003-61
Sequence 61, Application US/10169003
Sequence 61, Application WS/10169003
Sequence 61, Application No. US20030124119A1
Sequence 61, Application No. US20030124119A1
SEMBRAL INFORMATION:
TITLE OF INVENTION: SEADALIZED Antibody Composition and Pharmaceutical Preparation for TITLE OF INVENTION: Injection
FILE REFERENCE: PH-1093-PCT
CURRENT PAPLICATION NUMBER: US110/169,003
CURRENT PAPLICATION NUMBER: 200-26-26
SPRIOR APPLICATION NUMBER: J99112-28
SPRIOR FILING DATE: 1999-12-28
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                                                                                                                                                                                                                                                                                                                 APPLICANT: CHUGAL SEIYAKU KABUSHIKI KAISHA
TITLE OF INVENTION: THERAPEUTIC AND PREVENTIVE AGENTS FOR DENTAL DISEASES.
FILE REPERENCE: PH-1092-PCT
CURRENT APPLICATION NUMBER: US/10/182,018
CURRENT FILING DATE: 2002-07-24
PRIOR PILIAGIATION NUMBER: UF 2000-83034
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 61
LENGTH: 9
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                                                     Gaps
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Score 40; DB 14; Length 9;
Pred. No. 4e+05;
1; Mismatcheș 2; Indels
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Pred. No. 4e+05;
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; Sequence 61, Application US/10182018
; Publication No. US20030049211A1
; GENERAL INFORMATION:
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Best Local Similarity 66.7%;
Matches 6; Conservative 1
Similarity 66.7%; 6; Conservative 1
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66.7%;
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 61
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Best Local Similarity 66.7
Matches 6; Conservative
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OTHER INFORMATION: Description of Artificial Sequence: Amino acid CTHER INFORMATION: sequence of the L chain V region of RVLb US-09-509-098-134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40; DB 12; Length 107;
Pred. No. 17;
1; Mismatches 2; Indels
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/800,908
FILING DATE: 08-Mar-2001
CLASSIFICATION: UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/477,347
FILING DATE: -UNKNOWN>
FILING DATE: -UNKNOWN>
APPLICATION NUMBER: IL 106271
FILING DATE: -08-JUL-1993
ATTORNY/AGENT INFRWATION:
Sequence 134, Application US/09509098
Publication No. US20030103970A1
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, MASAYUKI
TITLE OF INVENTION: NATURAL HUMANIZED ANTIBODY
FILE REFERENCE: 053466/0274
CURRENT APPLICATION NUMBER: US/09/509,098
CURRENT FILING DATE: 1909-10-02
PRIOR PILING DATE: 1999-10-02
PRIOR PILING DATE: 1999-10-03
FRIOR APPLICATION NUMBER: UP 9-271726
PRIOR FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 203
SOFTWARE: PatentIn Ver: 2.1
SEQ ID NO 134
LENGTH: 107
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REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: WALLACH=10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 419 Seventh Street, N.W
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TITLE OF INVENTION: TWE LIGANDS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/09800908
Patent No. US20020111462A1
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: WALLACH, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BIGDA, Jacek
BELETSKY, Igor
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Best Local Similarity 66.7%;
Matches 6; Conservative
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US-09-800-908-11
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66.7%; Pred. No. 17;
cive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                   APPLICANT: TSUCHIYA, MASAYUKI
TILE OF INVENTION: NATURAL HUMANIZED ANTIBODY
FILE REFERENCE: 053466/0274
CURRENT APPLICATION NUMBER: US/09/509,098
CURRENT FILING DATE: 2000-03-22
FRIOR APPLICATION NUMBER: PCT/JP98/04469
FRIOR APPLICATION NUMBER: DP 9-271726
PRIOR APPLICATION NUMBER: JP 9-271726
PRIOR FILING DATE: 1998-10-03
PRIOR FILING DATE: 1997-10-03
NUMBER: PAPALICATION NUMBER: JP 3-271726
NUMBER: PEROFINION OFF: 203
SOFTWARE: PAPALICATION OFF: 203
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TITLE OF INVENTION: NATURAL HUMANIZED ANTIBODY
FILE REFERENCE: 053466/0274
CURRENT APPLICATION NUMBER: US/09/509,098
CURRENT FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: PCT/JP98/04469
PRIOR FILING DATE: 1998-10-02
PRIOR FILING DATE: 1997-10-03
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US-09-509-130
US-09-509-130
Sequence 130, Application US/09509098
Publication No. US20030103970A1
GENERAL INFORMATION:
                                                                                                                                                                                   ; Sequence 133, Application US/09509098; Publication No. US20030103970A1; GENERAL INFORMATION:
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ORGANISM: Artificial Seguence
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 130
LENGTH: 107
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Matches 6; Conservative
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89 QQHYSTPFT 97
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89 QQHYSTPFT 97
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                                                                                                           RESULT 14
US-09-509-098-133
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                         69.0%; Score 40; DB 11; Length 119; 66.7%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: KOISHIHARA, YASUO
APPLICANT: YOSHIMURA, YASUO
APPLICANT: YOSHIMURA, YASUSHI
TITLE O'NUENTION: THERAPEUTIC AGENT FOR LYMPHATIC TUMORS
FILE REFERENCE: 033466/0255
CURRENT APPLICATION NUMBER: US/09/155,925
CURRENT PILING DATE: 1999-08-11
PRIOR FILING DATE: 1999-08-12
PRIOR FILING DATE: 1990-02-12
PRIOR PLILOTATION NUMBER: UP 9-41410
PRIOR FILING DATE: 1997-02-12
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION TO ANALY ASUO
TITLE OF INVENTION: INHIBITOR OF LYMPHOCYTE ACTIVATION
TITLE OF INVENTION: INHIBITOR OF LYMPHOCYTE ACTIVATION
FILE REFERENCE: 053466/0295
CURRENT APPLICATION NUMBER: U8/09/760,723
CURRENT FILING DATE: 2001-05-29
PRIOR PAPLICATION NUMBER: P09/367,833
PRIOR FILING DATE: 1998-08-25
PRIOR FILING DATE: 1998-08-25
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                      1; Mismatches
                       LENGTH: 119 amino acids
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-800-908-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/09760723
Patent No. US20020034507A1
GENERAL INFORMATION:
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Patent No. US20020037288A1
GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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Matches 6; Conserv
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Matches 6; Conserv
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SEQ ID NO 6
LENGTH: 126
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LENGTH: 126
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US-09-760-723-6
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OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence OTHER INFORMATION: of reshaped human anti-HM 1.24 antibody L chain V region OTHER INFORMATION: version a
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OTHER INFORMATION: Description of Artificial Sequence: Amino acid of There Information: Sequence of L chain V region version a of CHER INFORMATION: humanized anti-HM1.24 antibody US-09-155-925-6
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Publication No. US20030045691A1

GENERAL INFORMATION:
APPLICANT: Ono, Voichiro
APPLICANT: Ono, Coichiro
APPLICANT: Ontomo, Toshihiko
APPLICANT: Stochiya, Masayuki
APPLICANT: Yoshimura, Yasuo
TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY
FILE REFERENCE: 35029-20007.00
CURRENT APPLICATION NUMBER: US/09/269,921
CURRENT FILING DATE: 1999-04-01
EARLIER APPLICATION NUMBER: PCT/JP97/03553
EARLIER FILING DATE: 1997-10-03
EARLIER FILING DATE: 1997-10-03
EARLIER FILING DATE: 1996-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Onco, Koichiro
APPLICANT: Onco, Toshihiko
APPLICANT: Tsuchiya, Masayuki
APPLICANT: Tsuchiya, Masayuki
APPLICANT: Yoshimura, Yasushi
APPLICANT: Yoshimura, Yasushi
APPLICANT: Yoshimura, Yasushi
APPLICANT: Yoshimura, Yasushi
APPLICANT: Yoshimura, Yasushi
APPLICANT: MUMBER: US/09/269,921
CURRENT FILENG DATE: 1999-04-01
CURRENT FILING DATE: 1999-04-01
EARLIER APPLICATION NUMBER: DF 264756
EARLIER FILING DATE: 1996-10-04
NUMBER OF SEQ ID NOS: 137
SEQ ID NOS: 137
SEQ ID NO 106
SEQ ID NO 106
                                                                                                                                                                2; Indels
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Pred. No. 20;
1; Mismatches 2;
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Pred. No. 20;
1; Mismatches 2
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; Sequence 106, Application US/09269921
; Publication No. US20030045691A1
                                                                                                                  69.0%;
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ORGANISM: Artificial Sequence
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                                                                                          Query Match
Best Local Similarity 66.70,
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Best Local Similarity
Matches 6; Conserva
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TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 66.7%;
Matches 6; Conservative
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Matches 6; Conserv
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                                                                                                                      FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence
OTHER INFORMATION: of reshaped human anti-HM 1.24 antibody L chain V region
US-09-269-921-107
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Pred. No. 20;
1; Mismatches 2; Indels
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66.7%; Pred. No. 20;
iive 1; Mismatches 2; Indels
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Publication No. US20030103970A1;
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, MASAYUKI
TITLE COF INVENTION: NATURAL HUMANIZED ANTIBODY
FILE REFREENCE: 053466/0274
CURRENT FILING DATE: 2000-03-22
PRIOR FILING DATE: 1996-10-02
PRIOR FILING DATE: 1997-10-03
PRIOR FILING DATE: 1997-10-03
PRIOR FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 203
SOFTWARE: PALENTIN OF SEQ ID NOS: 203
SEQ ID NO 14
LENGTH: 126
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US-09-509-098-12
Sequence 12, Application US/09509098
Sequence 12, Application US/09509098
Publication No. US20030103970A1
GENERAL INFORMATION:
APPLICANT: TSUCHIVA, MASAYUKI
FILLE REFRENCE: 053466/0274
CURRENT APPLICATION NUMBER: US/09/509,098
CURRENT FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: PCT/JP98/04469
PRIOR PILING DATE: 1999-10-02
PRIOR PILING DATE: 1999-10-03
PRIOR FILING DATE: 1997-10-03
SOFTWARE: PatentIN VOR: 203
SOFTWARE: PatentIN VET: 2.1
                                                                                                                                                                                                                                                  69.0%;
                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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NUMBER OF SEQ ID NOS: 137
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 107
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Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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US-09-509-098-14
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                                                               LENGTH:
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; OTHER INFORMATION: Amino acid sequence of anti-HM 1.24 antibody L chain V region US-09-269-921-104
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 131;
       INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/0950908
; Publication No. US20030103970A1
; GENERAL INFORMATION:
   APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: NATURAL HUMANIZED ANTIBODY
FILE REFERENCE: 053466/0274
; CURRENT FILING NUMBER: US/09/509,098
; CURRENT FILING NUMBER: US/09/509,098
; CURRENT FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: PCT/JP98/04469
; PRIOR APPLICATION NUMBER: P9-271726
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 203
; SEQ ID NO 2: 203
; SEQ ID NO 2: 2.1
; SEQ ID NO 2: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40; DB 12;
Pred. No. 21;
1; Mismatches 2
                                             CURRENT APPLICATION NUMBER: US/09/269,921
CURRENT FILING DATE: 1999-04-01
EARLIER APPLICATION NUMBER: PCT/JP97/03553
EARLIER FILING DATE: 1997-10-03
EARLIER FILING DATE: 1996-10-04
NUMBER OF SEQ ID NOS: 137
SEQ ID NO 104
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Pred. No.
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Publication No. US20030129185A1
GENERAL INFORMATION:
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APPLICANT: Ohtomo, Toshihiko
APPLICANT: Tsuchiya, Masayuki
APPLICANT: Yoshimura, Yasushi
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Best Local Similarity 66.,
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Best Local Similarity 66.7
Matches 6, Conservative
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ORGANISM: murine
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OTHER INFORMATION: of reshaped human anti-HM 1.24 antibody L chain V
OTHER INFORMATION: version b
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APPLICANT: KOISHIHARA, YASUO
APPLICANT: YOSHIMURA, YASUO
TILE OF INVENTION: THERAPEUTIC AGENT FOR LYMPHATIC TUMORS
FILE REPERNCE: 053466/0255
CURRENT APPLICATION NUMBER: US/10/315,125
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: PCT/JP98/00568
PRIOR FILING DATE: 1999-08-11
PRIOR FILING DATE: 1999-02-12
PRIOR FILING DATE: 1999-02-12
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 8
SOFFWARE: PALENTI VATE: 1997-02-12
NUMBER OF SEQ ID NOS: 8
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pred. No. 20;
1; Mismatches 2; Indels
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Pred. No. 20;
1; Mismatches 2; Indels
PRIOR APPLICATION NUMBER: PCT/JP97/03553
PRIOR FILING DATE: 1997-10-03
PRIOR APPLICATION NUMBER: JP 8-264756
PRIOR FILING DATE: 1996-10-04
NUMBER OF SEQ ID NOS: 137
SOFTWARE: Patentin Ver. 2.0
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Publication No. US20030045691A1
GENERAL INFORMATION:
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Publication No. US20030113334A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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APPLICANT: Ohtomo, Toshihiko
APPLICANT: Tsuchiya, Masayuki
APPLICANT: Yoshimura, Yasushi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Yoshimura, Yasush APPLICANT: Koishihara, Yasuo
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Best Local Similarity, 66.7-
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Best Local Similarity 66.7
Matches 6; Conservative
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                                                                                                                                            SEQ ID NO 107
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Gaps

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Indels

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Gaps

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Indels

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Sequence 16, Application US/10096246
Publication No US20030100060A1
GENERAL INFORMATION:
APPLICANT: The Minister of National Defence, Government of Canada
APPLICANT: Fulton, R E
APPLICANT: Fulton, R E
APPLICANT: APPLICANT: And APPLICANT: Fulton, R E
APPLICANT: Again E
APPLICANT: Nagata, Leslie
TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Matsushima, Kouji
Matsumoto, Yoshihiro
Yamada, Yoshiki
Sato, Koh
Tsuchiya, Masayuki
Yamazaki, Tatsumi
IITLE OF INVENTION: Reshaped Human Antibody
Interleukin-8
                                                                                                                                                                                                                                                        Score 39; DB 11;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                0; Mismatches
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CURRENT APPLICATION NUMBER: US/10/096,246
CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 37
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ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 83, Application US/09730857
Patent No. US20020082396A1
GENERAL INFORMATION:
                                               2001-03-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin version 3.1
SEQ ID NO 16
LENGTH: 110
                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative
; FILE REFERENCE: 089491/0201
; CURRENT APPLICATION NUMBER: UG
; CURRENT FILING DATE: 2001-03-
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 17
; LENGTH: 518
; TYPE: RRT
; ORGANISM: Homo sapiens
US-09-816-248-17
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COMPUTER READABLE FORM:
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||||| |:|
89 QHHYG-PFT 96
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COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                       499 HHYGTGY 505
                                                                                                                                                                                                                                                                                                                                             2 HHYGTPY 8
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                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Amino acid sequence of anti-HM 1.24 antibody L chain V region US-10-218-253-104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: CECH, THOMAS R.
TITLE OF INVENTION: PROTECTION-OF-TELOMERE-1 (POT-1) PROTEIN AND ENCODING
TITLE OF INVENTION: POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40; DB 14; Length 131;
Pred. No. 21;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.2%; Score 39; DB 15; Length 175; 66.7%; Pred. No. 39; 2; Indels ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Bayer AG
APPLICANT: Bull, Christof
TITLE OF INVENTION: Regulation of human Opsin-related GPCR
FILE REFERENCE: Lio039 foreign countries
CURRENT APPLICATION NUMBER: US/10/221,558
CURRENT FILING DATE: 2002-09-13
TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY FILE REFERENCE: 35029-20007.00
                  FILE REFERENCE: 35029-20007.00
CURRENT APPLICATION NUMBER: US/10/218,253
PRIOR APPLICATION NUMBER: US/09/269,921
PRIOR FILING DATE: 1999-04-01
PRIOR FILING DATE: 1999-04-03
PRIOR FILING DATE: 1997-03533
PRIOR FILING DATE: 1997-10-03
PRIOR FILING DATE: 1997-10-04
NUMBER OF SEQ ID NOS: 137
SEQ ID NO 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Xaa = any amino acid US-10-221-558-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/191,717
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 17, Application US/09816248; Patent No. US20020137703A1; GENERAL INFORMATION: APPLICANT: BAUMANN, PETER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/10221558
Publication No. US20030105316A1
GENERAL INFORMATION:
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Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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113 QOHYSTPFT 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QHHYGTPYT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QHHYGTPYT 9
                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 31
US-09-816-248-17
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LENGTH: 175
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                                                                                                                                                                                                                                                                                                LENGTH: 131
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CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/730,857
FILING DATE: Or-Dec-2000
CLASSIFICATION NUMBER: 09/16,557
APPLICATION NUMBER: 09/416,557
FILING DATE: 1999-10-12
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sato, Koh
Tsuchiya, Masayuki
Yamazaki, Tatsumi
TITLE OF INVENTION: Reshaped Human Antibody to
REFERENCE/DOCKET NUMBER: 35029-20001.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 35029-20001.10
                                                                                                                                                                                                                                                                                                           LUCATION: 1.7.19
COTHER INFORMATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 73:
US-09-730-857-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interleukin-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Matsushima, Kouji
Matsumoto, Yoshihiro
Yamada, Yoshiki
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TELEPHONE: 202-887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 77, Application US/09730857
Patent No. US20020082396A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,
                                                                               INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 126 amino acids
                                       TELEPHONE: 202-887-1500
TELEFAX: 202-822-0168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 202-822-0168
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INFORMATION FOR SEQ ID NO: 77
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                    Signal
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEOUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                   TELECOMMUNICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QHHYGTPYT 9
                                                                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: DC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF
                                                                                                                                                                                                                                                                              FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-730-857-77
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Pred. No. 4e+05;
1; Mismatches 2; Indels
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ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW, suite 5500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ_for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 73, Application US/09730857
Patent No. US2002082396A1
GENERAL INFORMATION:
MATEURION: MATEURION:
MATEURION: Yoshihiro
MATEURION: Yoshiki
Sato, Koh
Tsuchiya, Masayuki
Yamazaki, Tatsumi
TITLE OF INVENTION: Reshaped Human Antibody to
                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/730,857
                                                                                                                                                                                                                                                      NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 35029-20001.10
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEPAX: 202-822-0168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/09/730,857
FILING DATE: 07-Dec-2000
CLASSIFICATION: «UNKNOWN»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO: 83:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 09/416,557
                                                                                                                                                                      PRIOR APPLICATION DATA: APPLICATION NUMBER: 09/416,557
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REGISTRATION NUMBER: 29,959
                                                                                                                            FILING DATE: 07-Dec-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1999-10-12 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                  FILING DATE: 1999-10-12
                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                  TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 83
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 65.5
Best Local Similarity 66.7
Matches 6; Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibeault/Patent Department
STREET: Exchange Place, 53 State Street
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT SATENTIAN DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/887,853
FILING DATE: 21-Jun-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: US/08/133,804
*ILING DATA:
APPLICATION NUMBER: US/08/133,804
*ILING DATA:
APPLICATION NUMBER: US/08/133,804
*ILING DATA:
ATORNEY/AGENT INFORMATION:
RECISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                Score 38; DB 10; Length 127;
Pred. No. 42;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                      William David B. TITLE OF INVENTION: Imaging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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66.7%; Pred. No. 1.2e+02;
iive 0; Mismatches 3;
                   ; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-730-857-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Huston, James S. Oppermann, Hermann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09887853
Patent No. US20020168375A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/09899896
Patent No. US20020072588A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGIH: 250 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Massachusetts
    OTHER INFORMATION:
                                                                                Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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                                                                                                                                                                                          109 QHHFGFPRT 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
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                                                                                                                                                                  1 QHHYGTPYT
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US-09-899-896-8
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                                                                                                                                                                                                                                              65.5%; Score 38; DB 10; Length 126;
66.7%; Pred. No. 42;
iive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW, suite 5500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 27, Application US/09730857
Patent No. US20020396A1
GENERAL INFORMATION:
MATSUMOTO, Yoshiniro
Yamada, Yoshiki
Sato, Koh
Tsuchiya, Masayuki
Yamazaki, Tatamini
Yamazaki, Tatamini
TITLE OF INVENTION: Reshaped Human Antibody to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP:: 2006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/730,857
FILING DATE: O'-Dec-2000
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 35029-20001.10
TELECOMMUNICATION INFORMATION:
                                                                                                                       LOCATION: 0.19nal Sequence
LOCATION: 1...19
CHER INFORMATION: SEQUENCE DESCRIPTION: SEQ ID NO: 77:
US-09-730-857-77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 09/416,557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1999-10-12
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 127 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 202-822-0168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                   STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein FRAGMENT TYPE: internal FEATURE:
                                    TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPOLOGY: linear
TYPE: amino acid
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Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                             108 QHHFGFPRT 116
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                                                                                                                                                                                                                                                                                                                                   1 QHHYGTPYT 9
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LOCATION:
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APPLICANT: SHASHIDHARA, L.S.
TITLE OF INVENTION: IN VIVO ASSAY SYSTEM FOR SCREENING AND VALIDATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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US-09-880-748-2110

is Sequence 2110, Application US/09880748

publication No. US20030059937A1

is GENERAL INFORMATION:

APPLICANT: Ruben et al.

if TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PFS23

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT APPLICATION NUMBER: US/02/212

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR PELING DATE: 2000-06-15

PRIOR PELING DATE: 2000-06-15

PRIOR PELING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/270,379

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-18

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PATCHTIN VOY: 2.0
APPLICANT: Generally and the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the p
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1.6e+02;
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Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 66.7
Matches · 6; Conservative
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; ORGANISM: Homo sapiens
US-09-880-748-2110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89 OCHYSTPLT 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 8
LENGTH: 100
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

July 18, 2003, 15:03:05; Search time 11.7 Seconds (without alignments) 73.950 Million cell updates/sec

US-10-007-790-10. 58 1 QHHYGTPYT 9 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 ... Maximum DB seq length: 20000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

PIR 73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	q kappa	g kappa cha	g kappa chain v		g kappa chain V	g kappa	g kappa chain V	וט	b	וס	ש	σ	Ig kappa chain V r	hypothetical prote		hydrolase, probabl	glucose dehydrogen	hypothetical prote		Ig kappa chain V r	Ig kappa chain - m	Ig kappa chain pre	kappa rheum	hypothetical prote		abdominal segment	υ	hypothetical prote	ρι
SUMMARIES	ID	732	S31488	S24290	PH1069	KVMS49	S20810	PL0266	PH1053	PL0088	832191	832192	868212	PL0080	T26992	T26990	B81245	OPKEX .	T00826	A84845	A28840	S22024	S11245	A49138	D69536	439	N	279	99	7345
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hypothetical prote	hypothetical prote	hypothetical prote	Ig kappa chain pre	zinc finger protei	two-component resp	hypothetical prote	probable transcrip	transcription regu	homeotic protein m	unknown protein (i	probable membrane	hypothetical prote	adenomatous polypo	adenomatous polypo	PL7-6 antibody lig
D71101	D75139	T28876	830751	138617	E69747	AB0440	C81954	H81011	A43561	D86440	B70915	846115	RBHUAP	I49505	JC2270
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450	451	568	152	173	223	299	309	309	416	439	589	731	2843	2845	113
63.8	63.8	63.8	62.1	62.1	62.1	62.1	62.1	62.1	62.1	62.1	62.1	62.1	62.1	62.1	60.3
37	37	37	36	36	36	36	36	36	36	36	36	36	36	36	35
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1 B47329 IG kappa chain V region (PR1) - mouse C;Species: Mus musculus (house mouse) C;Date: 21-Sep-1993 #sequence_revision 17-Jul-1994 #text_change 21-Jan-2000 C;Date: 21-Sep-1993 #sequence_revision 17-Jul-1994 #text_change 21-Jan-2000 C;Date: 21-Sep-1993 #sequence_revision 17-Jul-1994 #text_change 21-Jan-2000 C;Date: 21-Sep-1993 #sequence_revision 17-Jul-1994 #text_change 21-Jan-2000 C;Date: 21-Sep-1993 #sequence_revision 17-Jul-1994 #text_change 21-Jan-2000 C;Date: 21-Sep-1993 #sequence_revision that is active on prostate cancer cells and that is constitute; prellumiary A;Reference number: A47329; MUID:93133825; PMID:8421689 A;Restaus: prellumiary A;Residues: 1-106 <bri>A;Residues: 1-106 <bri 1-106="" <bri="" <bri<="" a;residues:="" th=""></bri></bri></bri></bri></bri></bri></bri></bri></bri></bri></bri></bri></bri></bri></bri></bri></bri></bri></bri></bri></bri></bri></bri></bri></bri></bri></bri></bri></bri></bri></bri></bri></bri></bri></bri></bri></bri></bri></bri></bri></bri></bri>
Query Match Best Local Similarity 88.9%; Pred. No. 0.011; Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Qy 1 QHHYGTPYT 9 Db 89 QHHYGTPFT 97
RESULT 2 S31488 Ig kappa chain precursor V region (F11) - mouse (fragment) C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Accession: S1488 R;Bespalov, I.A.; Shiyanov, P.A.; Lukashevich, L.V.; Lunev, V.E.; Tribush, S.S.; Gaponov; submitted to the EMBL Data Library, December 1992 A;Reference number: S31488 A;Accession: S31488 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-13 < ABES A;Cross-references: EMBL:X69859; NID:g50929; PIDN:CAA49493.1; PID:g50930 C;Superfamily: immunoglobulin V region; immunoglobulin homology
C; Neywords: neceroterramer; immunoglobulin F;36-110/Domain: immunoglobulin homology < IMM> Query Match Best Local Similarity 88.9%; Pred. No. 0.013; Matches 8; Conservative 1; Mismatches 0; Gaps 0;

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A;Residues: 1-108 <APP>
A;Residues: 1-108 <APP>
A;Resperimental source: strain BALB/c
A;Note: this chain was isolated from a myeloma protein
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp c);Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lance;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;16-90/Domain: immunoglobulin homology <IMM>
F;16-90/Domain: immunoglobulin homology <IMM>
F;21-88/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Hoogenboom, H.; Dubois, P.; Raus, J.; Volckaert, G. submitted to the EMBL Data Library, September 1990
A;Description: Nucleotide sequences of the variable region cDNAs encoding a murine antibo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C,Accession: PL0266
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic ni
A;Reference number: PL0231; MUID:90111618; PMID:2104919
A;Accession: PL0266
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C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Accession: S20810
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C.Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-May-1997
                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pred. No. 0.19;
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Pred. No. 0.25;
1; Mismatches
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Best Local Similarity 77.8%;
Matches 7; Conservative
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88.9%;
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Best Local Similarity 88.2
Seconservative 8; Conservative
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A;Accession: S20810
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A; Residues: 1-101 <HOO>
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A;Residues: 1-62 <SHL>
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                                                                                                                                                                                                                                                                                                                    Rimoncharmont, B. submitted to the EMBL Data Library, September 1991
Submitted to the EMBL Data Library, September 1991
A) Foscription: Cloning and sequencing of the cDNA coding for the variable regions of the A) Reference number: $24287
A) Accession: $24290
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IG kappa chain V region (M149) -- mouse

C;Species: Mus musculus (house mouse)

C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 16-Aug-1996

C;Accession: A01919

R;Appella, E; Alvarez, V.L.

Mol. Immunol. 17, 1507-1513, 1980

A;Title: Amino acid sequence of the variable region of M149 mouse myeloma light chain:
A;Recession: A01919; MUID:82057806; PMID:6795447

A;Molecule type: protein
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19 light chain V region (clone 185-cl) - mouse (fragment)
C;Species: Wus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1069
B;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
A;Tille: Both IgM and IgG anti-DNA antibodies are the products of clonally selective BA;Reference number: PH0971; MUID:92381444; PMID:1512540
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C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
C;Accession: S24290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X62704; NID:g51693; PIDN:CAA44580.1; PID:g1333967
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
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C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: immunoglobulin homology < IMM>
F;16-90/Domain: immunoglobulin homology < IMM>
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88.9%; Pred. No. 0.12;
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                                                                  QHHYGTPFT 117
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QHHYGTPYT
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nes 8; Conserv
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les 8; Conserv
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A;Molecule type: mRNA
A;Residues: 1-107 <MON>
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A; Residues: 1-98 <TIL>
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Best Local S
Matches 8
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R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
FBBS Lett. 375, 273-276, 1995
A;Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin F
A;Reference number: 868211; MUID:96085223; PMID:7498516
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C;Species: Mus musculus (house mouse)
C;Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 11-Jan-2000
C;Accession: S68212
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig kappa chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
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C;Species: Mus musculus (house mouse)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 21-Jan-2000
C;Accession: PLO080
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
  A;Cross-references: EMBL:X70095; NID:g288260; PIDN:CAA49700.1; PID:g288261 C.Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin homology riM-90/Domain: immunoglobulin homology <IMM>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
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                                                                                                                                    Score 44; DB 2; Length 107;
Pred. No. 0.69;
0; Mismatches 2; Indels
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A; Status: preliminary; nucleic acid sequence not shown
A; Molecule type: mRNA
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submitted to the EMBL Data Library, February 1993
A,Reference number: S32185
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                                                                                                                                       Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative
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Matches 7; Conservative
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nes 7; Conserv
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A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-107 <IZU>
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PLO088
Ig kappa chain V regions (12518-1, 12528-16) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 21-Jan-2000
C;Accession: PL0088
R;Meek, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.; Ca
J. Exp. Med. 169, 519-533, 1889
A;Title: Structural characterization of antiidiotypic antibodies; evidence that Ab2s are
A;Reference number: PL0080; MUID:89094248; PMID:2492056
A;Accession: PL0088
A;Molecule type: mRNA
A;Residues: 1-106 <MEE>
A;Cross-references: GB:X58581; GB:Y00794; NID:951592; PIDN:CAA41457.1; PID:9930151
A;Note: the sequence shown here is from the V kappa regions an antiidiotypic monoclonal C;Superfamily: immunoglobulin V region; immunoglobulin homology cIMM>
F;16-89/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                      Ig light chain V region (clone 163.100) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: PH1053
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
C;Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective is A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1053
A;Accession: PH1053
A;Accession: PH1053
A;Accession: PH1053
A;Stefarence number: Bequence not shown
A;Molecule type: mRNA
A;Residues: 1-104 <TIL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin homology <IMM>
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C;Species: Mus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
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K;Izul, S.
submitch to the EMBL Data Library, February 1993
A;Reference number: S32185
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45 ONHYGIPYT 53
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Best Local Similarity
7; Conservi
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A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-107 <IZU>
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Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                         2 HHYGTPY
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A;Experimental source: strain BALB/c
A;Note: 106-Leu is translated from the codon CUN
A;Note: the sequence shown here is from the V kappa region of an antiidiotypic monoclona
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
R;Meek, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.; Ca
J. Exp. Med. 169, 519-533, 1989
A;Title: Structural characterization of antiidiotypic antibodies; evidence that Ab2s are
A;Reference number: PLO080; MUID:89094248; PMID:2492056
A;Accession: PLO080
A;Molecule type: mRNA
A;Residues: 1-107 <MEE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:AL032642; PIDN:CAA21653.1; GSPDB:GN00021; CESP:Y48A6C.3 A;Experimental source: clone Y48A6C C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:AL032642; PIDN:CAA21651.1; GSPDB:GN00021; CESP:Y48A6C.1
A;Experimental source: clone Y48A6C
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Cispecies: Caenorhabditis elegans
Cispecies: Tacot-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
Ciscossion: Tacot-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
Rigardner, A. Rigardner, A. Rigardner, A. Reference number: Z20296
A; Reference number: Z20296
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from A; Residues: 1-332 WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein Y48A6C.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 15-Oct.1999
C;Accession: T26990
R;Gardner, A.
8ubmitted to the EMBL Data Library, October 1998
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A;Introns: 27/3; 37/2; 87/2; 126/3; 149/3; 349/3; 385/3; 426/1; 465/3
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T26992
hypothetical protein Y48A6C.3 - Caenorhabditis elegans
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A;Molecule type: DNA
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Pred. No. 1.6;
1; Mismatches
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ilarity 85.7%; Pred. No. 5
Conservative 0; Mismatch
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A;Introns: 20/2; 70/2; 109/3; 132/3
                                                                                                                                                                                                                                                                                                                                                                                       72.4%;
85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
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89 QHHYGSP 95
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Ritetelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver A;Authers: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID: 20175755; PMID: 10710307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-237 <TET>
A;Cross-references: GB:AE002364; GB:AE002098; NID:g7225269; PIDN:AAF40511.1; PID:g722526(
A;Experimental source: serogroup B, strain MC58
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C;Superfamily: glucose dehydrogenase (pyrroloquinoline-quinone)
C;Keywords: oxidoreductase; pyrroloquinoline quinone; respiratory chain; transmembrane p)
F;9-28/Domain: transmembrane #status predicted <TM1>
F;35-54/Domain: transmembrane #status predicted <TM2>
F;60-76/Domain: transmembrane #status predicted <TM3>
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                                                                                                                                                                                                                                                                                                                                                                                                 hydrolase, probable NMB0040 [imported] - Neisseria meningitidis (strain MC58 C;Species: Neisseria meningitidis C;Date: 31-Mar-2000 #text_change 19-Jan-2001
                                                                       Gaps
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DB 2; Length 474; 7.8;
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                                                                   1; Indels
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Residues: 1-212,'A',214-808 <GOO>
Cross-references: EMBL:X62710; NID:g58416; PID:g58417
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F;122-138/Domain: transmembrane #status predicted <TM5>
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Pred. No. 8.5;
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                                                                       0; Mismatches
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   Score 42;
Pred. No.
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Best Local Similarity 75.0%;
Matches 6; Conservative
72.4%;
85.7%;
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A;Residues: 1-808 <CLE>
A;Cross-references: EMBL:X62710
                                                                   6; Conservative
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FOILEY, P., Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau, M.
EMBO J. 4, 3681-3688, 1985
A.Title: The idiotypic network and the internal image: possible regulation of a germ-line
A;Reference number: A91028; MUID:86136012; PMID:3937730
A;Recession: A28840
A;Molecule type: mRNA
A;Residues: 1-79 -OLL.
A;Cross-references: GB:X03387; NID:952168; PIDN:CAA27118.1; PID:g52169
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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R,Caulfield, M.J.
submitted to the EMBL Data Library, September 1991
A,Description: Nucleotide sequences of the mRNA/cDNA encoding a pathogenic anti-erythrocy
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C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
                                                                            C;Species: Mus musculus (house mouse)
C;Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Jul-1999
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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                                               (g kappa chain V region (HP21) - mouse (fragment)
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Pred. No. 4.1;
2; Mismatches
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A;Residues: 1-134 <WEL>
A;Cross-references: EMBL:X53484
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Best Local Similarity 66.7
Matches 6; Conservative
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                                                                                                                                             C; Accession: A28840; M25114
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Best Local Similarity
Matches 6; Conserv
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A;Molecule type: mRNA
A;Residues: 1-81 <CAU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein T32G6.22 - Arabidopsis thaliana (fragment)
(;Species: Arabidopsis thaliana (mouse-ear cress)
(;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 23-Mar-2001
(;Accession: T00026
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul submitted to the EMBL Data Library, November 1997
A;Description: Arabidopsis thaliana chromosome II BAC T32G6 genomic sequence.
A;Reference number: Z14163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Introns: 33/3; 95/2; 113/3; 137/3; 168/3; 361/3; 421/2; 432/3; 493/3; 521/3; 535/3; 56
A;Note: T32G6.22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable ABC transporter [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (c;Species: Arabidopsis thaliana (mouse-ear cress) (c;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;Accession: A84645 (c;A
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A;Reference number: A84420; MUID:20083487; PMID:10617197
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Pred. No. 50;
1; Mismatches 2; Indels
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F;91,93/Binding site: ubiquinone (Arg, Asp) #status predicted F;470/Active site: Asp #status predicted
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A;Cross-references: EMBL:AC002510; NID:g2618683; PID:g2618705
A;Experimental source: cultivar Columbia
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                                                                                                                                                                          1; Mismatches
                                                                                                     Score 40;
Pred. No. 3
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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Local Similarity 66.7%;
les 6; Conservative 1
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Best Local Similarity 75.0%;
Matches 6; Conservative
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100 KHHYGVGYT 108
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670 KHHYGVGYT 678
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647 QHNYGIPY 654
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A; Map position: 2

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Query Match

A;Accession: A84845 A;Status: preliminary A;Molecule type: DNA

1-1816

A;Residues:

C;Genetics: A;Gene: At2g41700 A; Map position: 2

1 QHHYGTPYT

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A;Residues: 1-393 <BUL>
A;Cross-references: GB:U67519; GB:L77117; NID:g1591436; PIDN:AAB98728.1; PtD:g1591446; T1
C;Genetics:
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, C. Feich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Science J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science J.J.; 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C. A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A;Reference number: A64300; MJID:96337999; PMID:8688087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: T04242
S. Bevan, M.; Petersrs, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Hohelsel, J.; Mewe
submitted to the Protein Sequence Database, March 1999
A;Reference number: Z15262
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A;Description: Light chain V region gene usage restriction and peculiarities in myeloma-a, A;Reference number: S52789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thaliana
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A,Status: preliminary, nucleic acid sequence not shown; translation not shown
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C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000
C;Accession: S52792
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A;Introns: 100/1; 145/3; 505/1; 576/3; 612/3; 683/3; 720/3; 785/3; 843/1
A;Note: F14M19.160
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Pred. No. 76;
0; Mismatches
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Pred. No. 33;
0; Mismatches
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C;Superfamily: Methanobacterium flavoprotein A
C;Keywords: flavoprotein
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A,Residues: 1-849 <BEV>
A,Cross-references: EMBL:AL049480
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ilarity 75.0%;
Conservative
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Best Local Similarity
Matches 6; Conserv
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Best Local
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C;Specias; Archaeoglobus fulgidus
C;Specias; Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 04-Mar-2000
C;Accession: D69536
R;KLenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec
A;Recession: D69536
A;Accession: D69536
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1.287 <KLE>
A;Cross-references: GB:AE000946; GB:AE000782; NID:g2689269; PIDN:AAB88967.1; PID:g264823
C;Superfamily: Archaeoglobus fulgidus hypothetical protein AF2292
                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: A49138
R;Gause, A.; Kuppers, R.; Mierau, R.
Clin. Exp. Immunol. 88, 430-434, 1992
A;Title: A somatically mutated V kappa IV gene encoding a human rheumatoid factor light A;Reference number: A49138; MUID:92298590; PMID:1606727
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C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: D64391
                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:S37926; NID:g298207; PIDN:AAB22366.1; PID:g298208 A;Note: sequence inconsistent with the nucleotide translation A;Note: sequence extracted from NGBI backbone (NCBIN:106633, NCBIP:106637) C;Superfamily: immunoglobulin v region; immunoglobulin homology r/Ama
                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 38; DB 2; Length 106;
Pred. No. 8.2;
1; Mismatches 2; Indels
                                            Indels
                                                                                                                                                                                                                                                                                                                        IgA kappa rheumatoid factor variable - human (fragment)
                                            ..
               Pred. No. 8.6;
                                            1, Mismatches
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         77.8%;
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Best Local Similarity 62.5
Matches 5; Conservative
            Best Local Similarity 77.8
Matches 7; Conservative
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Matches 6; Conservative
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OHHYG-PFT 117
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QHYYGAPF 219
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1 OHHYGIPYT 9

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Query Match

A; Residues: 1-106 <GAU> A;Status: preliminary A;Molecule type: DNA

1 QHHYGTPY 8

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Cispecies: Pyrococcus horikoshii
Cibate: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 05-Nov-1999
Cipaccession: D7101
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekint M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, DNA Res. 5, 55-76, 1998
A;Title: Complète sequence and gene organization of the genome of a hyper-thermophilic and A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Reference number: A71001
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-450 «KAW»
A; Cross-references: GB:AP000004; NID:g3236131; PIDN:BAA30170.1; PID:d1031113; PID:g325746
A; Experimental source: strain OT3
A; Note: this accession replaces an interim accession for a sequence replaced by GenBank
C; Genetics:
A; Gene: PH1071
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R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struct
A;Reference number: A75001
A;Accession: D75139
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A;Experimental source: strain Orsay
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A,Molecule type: DNA
A,Residues: 1-568 <MIL>
A;Residues: 1-568 <MIL>
A;Cross-references: EMBL:U41538; PIDN:AAC48176.1; GSPDB:GN00028; CESP:R04E5.10
A;Experimental source: strain Bristol N2; clone R04E5
C;Genetics:
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C,Species: Caenorhabditis elegans
C,Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
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hypothetical protein PAB1751 - Pyrococcus abyssi (strain Orsay)
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59;
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R,Miller, N.
submitted to the EMBL Data Library, December 1995
A,Description: The sequence of C. elegans cosmid R04ES.
A,Reference number: Z20535
A,Accession: T28876
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       hypothetical protein PH1071 - Pyrococcus horikoshii
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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A;Molecule.type: DNA
A;Residues: 1-451 <KAW>
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A;Gene: PAB1751
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C;Species: Lactococcus lactis subsp. lactis
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession. B86659
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: B86659
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-199 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ritimelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R. Nucleic Acids Res. 24, 4420-4449, 1996
Nucleic Acids Res. 24, 4420-4449, 1996
A; Title: Complete Gequence analysis of the genome of the bacterium Mycoplasma pneumoniae A; Reference number: S73327; MUID:97105885; PMID:8948633
A; Accession: S73455
A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Residues: 1-288 cHIM>
A; Residues: 1-288 cHIM>
A; Residues: L288 cHIM>
A; Residu
                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein nrdG [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
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A;Experimental source: strain IL1403
C;Genetics:
A;Gene: nrdG
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                                       Length 129;
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                                                                                                           2; Indels
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Pred. No. 36;
1; Mismatches
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100.0%; Pred. No. ...
0; Mismatches
                                   Score 37; DB 2
Pred. No. 15;
1; Mismatches
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C; Superfamily: fructose-bisphosphate aldolase II
C; Keywords: aldehyde-lyase; carbon-carbon lyase
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                                       63.8%;
Query Match
Best Local Similarity 66.77
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| OHHYAVPH 21
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Best Local Similarity
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YGTPYT 64
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C; Accession: E69747

R; Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berterc C; Accession: E69747

R; Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berterc A.; Brulich, S.D.; Brauerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A; Authores: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerc A; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holeappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Lavine, A.; Liu, H.; Masuda, S.; Maueel, A.; Authores: Lauber, J.; Lazarevic, V.; Ees, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y.; M.; Ogawa, A.; Odega, B.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, Y.; M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Authores: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sato, T.; Scanlon, A; Huthores: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sato, T.; Scanlon, A; Tomatel, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Minters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Altele: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Reference number: A69580; MulDisgody4033; PMID: 3984377

A; Altele: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
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C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AB0440
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B., deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; I il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, E Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-223 <KUN> A;Residues: 1-223 <KUN> A;Cross-references: GB:Z99105; GB:AL009126; NID:g2632457; PIDN:CAB11994.1; PID:g2632486 A;Experimental source: strain 168 C;Genetics:
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                                       C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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response regulator [YbdK] homolog ybdJ - Bacillus subtilis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
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F;52/Binding site: phosphate (Asp) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 223;
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Pred. No. 57;
1; Mismatches 0; Indels
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C, Keywords: phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36; DB 2;
Pred. No. 42;
1; Mismatches
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83.3%;
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Matches 5: Conservative
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117 EHHYGT 122
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C81954
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Cispecies: Homo sapiens (man)

Cjate: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 05-Nov-1999

CjAccession: 138617

R;Tommerup, N; Vissing, H.

R;Tommerup, N; Vissing, H.

R;Tommerup, N; Vissing, H.

R;Title: Isolation and fine mapping of 16 novel human zinc finger-encoding cDNAs identif A;Reference number: A57785; MUID:96044430; PMID:7557990

R;Accession: 138617

R;Accession: I38617

R;Accession: I38617

R;Accession: I38617

R;Reference number: A57785; MUID:96044430; PMID:7557990

R;Reference number: A57785; MUID:96044430; PMID:7557990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 33
S10751
Ig kappa chain precursor V region - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Decies: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jan-2000
C;Accesaion: S10751
R;Grant, F.J.; Levin, S.D.; Gilbert, T.; Kindsvogel, W.
Nucleic Acids Res. 15, 5496, 1987
A;Title: Improved RNA sequencing method to determine immunoglobulin mRNA sequence.
A;Reference number: S10751
A;Accession: S10751
A;Accession: S10751
A;Residues: 1-152 <GRA>
A;Cross-references: EMBL:X05877; NID:G52195; PIDN:CAA29301.1; PID:G52196
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin homology
F;138-152/Domain: C region (C-kappa) (fragment) #status predicted <CRE>
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C; Genetics:
                                                                                                                                                                                                                                                       Gaps
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       A;Gene: CESP:R04E5.10
A;Map posttion: X
A;Introns: 70/3; 108/3; 141/2; 308/3; 331/3; 386/3; 441/1; 474/3; 526/3
C;Superfamily: intermediate filament protein Av71
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Pred. No. 32;
0; Mismatches 1; Indels
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Pred. No. 28;
0; Mismatches 3; Indels
                                                                                                                                                                              Length 568
                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                              Score 37; DB 2;
Pred. No. 75;
2; Mismatches
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66.7%;
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62.5%;
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85.7%;
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Best Local Similarity 62...
Pocal 5; Conservative
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A;Map position: 2q34-2q35
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Matches 6; Conservative
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Matches 6; Conservative
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1 QHHYGTPYT 9

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111 ||| QHHPGTP 81

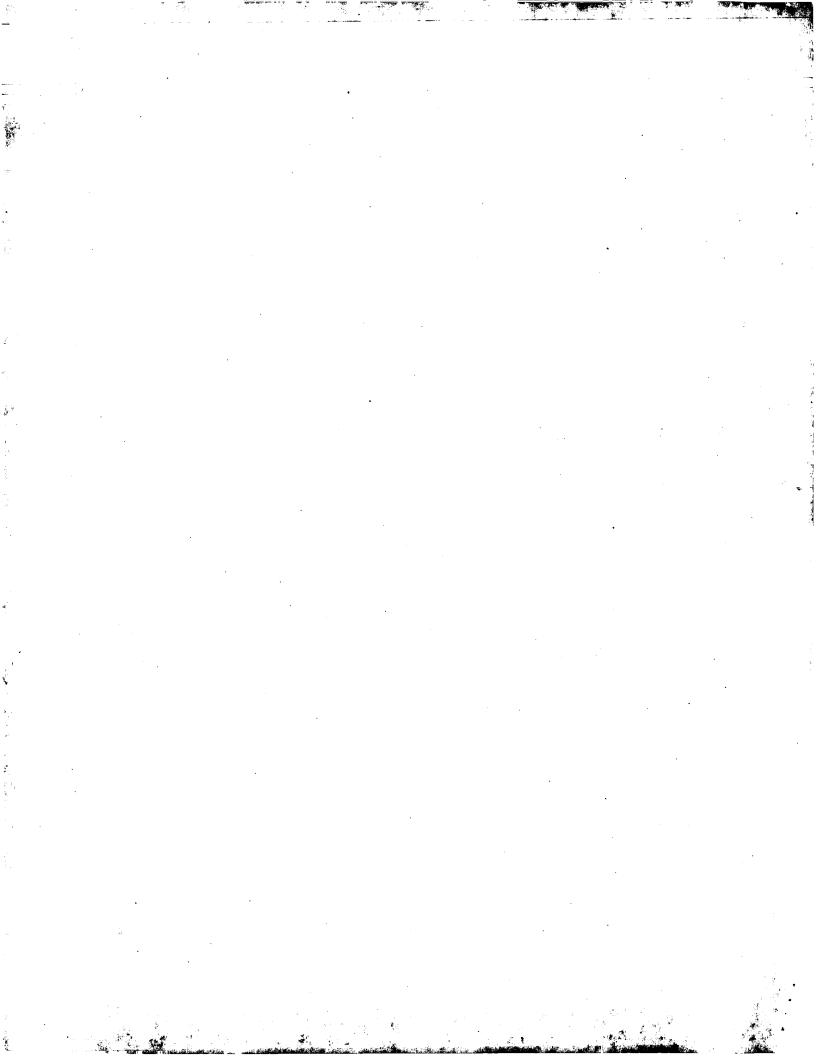
ઠ g RESULT 35 E69747

A; Gene: GDB: ZNF142

Query Match

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A;Molecule type: mRNA
A;Residues: 1-416 <BOD>
A;Residues: 1-416 <BOD>
A;Cross-references: GB.X55192; NID:g10345; PIDN:CAA38978.1; PID:g10346
R;Kim, Y.; Nirenbergy
B;Kim, Y.; Ni
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Best Local Similarity 62.5%;
Matches 5; Conservative
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71.4%;
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Best Local Similarity 71.4
Matches 5; Conservative
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140 QHHHGHPH 147
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Habili
transcription regulator, LygR family NMB2055 [imported] - Neisseria meningitidis (strain c.Species: Neisseria meningitidis
C.Species: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C.Jacession: HB1011
R.Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Hi, H.; Olin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
probable transcription activator protein METR NWA0381 [imported] - Neisseria meningitidi Cispecies: Neisseria meningitidis Cispecies: Neisseria meningitidis Cipate: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001 CiAccession: C81954
R;Parkhill, J; Achtman, M; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel Nature 404, S02-506, 2000 A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491. A;Reference number: A81775; MuID:20222556; PMID:10761919 A;Reterence T81954 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB83682.1; PID:g737913
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
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A;Residues: 1-309 <TET>
A;Cross-references: GB:AE002555; GB:AE002098; NID:g7227310; PIDN:AAF42375.1; PID:g722731
A;Experimental source: serogroup B, strain MC58
C;Genetics:
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Pred. No. 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 62.1%; Score 36; DB Best Local Similarity 71.4%; Pred. No. 59; Matches 5; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      d. No. 59;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Gene: metR, NMA0381
C,Superfamily: regulatory protein lysR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Gene: NMB2055
C,Superfamily: regulatory protein lysR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A43561
homeotic protein msh-2 - fruit fly
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71.4%;
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Best Local Similarity
'... 5; Conserv?
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ENHYGTP 50
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ENHYGTP 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-309 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QHHYGTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: H81011
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Chin, Cow, Chung, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: D86440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: D86440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
A,Accession: D33976
A,Accession: D33976
A,Molecule type: DNA
A,Residues: 267-416 KKM>
A,Cross-references: GB:M27292; NID:g157639; PIDN:AAA28619.1; PID:g552094
C,Genetics:
A,Gene: FlyBase:tin
A,Cross-references: FlyBase:FBgn0004110
                                                                                                                                                                                                                                               C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;3102-358/Domain: homeobox homology <HOX>
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Pred. No. 81;
2; Mismatches 1; Indels
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86;
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Pred. No.
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July 18, 2003, 15:03:05; Search time 6.5 Seconds (without alignments) 73.950 Million cell updates/sec Run on:

US-10-007-790-6 30 1 SCYNA 5 Title: Perfect score: Sequence:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

283224 segs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%.
Maximum Match 100%
Listing first 45 summaries

Database

PIR 73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote	e-tR	hypothetical prote	ORF MSV162 probabl	gp86 protein - Myc	86 proteir	het	precu	anthranilate synth		trai	cell surface glyco	netical		_	d hyp		4				>	transcription fact					o	iption
SUMMARIES	Ω	S19431	13	C64154	T28323	B72809	831031	T14799	S22515	T11982	T51829		B47629	T25314	T23637	H81309	AI0422	AG0900	C65106	H91133	C85979	T33297	35	5	173	A55973	5173	5173	919	55
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df		100.0	100.0	100.0	100.0	90.0	0.06	90.0	90.0	90.0	90.0	0.06	90.0	90.0	90.0	90.0	90.0	90.0	90.0	90.0	90.0	90.0	90.0	90.0	90.0	0.06	0.06	90.0	90.0	0.06
	Score				30	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27		27	27	27		27		27		27
	Result No.	1	7	m	4	ß	9	7	Φ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

purple acid phosph hypothetical prote		unknown protein [i pherophorin II - V	aldehyde dehydroge	aldehyde dehydroge hypothetical 58.0K	hypothetical prote	conserved hypothet	serine-type carbox	nitrous-oxide redu	propionate-CoA lig	hypothetical prote	F16F4.8 protein -
T49253 B71414	C91296 A84940	A96555 S36339	S74224	A55684 S56604	E86137	AB1073	JC7666	T44660	AE3290	T25228	F86345
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388 396	422	460 484	499	512 516	516	516	552	650	663	665	714
90.06	90.0	90.0	90.0	0.06	90.0	0.06	90.0	90.0	0.06	0.06	0.06
27	27	27 27	27	227	27	27	27	27	27	27	27
30 31	32 33	3.4 3.5	36	37 38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1 S19411 hypothetical protein YCR020c - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae · C;Date: 31-Mar-1992 #Sequence_revision 31-Mar-1992 #text_change 29-Oct-1999 · C;Accession: 819431; S07692
 R;Feldmann, H.; Mannhaupt, G.; Vetter, I. submitted to the Protein Sequence Database, March 1992 A;Reference number: S19429
 A;Accession: S19431 A;Molecule type: DNA A;Residues: 1-215 <fel> A;Cross-references: EMBL:X59720; NID:q1907116; PIDN:CAA42311.1; PID:e264484; PID:q190716</fel>
R,Toh-e, A.; Sahashi, Y. Yeast 1, 159-171, 1985
A,Title: The PET18 locus of Saccharomyces cerevisiae: a complex locus containing multiple A,Reference number: S07692; MUID:89131254; PMID:3916862 A,Accession: S07692
A;Molecule type: DNA A;Residues: 1-39,'M',41-103,'G',105-121,'S',123-215 <toh> C;Genetics:</toh>
 A;Gene: SGD:PET18 A;Cross-references: SGD:S0000613; MIPS:YCR020c A;Map position: 3R
 Query Match 100.0%; Score 30; DB 2; Length 215; Best Local Similarity 100.0%; Pred. No. 60; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SCYNA 5         Db 211 SCYNA 215

Glutamate-tRNA ligase (EC 6.1.1.17) Cj1288c [imported] - Campylobacter jejuni (strain NC7 C; Species: Campylobacter jejuni
C; Species: Campylobacter jejuni
C; Species: Campylobacter jejuni
C; Species: Campylobacter jejuni
C; Species: Campylobacter jejuni
R; Parkill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
C; M.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel)
Nature 403, 665-668, 2000
A; Fitle: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hype
A; Reference number: A81250; MUID:20150912; PMID:10688204

A; Accession: A81337

A; Status: preliminary A; Molecule type: DNA

A;Residues: 1-463 <PAR>
A;Residues: 1-463 <PAR>
A;Cross-references: GB:AL139077; GB:AL111168; NID:g6968444; PIDN:CAB73541.1; PID:g696872(
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:

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C;Species: Mycobacterium phage L5
C;Stecies: Mycobacterium phage L5
C;Accession. 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 08-Oct-1999
C;Accession. 331031
R;Donnelly-Wu, M.K.; Jacobs Jr., W.R.; Hatfull, G.F.
Mol. Microbiol. 7, 407-417, 1993
Mol. Microbiol. 7, 407-417, 1993
A;Title: Superinfection immunity of mycobacteriophage L5: applications for genetic transfl A;Reference number: S30949; WUID:93211283; PMID:8459767
A;Accession: S31031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:218946; NID:g15859; PIDN:CAA79462.1; PID:g15942
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992
C;Genetics:
                                                                                                             Artitle: Genome structure of mycobacteriophage D29: Implications for phage evolution. A;Reference number: A72800; MUID:98300335; PMID:9636706
A;Accession: B72809
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-88 <FOR>
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C;Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology
                                                                                                                                                                                                                                                                              A;Cross-references: GB:AF022214; NID:93172250; PIDN:AAC18516.1; PID:93172323 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein DKF2p434N221.1 - human
C,Species: Homo sapiens (man)
C,Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 02-Jun-2000
12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 20-Apr-2001
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                              C;Accession: B72809
R;Ford, M.E.; Sarkis, G.J.; Belanger, A.E.; Hendrix, R.W.; Hatfull, G.F.
J. Mol. Biol. 279, 143-164, 1998
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R;Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, submitted to the Protein Sequence Database, August 1999
A;Reference number: Z18183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 27; DB 2; Length 88; Pred. No. 1.2e+02; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             Score 27; DB 2; Length 88;
Pred. No. 1.2e+02;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene 86 protein - Mycobacterium phage L5
                                                                                                                                                                                                                                                                                                                                                                                                             90.0%;
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80.0%;
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Similarity 80.0%;
4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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Matches 4; Conserv
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Best Local Similarity
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51 ACYNA 55
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A; Residues: 1-88 < DON>
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A;Residues: 1-108 <POI
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                                                                                                                                                                                                                                                                                                                                                          A; Gene: 86
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A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-514 <TIGR>
A;Cross-references: GB:U32734; GB:L42023; NID:g1573498; PIDN:AAC22179.1; PID:g1573504;
A;Note: best homolog was a hypothetical protein from Escherichia coli
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ORF MSV162 probable NAD+ dependent DNA ligase - Melanoplus sanguinipes entomopoxvirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein HI0521 - Haemophilus influenzae (strain Rd KW20) C;Species: Haemophilus influenzae (5.pate: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999 C;Accession: C64154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Melanoplus sanguinipes entomopoxvirus
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
                                                                                                                                                                                Gaps
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R;Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
J. Virol. 73, 533-552, 1999
A;Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A;Reference number: 220484; MUID:99102612; PMID:9847359
A;Gene: gltX2; Cj1288c
C;Superfamily: glutamate-tRNA ligase; glutamine-tRNA ligase homology
C;Keywords: ligase
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100.0%; Score 30; DB 2; Length 514;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: nucleic acid sequence not shown; translation not shown
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llarity 100.0%; Pred. No. 1.2e+02;
Conservative 0; Mismatches 0; Indels
                                                                                                                      Length 463;
                                                                                                                100.0%; Score 30; DB 2; L
100.0%; Pred. No. 1.1e+02;
iive 0; Mismatches 0;
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A;Molecule type: DNA
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C,Species: Mycobacterium phage D29
                                                                                                                                                                                Conservative
                                                                                                                Query Match
Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                     299 SCYNA 303
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SCYNA 234
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                                                                                                                                                                                                                                   1 SCYNA 5
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RESULT 5 B72809

Gaps

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probable transcription regulator PA4288 [imported] - Pseudomonas aeruginosa (strain PAO1)
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Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog A;Reference number: A62950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AE004845; GB:AE004091; NID:g9950507; PIDN:AAG07676.1; GSPDB:GN001; A;Experimental source: strain PA01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X53517; NID:955911; PIDN:CAA37596.1; PID:955912
C;Comment: This antigen is expressed abundantly on B lymphocytes and is also seen at lowe
C;Superfamily: CD9 antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alternate names: leukocyte aniigen CD37; Species: Rattus norvegicus (Norway rat); Species: Rattus norvegicus (Norway rat); Pate: 03-Feb-1994 #sequence_revision 09-Aug-1996 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: B83109
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                                                                                                                                                                                                                                                                                                C; Superfamily: Arabidopsis thaliana hypothetical protein F16G20.50
                                                                                                                                                                                                                                                                                                                                                                 Score 27; DB 2; Length 246;
Pred. No. 2.6e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 27; DB 2; Length 267; Pred. No. 2.8e+02;
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A,Accession: T51829
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
                                                                                                                                                 A; Cross-references: EMBL: AJ011845; PIDN: CAA09808.1
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80.0%;
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Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity 80.C
Matches 4; Conservative
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                                                                                                               A; Residues: 1-246 < AUB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 SCYNS 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-267 <STO>
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A; Residues: 1-281 < CLA>
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A, Map position: 4
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                                                                                                                                                                                                                                                                                                           Nillouin precursor, text. Carrier partial precursor, text. Change 17-Mar-1999
C;Species: Hordeum vulgare (barley)
C;Species: Hordeum vulgare (barley)
C;Species: Hordeum vulgare (barley)
C;Accession: 522515
R;Andresen, I; Becker, W.; Schlueter, K.; Burges, J.; Parthier, B.; Apel, K.
R;Andresen, I.; Becker, W.; Schlueter, K.; Burges, J.; Parthier, B.; Apel, K.
R;Andresen, I.; Becker, W.; Schlueter, K.; Burges, J.; Parthier, B.; Apel, K.
R;Andresen, I.; Becker, W.; Schlueter, K.; Burges, J.; Parthier, B.; Apel, K.
A;Reference number: 522514; MuID:92322947; PMID:1377959
A;Accession: 522515
A;Anolecule type: mRNA
A;Anolecule type: mRNA
A;Residues: 1-137 <a href="https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/10.1007/j.nl/">https://doi.org/
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A;Description: Organisation of 46 kb of the Cyanidium caldarium RK1 plastid genome.
A;Reference number: 217374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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T51829
IBIC3-1 protein [imported] - Arabidopsis thaliana (fragment)
[Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 17-Nov-2000
C;Accession: T51829
R;Aubourg, S.
Submitted to the EMBL Data Library, October 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: chloroplast Cyanidium caldarium
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 05-May-2000
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Pred. No. 1.7e+02;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Superfamily: glutamine amidotransferase; trpG homology
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A;Molecule type: DNA
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C;Keywords: chloroplast
F;2-190/Domain: trpG homology <TRG>
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                                                                                                                                                                                                                                                                                        thionin precursor, leaf - barley
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Matches 4; Conservative
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Matches 4; Conservative
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NCYNA 66
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87 TCYNA 91
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A;Cross-references: EMBL:281132; PIDN:CAB03439.1; GSPDB:GN00023; CESP:T26E4.13
A;Experimental source: clone T26E4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted to the EMBL Data Library, November 1996
A;Reference number: Z19776
A;Accession: T23637
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Redus: L-287 <WIL>
A;Coss-references: EMBL:Z83116; PIDN:CAB05562.1; GSPDB:GN00023; CESP:M01B2.4
A;Experimental source: clone M01B2
                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein T26E4.13 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 26-May-2000 C;Accession: T25314 R;McMurray, A. Bubmitted to the EMBL Data Library, October 1996 A;Reference number: Z20013
F;242-267/Domain: transmembrane #status predicted <TM4>
F;268-278/Domain: intracellular #status predicted <CY3>
F;170,183,188/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 26-May-2000
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A;Introns: 206/2
C;Superfamily: Caenorhabditis elegans hypothetical protein B0250.6
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                                                                                                 Query Match 90.0%; Score 27; DB 1; Length 281; Best Local Similarity 80.0%; Pred. No. 2.9e+02; Matches 4; Conservative 1; Mismatches 0; Indels
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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80.0%; Pred. No. 3e+02;
tive 1; Mismatches
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Best Local Similarity 80.0
Matches 4; Conservative
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SCYNS 170
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164 SCYNS 168
                                                                                                                                                                                                                                     180 SCYNS 184
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A: Map position: 5
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R, Lloyd, C.
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C.Species: Campylobacter jejuni
C,Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C,Accession: H81300
C,Accession: H81300
C,W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell
Nature 403, 665-668, 2000
A,Title: The genome sequence of the food-borne pathogen Campylobacter jejuņi reveals hype
A,Reference number: A81250; MUID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Cross-references: GB:AL139077, GB:AL111168; NID:g6968444, PIDN:CAB73324.1; PID:g696850:
A,Experimental source: serotype O2, strain NCTC 11168
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C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Accession, A10422
B;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; I
II, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, I
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague:
A;Reference number: AB0001; MUID:21470413; PMID:11586360
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Nature, 413, 48-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serove
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       conserved hypothetical protein STY3458 [imported] - Salmonella enterica supsp. enterica C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001 C;Accession: AG0900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       conserved hypothetical protein YPO3480 (imported) - Yersinia pestis (strain CO92)
yypothetical protein Cj1069 [imported] - Campylobacter jejuni (strain NCTC 11168)
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80.0%; Pred. No. 3e+02;
tive 1; Mismatches 0; Indels
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Pred. No. 3e+02;
1; Mismatches 0; Indels
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Best Local Similarity 80.0%;
Matches 4; Conservative
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A Molecule type: DNA
A, Residues: 1-292 <KUR>
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117 NCYNA 121
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63 ACYNA 67
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A;Cross-references: GB:AE005174; NID:g12517767; PIDN:AAG58295.1; GSPDB:GN00145; UWGP:245; A;Experimental source: strain O157:H7, substrain EDL933
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G;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000
C;Accession: T33297
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C,Superfamily: Escherichia coli hypothetical 33.2K protein b3159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 90.0%; Score 27; DB 2; Length 298; Similarity 80.0%; Pred. No. 3.1e+02; 4; Conservative 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Superfamily: Caenorhabditis hypothetical protein C49G7.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Miller, N. ubmitted to the EMBL Data Library, May 1998
1Description: The sequence of C. elegans cosmid H05B21.
1Reference number: Z21317
1Accession: T33297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.0%; Score 27; DB 2; I ilarity 80.0%; Pred. No. 3.3e+02; Conservative 1; Mismatches 0;
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Best Local Similarity
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Best Local Similarity
Matches 4; Conserv
                                                                             123 NĊŸNÄ 127
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A; Residues: 1-298 <STO>
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NCYNA 6
                                 1 SCYNA 5
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C65106
hypothetical 33.2K protein b3159 - Escherichia coli (strain K-12)
C.Species: Escherichia coli
C.Species: Escherichia coli
C.Species: Escherichia coli
C.Species: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C.Accession: C65106
R.Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A./Title: The complete genome sequence of Escherichia coli K-12.
A.Reference number: A64720; MUID:97426617; PMID:9278503
A./Accession: C65106
A.Status: preliminary; nucleic acid sequence not shown; translation not shown
A.Residues: 1-298 «BLAT»
A.Cross-references: GB:AE000396; GB:U00096; NID:g1789536; PIDN:AAC76193.1; PID:g1789549;
A.Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C,Accession: H91133
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gench A;Reference number: A99629; MUID:21156231; PMID:11258796
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                                                                                                                    A,Cross-references: GB:AL513382; PIDN:CAD07797.1; PID:g16504345; GSPDB:GN00176 C,Genetics: A;Gene: STY3458 C,Superfamily: Escherichia coli hypothetical 33.2K protein b3159
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A;Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Species: Bscherichia coli
Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
                                                                                                                                                                                                                                                                                                        Gaps
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C;Superfamily: Escherichia coli hypothetical 33.2K protein b3159
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Superfamily: Escherichia coli hypothetical 33.2K protein b3159
                                                                                                                                                                                                                                               Score 27; DB 2; Length 292;
Pred. No. 3e+02;
1; Mismatches 0; Indels
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A; Reference number: AB0502; PMID:11677608
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Best Local Similarity 80.0
Matches 4; Conservative
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les 4; Conservative
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117 NCYNA 121
                                                                      A; Molecule type: DNA
A; Residues: 1-292 < PAR>
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123 NCYNA 127
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Residues: 1-298 <HAY>
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                         A; Accession: AG0900
A; Status: preliminary
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Dev. Dyn. 199, 1-11, 1994
A,Tile: Developmental regulation of islet-1 mRNA expression during neuronal differentiat
A,Reference number: 151739; MUID:94220748; PMID:8167375
C;Date: 13-Mar-1997 #sequence_revision 13-Mar-1997 #text_change 16-Jul-1999
C;Accession: 151739
R;Inoue, A.; Takahashi, M.; Hatta, K.; Hotta, Y.; Okamoto, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: mRNA;Residues: 1-358 <GON>;Cross-references: EMBL:X64885
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les 4, Conservative
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Best Local Similarity
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Best Local S:
Matches 4
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N;Alternate names: insulin enhancer-binding protein isl-2b; islet-2b protein
N;Alternate names: insulin enhancer-binding protein isl-2b; islet-2b protein
C;Species: Oncorhynchus tschawytscha (chinook salmon)
C;Date: 03-Oct-1995 #sequence revision 03-Oct-1995 #text_change 16-Jul-1999
C;Accession: B55973; S52091; S19956
N;Gong, Z.; Hui, C.; Hew, C.L.
J; Biol. Chem. 270, 3335-3345, 1995
A;Title: Presence of isl-1-related LIM domain homeobox genes in teleost and their simila A;Reference number: A55973; MUID:95155429; PMID:7852419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-340 <GON>
A; Cross-references: EMBL:X64884; NID:g64208; PIDN:CAA46102.1; PID:g64209
A; Cross-references: EMBL:X64884; NID:g64208; PIDN:CAA46102.1; PID:g64209
A; Notes: authors translated the codon CTG for residue 251 as Met, and ATG for residue 256
R; Gong, Z.; Hew, C.L.
Biochim. Biophys. Acta 1260, 349-354, 1995
A; Title: Several splicing variants of isl-1 like genes in the chinook salmon (Oncorhynch
A; Reference number: $52089; MUID:95178560; PMID:7873614
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A;Note: the authors translated the codon CAG for residue 105 as His, GTG for residue 107
C;Genetics:
                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE004111; GB:AE003852; NID:99654614; PIDN:AAF93388.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype E1 Tor
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C,Superfamily: transcription factor isl-1; homeobox homology; LIM metal-binding repeat
C,Keywords: DNA binding; duplication; homeobox; nucleus; transcription regulation; zinc
F;9-62/Domain: LIM metal-binding repeat homology <LIM1>
F;71-124/Domain: LIM metal-binding repeat homology <LIM2>
F;173-229/Domain: homeobox homology <HOX>
            Gwinn, M.L.; Dodson, R.J.
H.; Dragoi, I.; Sellers,
      R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sells, I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Status; preliminary
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Pred. No. 3.3e+02;
1; Mismatches 0; Indels
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80.0%;
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Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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A;Residues: 1-340 <GO2>
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SCYNS 256
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                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-325 <HEI>
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-349 - 61NO>
A;Achessidues: 1-349 - 61NO>
A;Cross-references: GB-D21135; NID:g497897; PIDN:BAA04670.1; PID:g497898
C;Superfamily: transcription factor isl-1; homeobox homology; LIM metal-binding repeat hc
C;Keywords: DNA binding; duplication; homeobox; nucleus; transcription regulation; zinc
F;77-07/Domain: LIM metal-binding repeat homology <LIMI>
F;79-112/Domain: LIM metal-binding repeat homology <LIMI>
F;182-238/Domain: homeobox homology <HOX>
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R; Gong, Z.; Hui, C.; Hew, C.L.

J; Biol. Chem. 270, 3335-3345, 1995
A; Title: Presence of isl-1-related LIM domain homeobox genes in teleost and their similary A; Reference number: A55973; MUID:95155429; PMID:7852419
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Blochim. Blophys. Acta 1260, 349-354, 1995
Aritle: Several splicing variants of isl-1 like genes in the chinook salmon (Oncorhynch
Areference number: S52089; MUID:95178560; PMID:7873614
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C;Keywords: alternative splicing; DNA binding; duplication; homeobox; nucleus; transcripti
F;7-780/Domain: LIM metal-binding repeat homology <LIM1>
F;89-142/Domain: LIM metal-binding repeat homology <LIM2>
F;191-247/Domain: homeobox homology <HOX>
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A;Note: the authors translated the
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NyAlternate names: protein T4D2.70
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 18-Feb-2000
C;Accession: T46160
R;NyAkatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.; N
submitted to the Protein Sequence Database, December 1999
A;Reference number: Z23025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transcription factor isl-3 - chinook salmon
NyAlternate names: insulin enhancer-binding protein isl-3; islet-3 protein
C;Species: oncorhynchus tschawytscha (chinook salmon)
C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 07-May-1999
C;Accession: C55973; 852090
R;Gong, Z.; Hui, C.i.
J. Biol. Chem. 270, 3335-3345, 1995
A;Title: Presence of isl-1-related LIM domain homeobox genes in teleost and their similar
A;Reference number: A55973; MUID:95155429; PMID:7852419
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Biochim. Biophys. Acta 1260, 349-354, 1995
A;Title: Several splicing variants of isl-1 like genes in the chinook salmon (Oncorhynch)
A;Reference number: S52089; MUID:95178560; PMID:7873614
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F;89-142/Domain: LIM metal-binding repeat homology <LIM2>
F;89-248/Domain: homeobox homology <HOX>
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-359 <NYA>
A;Cross-references: EMBL:AL132958
A;Experimental source: cultivar Columbia; BAC clone T4D2
C;Genetics:
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Pred. No. 3.6e+02;
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80.0%; Pred. No. 3.6e+02;
iive 1; Mismatches 0
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A,Residues: 1-82, TWNKMCKWQPGIQQO'
A,Cross-references: EMBL:X64883
A,Note: alternative splice form
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Introns: 126/3; 239/1; 260/3
A;Note: T4D2.70
C;Superfamily: O-methyltransferase
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Best Local Similarity 80.0%;
Matches 4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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A,Residues: 1-363 <GON>
A,Cross-references: GB:X64883
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277 NCYNA 281
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208 TCYNA 212
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C;Species: Brachydanio rerio (zebra fish)
C;Date: 13-Mar-1997 #sequence_revision 13-Mar-1997 #text_change 16-Jul-1999
C;Accession: 151735
R;Tokumoto, M.; Gong, Z.; Tsubokawa, T.; Hew, C.L.; Uyemura, K.; Hotta, Y.; Okamoto, H. Dev. Biol. 171, 578-589, 1995
A;Title: Molecular heterogeneity among primary motoneurons and within myotomes revealed A;Reference number: 151734; MUID:96005022; PMID:7556938
A;Status: preliminary; translated from GB/EMBL/DDBJ
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F;89-142/Domain: LIM metal-binding repeat homology <LIM2>
F;192-248/Domain: homeobox homology <HOX>
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NyAlternate names: insulin enhancer-binding protein isl-2; islet-2 protein

NyAlternate names: insulin enhancer-binding protein isl-2; islet-2 protein

Species Brachydanio rerio (zebra fish)

C;Date: 13-Mar-1997 #sequence_revision 13-Mar-1997 #text_change 16-Jul-1999

C;Accession: I51734; S57407

C;Accession: I51734; S57407

Bry Tokumoro, M.; Aong, Z.; Tsubokawa, T.; Hew, C.L.; Uyemura, K.; Hotta, Y.; Okamoto, H.

Dev. Biol. 171, 578-589, 1995

A;Title: Molecular heterogeneity among primary motoneurons and within myotomes revealed

A;Reference number: I51734; MUID: 96005022; PMID: 7556938
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R; Appel, B.; Korzh, V.; Glasgow, E.; Thor, S.; Edlund, T.; Dawid, L.; Eisen, J.
submitted to the EMBL Data Library, June 1995
A; Description: Motoneuron fate specification and patterned LIM homeobox gene expression
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A.Moleoule type: mRNA
A.Residues: 1-359 <ARP>
A.Cross-references: EMBL:X88805; NID:g871000; PIDN:CAA61283.1; PID:g871001
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A;Accession: 151734 A;Status: preliminary; translated from GB/EMBL/DDBJ

A; Residues: 1-359 <TOK>

A; Molecule type: mRNA

A; Description: Motoneuron A; Reference number: S57407

A; Accession: S57407

A;Gene: isl-2

90.0%; Score 27; DB 1; Length 358; 80.0%; Pred. No. 3.6e+02;

1; Mismatches

Local Similarity 80.0 les 4; Conservative

Best Loc Matches

Query Match

208 TCYNA 212

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1 SCYNA 5

A; Molecule type: mRNA A; Residues: 1-358 <TOK>

A;Gene: isl-3

C, Genetics:

0; Indels

RESULT 30 T49253

90.0%; Score 27; DB 1; Length 359; 80.0%; Pred. No. 3.6e+02; ive 1; Mismatches 0; Indels

Similarity 80.0%; 4; Conservative

:|||| 208 TCYNA 212

28

RESULT T46160

1 SCYNA 5

Best Local Similarity

Matches

Query Match

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4; Conservative
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Matches 4; Conserv
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326 NCYNA 330
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A,Status: preliminary
A,Molecule type: DNA
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A;Molecule type: DNA
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A; Map position: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein - Arabidopsis thaliana (G.Species: Arabidopsis thaliana (Mouse-ear cress)

C.Species: Arabidopsis thaliana (Mouse-ear cress)

C.Species: O3-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 20-Jun-2000

C.SAccession: B71414

R.Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk R.Bevan, M.; Bancroft, I.; Bancroft, R.; Weiler, T.; Pohl, T.M.; Terryn, N.; Giel avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B. Nature 391, 485-488, 1998

A.Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans C.; Chalwatzis, N.
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A;Accession: B71414
purple acid phosphatase-related protein F12M12.90 [similarity] - Arabidopsis thaliana CiSpecies: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 14-Dec-2001
C;Accession: T49233
R;Jordan, N:/ Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Rudd, S.; submitted to the Protein Sequence Database, May 2000
A;Reference number: Z25020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 3
A;Introns: 56/3; 126/3; 191/3; 219/3; 323/2
C;Superfamily: kidney bean purple acid phosphatase; phosphoesterase core homology
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C;Superfamily: Arabidopsis thaliana hypothetical protein F16G20.50
                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-388 <JOR>
A;Cross-references: EMBL:AL355775; GSPDB:GN0061; ATSP:F12M12.90
A;Experimental source: cultivar Columbia; BAC clone F12M12
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Pred. No. 3.8e+02;
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Pred. No. 3.9e+02;
1; Mismatches 0;
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80.0%;
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Best Local Similarity 80.0
Local 4; Conservative
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Best Local Similarity
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ACYNA 53
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A;Status: preliminary
A;Molecule type: DNA
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C;Species: Buchnera sp.
C;Daces: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: A49440
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. AI
A;Title: Genome sequence of the NUID:20445173; PMID:10993077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ritheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-802, 2000
A.; Albures: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.K.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, II
A;Authors: Salzberg, S.L.; Schwartz, J.K.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, II
A;Attle: Sequence and analysis of chromosome I of the plant Arabidopsis.
A;Reference number: A66141; MUID:21016719; PMID:11130712
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A;Accession: C91296
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-422 - HAX>
A;Cross-references: GB:BA000007; PIDN:BAB38762.1; PID:g13364817; GSPDB:GN00154
A;Cross-references: strain O157:H7, substrain RIMD 0509952
C;Genetics: A;Gene: EC85339
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A;Cross-references: GB:AE005173; NID:g11094774; PIDN:AAG29707.1; GSPDB:GN00141
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: A96555
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80.0%; Pred. No. 4.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
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C,Superfamily: Escherichia coli pmbA protein
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C;Accession: A55684
A;HBu, L.C.; Chang, W.C.; Hiraoka, L.; Hsieh, C.L.
Genomics 24, 333-341, 1994
A;Title: Molecular cloning, genomic organization, and chromosomal localization of an addu
A;Reference number: A55684; MUID:95213025; PMID:7698756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical 58.0K protein (osmY-deoC intergenic region) - Escherichia coli (strain K-12) NiAlternate names: hypothetical protein f516 C;Species: Bscherichia coli (c)species: Bscherichia coli C;Species: Bscherichia coli C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 01-Mar-2002 C;Accession: S56604; C65253 R;Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R. Nucleic Acids Res. 23, 2105-2119, 1995 A;Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.8 A;Reference number: S56314; MUID:95334362; PMID:7610040
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A; Residues: 1-516 <BUR>
A; Residues: 1-516 <BUR>
A; Residues: 1-516 <BUR>
A; Cross-references: EMBL:U14003; NID:g1263172; PIDN:AAA97276.1; PID:g537220
A; Cross-references: EMBL:U14003; NID:g1263172; PIDN:AAA97276.1; PID:g337220
A; Cross-reference as submitted to the EMBL Data Library, August 1994
A; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A Description: catalyzes oxidation of an aldehyde to an acid using NAD+ and water A;Note: enzymes with this activity are involved in diverse metabolic pathways in various C;Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology C;Keywords: NAD; oxidoreductase; saliva F;70-334/Domain: aldehyde dehydrogenase homology <ALDD> F;280,314/Active site: Glu, Cys #status predicted F;467/Binding site: NAD (Cys) #status predicted
                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-512 cHSU>
A;Cross-references: GB:U07919; NID:g995897; PIDN:AAA79016.1; PID:g544482
C;Comment: This isozyme is found at highest levels in saliva, stomach, and kidney and at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: 15q26-15q26
A;Introns: 33/3; 68/3; 115/3; 159/1; 179/3; 222/3; 260/3; 295/1; 356/3; 411/3; 464/2; 485
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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                                                            C;Species: Homo sapiens (man)
C;Date: 03-Mar-1995 #sequence_revision 31-Jan-1997 #text_change 03-Jun-2002
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                                   (EC 1.2.1.3) 6 precursor,
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Pred. No. 4.8e+02;
1; Mismatches 0;
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4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
                                      dehydrogenase (NAD)
                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA; DNA
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466 NCYNA 470
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A; Residues: 1-516 <B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene: GDB:ALDH6
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Matches
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R; Zhao, D.; McGaffery, P.; Ivins, K.J.; Neve, R.L.; Hogan, P.; Chin, W.W.; Draeger, U.C. Bur, J. Biochem. 240, 15-22, 1996
A; Title: Molecular identification of a major retinoic-acid-synthesizing enzyme, a retinal A; Reference number: S74224; MUID:96390857; PMID:8797830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X99273; NID:g1430868; PIDN:CAA67666.1; PID:g1430869
A;Experimental source: strain C3H/He; cell type embryonal carcinoma; cell line P19 terat
C;Genetics:
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                                                                                                                                                                                                                                                                                                  pherophorin II - Volvox carteri (fragment)
C;Species: Volvox carteri
C;Species: Volvox carteri
C;Species: Volvox carteri
C;Species: Volvox carteri
C;Species: Volvox carteri
C;Species: Volvox carteri
C;Species: Volvox carteri
C;Species: Volvox carteri
C;Species: Volvox carteri
S;Supper, M; Berg, E; Wenzl, S; Godl, K.
EMBO J; 12, 831-865, 1993
A;Title: How a sex pheromone might act at a concentration below 10(-16) M, A;Reference number: S36338; WUID:93209229; PMID:8458341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aldehyde dehydrogenase (NAD) (EC 1.2.1.3) 2 - mouse
N;Alternate names: retinaldehyde-specific dehydrogenase
C;Species: Mus musculus (house mouse)
C;Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.Residues: 1-484 <SUM>
A.Cross-references: EMBL:X69802; NID:g311360; PIDN:CAB56809.1; PID:g6006628
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      Length 460;
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F;57-321/Domain: aldehyde dehydrogenase homology <ALDD>F;193-273/Domain: NAD binding #status predicted <NAD>F;267,301/Active site: Glu, Cys #status predicted
F;454/Binding site: NAD (Cys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 27; DB 2; I
Pred. No. 4.5e+02;
                                   4.4e+02;
      DB 2;
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                                                               1; Mismatches
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   Score 27;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: protein
A;Residues: 1-13;182-215;413-441 <SU2>
C;Keywords: pheromone
90.0%;
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Best Local Similarity 80.0.
Local 4; Conservative
                                                            Conservative
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Query Match
Best Local Similarity
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Matches 4; Conserv
                                                                                                                                                                               296 TCYNA 300
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TCYNA 380
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A; Residues: 1-499 <ZHA>
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NCYNA 457
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                                                                                                                         SCYNA 5
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A;Accession: S74224

A; Gene: RALDH-2

A; Accession: S37760

1 SCYNA 5

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453

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RESULT

Query Match

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RESULT 40
AB1073
Conserved hypothetical protein STY4917 [imported] - Salmonella enterica subsp. enterica
C;Species: Salmonella enterica subsp. enterica serovar Typhi
C;Species: Balmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C;Accession: AB1073
R;Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T; Connerton, P; Cronin, A; Davis, P; Davies, R.M.; Dowd, L; White, N.; Farrar,
S; Mouthe, S; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; PMID:11677608
A;Residues: Psellaninary
A;Residues: 1-516 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD03401.1; PID:g16505670; GSPDB:GN00176
                                                                                                                                                                                 hypothetical protein yjji [imported] - Escherichia coli (strain O157:H7, substrain EDL93 C;Species: Escherichia coli C;Species: Escherichia coli C;Species: Escherichia coli C;Species: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: E86437 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotheck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001 A;Reference number: A86480; MUID:21074935; PMID:11206551 Coli O157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-516 <STO>
A;Cross-references: GB:AE005174; NID:g12519407; PIDN:AAG59561.1; GSPDB:GN00145; UWGP:Z59
A;Cross-reference: strain 0157:H7, substrain EDL933
C;Genetics:
A;Gene: yjjI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.0%; Score 27; DB 2; Length 516; 80.0%; Pred. No. 4.8e+02;
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Matches 4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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235 SCYNS 239
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Search completed: July 18, 2003, 15:10:43 Job time : 7.5 secs

235 SCYNS 239

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

July 18, 2003, 15:02:20 ; Search time 3.1 Seconds (without alignments) 66.897 Million cell updates/sec

US-10-007-790-6 30 1 SCYNA S Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 segs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ption			haemophilus	mycobacteri	mycobacteri	hordeum vul	cyanidium c	-			-	brachydanio	oncorhynchu	brachydanio	brachydanio		drosophila	rattus norv	homo sapien	mus m		volvo	homo	mus m	rattus		homo sa			schizosacch	rattu	homo	mus musculu
	Description	P25362	052914	~	064267	005303	P09617	019914	061470	P31053	P45475	P50212	P53405	P53408	P53407	P53406	P53409	016867	Q912w6	94vn6Q	091ze0	P57191	P81132	094788	062148	063639	093344	P47895	P37342	094049	Q09764	P97846	P78357	054991
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SUMMARIES	QI	PT18 YEAST		YJJI HAEIN	VG86 BPMD2	VG86_BPML5		TRPG_CYACA	CD37_MOUSE	CD37 RAT	YHBV_ECOLI	IS2B ONCTS	ISL1 BRARE	IS2A ONCTS	ISL3_BRARE		IST3 ONCIS		TMLH RAT	TMLH HUMAN	TMLH MOUSE		PER2_VOLCA	DHA2_HUMAN	DHA2_MOUSE	DHA2 RAT	DHAS CHICK	DHA6 HUM	YJJI ECOLI	ACSA CANAL	YA7B SCHPO			CTA1_MOUSE
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d	Query Match I	100.0	100.0	100.0	0.06	0.06	0.06	0.06	90.0	90.0	90.0	90.0	0.06	0.06	90.0	90.0	90.0	90.0	90.0	90.0	90.0	90.0	90.0	90.0	0.06	0.06	0.06	0.06	0.06	0.06	0.06	0.06	0.06	90.0
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463 AA.

PRT;

STANDARD;

RESULT 2 SYE2\_CAMJE ID SYE2\_CAMJE

P25304 rattus norv				P25496 laticauda c		P10455 laticauda c		10	P01435 laticauda s	P41707 autographa	Q9psv3 columba liv		
AGRI RAT	TX3C_AGEAP	NXS2_LATCO	NXSA_LATCR	NXSB_LATCR	NXSB_LATLA	NXSC_LATCO	NXSD_LATCO	TX3B_AGEAP	NXS1_LATSE	Y150 NPVAC	KRF4_COLLI	ALIGNMENTS	
٦	П	ч	Н	-	Н	н	Н	٦	٦	Н	Н		
1959	43	62	62	62	62	62	62	16	83	66	100		
90.0	86.7	86.7	86.7	86.7	86.7	86.7	86.7	86.7	86.7	86.7	86.7		
27	26	56	56	56	56	26	26	56	56	56	56		
34	35	36	37	38	39	40	41	42	43	44	45		

RESULT 1 PT18_YEAST PT18_YEAST STANDARD; PRT; 215 AA.	01-MAY-1992 (Rel. 22, 01-MAY-1992 (Rel. 22,	15-DEC-1998 (Rel.	PETIB protein. PETIB OR HITZ	Saccharomyces cerevisiae (Baker's yeast). In Eukarvota: Fundi: Ascomycota: Saccharomycotina: Saccharomycetes:	Saccharomycetales; Saccharomycetaceae; Saccharom	XX NCBI_TaxID=4932;	SEQUENCE FROM N.A.	Feldmann H., Mannhaur	Submitted (MAK-1992) to the EMBL/Genbank/Dubb [2]		MEDLI		containing multiple genes.";	Yeast 1:159-171(1985).	C This cutto DDOT party, is convidit It is produced through a collaboration	between the Swiss Institute of Biol	the European Bioinformatics Institute. There are no restrictions on	use by non-profit institutions as long as its content is	(C modified and this statement is not removed. Usage by and for commercial (See http://www.ish.sib.ch/announce/	or send an email to license@isb-sib.ch).		EMBL; X59720;	NR PURK; 807692.	SGD; S0000613	InterPro; IPR004305;	Pfam; PF03070; TENA_THI-4; 1.	CONFLICT 104 104 D -> G (IN REF.	CONFLICT 122 122 D -> S (IN REF.	SEQUENCE 215 AA; 25223 MW; 71A2D7C5695CEA	Query Match 100.0%; Score 30; DB 1; Length 215;	Sir Conservative 0; Mismatch	y 1 SCYNA 5	b 211 SCYNA 215
RES PT1 ID	APP	占	d G	S C	88	X X	RP	RA:	Z Z	RP	XX 6	£ 5	RT	RL	ပ္ပင္	ยูย	ပ္ပ	ပ္ပ	ပ္ပင်	ខ្លួ	ပ္ပ	H I	DR G	í i	DR	Z E	I E	FT	SO	Οr	uΣ	ò	gg

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                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                         MEDLINE=95350630; PubMed=7542800;

REDLINE=95350630; PubMed=7542800;

Relavage A.R., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback F., Phillips C.A., Spriggs T., Hedblom E. Cotton M.D.,

Rine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98300335; PubMed=9636706;
Ford M.E., Sarkis G.J., Belanger A.E., Hendrix R.W., Hatfull G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Langen H., Takacs B., Evers S., Berndt P., Lahm H.W., Wipf B., Gray C., Fountoulakis M.;
"Two-dimensional map of the proteome of Haemophilus influenzae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          no RNA stage; Caudovirales; Siphoviridae;
                                                                                                                         Bacteria, Proteobacteria, gamma subdivision, Pasteurellaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 30; DB 1; Length 514; Pred. No. 41;
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Electrophoresis 21:411-429(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTIFICATION BY MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20137488; PubMed=10675023;
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100.0%;
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TIGR; HI0521; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; dsDNA viruses, no
unclassified Siphoviridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Conservative
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                                                                                                      Haemophilus influenzae.
(Rel. 32, (Rel. 32, 1) (Rel. 32, 1) (Rel. 41, 1)
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Best Local Similarity
                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                 NCBI_TaxID=727;
                                                            Protein HI0521.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Venter J.C.;
                                                                                                                                                    Haemophilus
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VG86_BPMD2
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PROSITE; PS00178; AA TRNA_LIGASE I; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                      MEDLINE=20150912; PubMed=10688204;
Parkhill J. Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitchead S., Barrell B.G.;
"The genome sequence of the food-borne pathogen Campylobacter jejuni
reveals hypervariable sequences.";
Nature 403:665-668(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=129108;
Wosten M.M.S.M., Boeve M., Koot M.G.A., Nuenen A.C.,
van der Zeijet B.A.M.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
-i phosphate + L-glutamyl-tRNA(Glu).
-!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                 Campylobacter jejuni.
Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
                     30-MAY-2000 (Rel. 39, Created)
LoCOT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Glutamyl-tRNA synthetase 2 (EC 6.1.1.17) (Glutamate--tRNA ligase
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ATP (BY SIMILARITY).
D60A0032963E6BED CRC64;
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InterPro; IPR00024; Glu ERNA-synt lc.
InterPro; IPR001412; tRNĀ-synt l.
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PRINTS; PR00987; TRNASYNTHGLU.
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243
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5; Conserve
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                                                                                                                                                                                      Campylobacter.
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ID YJJI HAEIN
AC P44744;
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                                                                                                                                                                                                                                                                                                                                                  Leaf-specific thionin precursor (Clones PKG1348, PKG1940, PKG2872 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                      Hordeum vulgare (Barley).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, M19046; AAA32976.1; -.
EMBL, M19047; AAA32977.1; -.
EMBL, M19048; AAA32978.1; -.
EMBL, M19048; AAA32978.1; -.
HSSP, P01643; IBHP.
InterPro; IPR001010; Thionin.
Pfam, PF00321; plant_thionins; 1.
PROSITE; PS00271; THIONIN; 1.
Plant defense; Thionin; Plant toxin; Signal; Multigene family.
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80.0%; Pred. No. 50;
.ive 1; Mismatches 0; Indels
                                                                                                                                                              "Thionin genes specifically expressed in barley leaves.";
Planta 171:241-246(1987).
                                                                                                                                                                                                                                                                 Apel K.;
"The identification of leaf thionin as one of the main jasmonate-induced proteins of barley (Hordeum vulgare).";
Plant Mol. Biol. 19:193-204(1992).
                                                                                                                                                                                                                                                    Andresen I., Becker W., Schluter K., Burges J., Parthier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FD00C2DBF6632797 CRC64;
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ACIDIC PROTEIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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V -> L (IN REF. 2).
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                                                                                                                                                                                                                       STRAIN=cv. Carina;
MEDLINE=92322947; PubMed=1377959;
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137 AA;
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Matches 4; Conserv
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39 NCYNA 43
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                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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"DNA sequence, structure and gene expression of mycobacteriophage L5:
a phage system for mycobacterial genetics.";
Mol. Microbiol. 7:395-405(1993).
                                                                                                                                                                                                                                                     Gaps
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"Genome structure of mycobacteriophage D29: implications for phage
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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
L5-like viruses.
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Pred. No. 34;
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(Rel. 17, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                            or send an email to license@isb-sib.ch).
                           J. Mol. Biol. 279:143-164(1998)
                                                                                                                                                                                                                     90.04;
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les 4; Conservative
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51 ACYNA 55
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01-FEB-1991 (
15-JUN-2002 (
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ID THNS_HORVU
AC P09617;
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Leukocyte antigen CD37.
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Best Local Similarity
Matches 4; Conserv
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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                                                                                                    NCBI_TaxID=10090;
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ID _CD37_RAT

AC P31053,
DT 01-JUL-195

DT 01-JUL-195

DT 16-OCT-206

DE Leukocyte
GN CD37.

CD37.

CD37.

Mammalia,
OX MCBI_TAXIII

RP SEQUENCE I
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pyruvate + L-glutamate.

PATHWAY: Tryptophan biosynthesis; first step.
SUBUNIT: TETRAMEN OF TWO COMPONENTS I AND TWO COMPONENTS II.
MISCELLAMENGOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE
USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES
GLUTAMINE AMIDOTRANSFERASE ACTIVITY.
                                                                                                                                                                                                                                                                                       Chloroplast.
Eukaryota; Rhodophyta; Bangiophyceae; Porphyridiales; Porphyridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS 1 TYPE-1 GLUTAMINE AMIDOTRANSFERASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIJNE=20496959; PubMed=11040290;
Gloeckner G., Rosenthal A., Valentin K.-U.;
"The structure and gene repertoire of an ancient red algal plastid
                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Anthranilate synthase component II (EC 4.1.3.27) (Glutamine amido-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               401. Evol. 51:382-390(2000).
CATALYTIC ACTIVITY: Chorismate + L-glutamine = anthranilate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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PROSITE; PS00442; GATASE TYPE I; 1.
Tryptophan biosynthesis; Lyase; Glutamine amidotransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 27; DB 1; Length 195;
Pred. No. 68;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51C53AE010352AD0 CRC64;
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01-NOV-1997 (Rel. 35, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Leukocyte antigen CD37.
                                                      195 AA
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BY SIMILARITY.
BY SIMILARITY.
                                                      PRT;
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InterPro; IPR002385; Anth_synthII.
InterPro; IPR000991; GATase_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam, PF00117, GATase, 1. PRINTS, PR00097, ANTSNTHASEII. PRINTS, PR00096, GATASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173 173 B
175 175 B
195 AA; 21984 MW;
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                                                      STANDARD;
                                                                                                                                                                                                                                                                  Cyanidium caldarium.
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Best Local Similarity
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TCYNA 91
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                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=2771;
                                                                                                                                                                                                                 transferase).
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CD37 MOUSE
ID CD37 MOUSE
AC Q61470;
DT 01-NOV-1997
DT 16-OCT-2001
DE Leukocyte an
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=RK-1
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                                                      CYACA
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ACT_SITE
SEQUENCE
RESULT 7
TRPG CYACA
ID TRPG CYACA
AC 019914;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)

N-LINKED (GLCNAC. .) (POTENTIAL)
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                                                                                                                                                                        STRAIN=129/Sv; TISSUE-Liver;
MEDLINE=97002026; PubMed=8845018;
MEDLINE=97002026; PubMed=8845018;
"Characterisation of mouse CD37: cDNA and genomic cloning.";
MOI. Immunol. 33:867-872(1986).
-i- SUBCELULAR LOCATION: Integral membrane protein.
-i- SIMILARITY: BELONGS TO THE TETRASPANIN (TM4SF) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 281; 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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EXTRACELLULAR (POTENTIAL).
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             281 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 27;
Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, U18372; AAB39500.1; -... EMBL, U18367; AAB39500.1; JOINED. EMBL, U18368; AAB39500.1; JOINED. EMBL, U18370; AAB39500.1; JOINED. EMBL, U18371; AAB39500.1; JOINED. EMBL, U18371; AAB39500.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000301; Transmem_4. Pfam; PF00335; transmembrane4; 1.
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01-JUL-1993 (Rel. 26, Last seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00259; TMFOUR.
PROSITE; PS00421; TM4_1; 1.
Glycoprotein; Antigen; Tran
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                            90.0%; Score 27; DB 1; Length 298; 80.0%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                   Hypothetical protein; Complete proteome.
SEQUENCE 298 AA; 33192 MW; 671EF53407233EA8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          340 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
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MEDLINE=95178560; PubMed=7873614;
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MEDLINE=95155429; PubMed=7852419;
                                                                                                                                                                                                                                            AE000396; AAC76193.1; -.
                                                                                                                                                                                                                    EMBL; U18997; AAA57962.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                        EcoGene; EG12791; yhbV.
                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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123 NCYNA 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P502<u>1</u>2;
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IS2B ONCTS
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                     EMBL;
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STRAIN=PVG X DA;

MEDLINE=90354767; PubMed=2388030;

Classon B.J., Willians A.C., Seed B., Stamenkovic I.;

Classon B.J., Willians A.C., Willis A.C., Seed B., Stamenkovic I.;

"The primary structure of the human leukocyte antigen CD37, a species homologue of the rat MRC OX-44 antigen.";

J. EXP. Med. 172:1007-1007(1990).

-! SUBCELLULAR LOCATION: Integral membrane protein.

-! TISSUE SPECIFICITY: BLYMPHOCYTES.

-! SIMILARITY: BELONGS TO THE TETRASPANIN (TWASF) FAMILY.
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STRAIDKIZ / MG1655;
MEDLINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMed=9278503;
MEDLINE=FR., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Lavis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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CYTOPLASMIC (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
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Glycoprotein; Antigen; Transmembrane.
DOMAIN 1 17 CYTOPLASMIC (POTENTIAL).
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seq
15-UTN-2002 (Rel. 41, Last ann
Hypothetical protein yhbv.
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PIR; JC1501; JC1501.
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180 SCYNS 184
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb.sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Several splicing variants of isl-1 like genes in the chinook salmon (Oncorhynchus tschawytscha) encode truncated transcription factors containing a complete LIM domain.";
                                                                                                                                                                                                                                                                                                                                Gong Z., Hui C.-C., Hew C.L.;
"Presence of isl.1-related LIM domain homeobox genes in teleost and their similar patterns of expression in brain and spinal cord.";
Their similar patterns of expression in brain and spinal cord.";
J. Biol. Chem. 270:3335-3346 (1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.
-!- SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochim. Biophys. Acta 1260:349-354 (1995).
-!- FUNCTION: BINDS TO ONE OF THE CIS-ACTING DOMAIN OF THE INSULIN GENE ENHANCER. MAY BE INVOLVED IN SUBTYPE SPECIALIZATION OF PRIMARY MOTONEURONS.
                                                                                                                                  Oncorhynchus tschawytscha (Chinook salmon) (King salmon).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Buteleostei,
Protacanthopterygii, Salmoniformes; Salmonidae, Oncorhynchus.
                                     01-OCT-1996 (Rel. 34, Created)
1-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Insulin gene enhancer protein ISL-2B (Islet-2B) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001356; Homeobox.
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Gaps

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Score 27; DB 1; Length 349; Pred. No. 1.1e+02;

90.0%;

1; Mismatches

39181 MW; F6F898870B4E378E CRC64;

HOMEOBOX GLN-RICH

133 240 250

LIM 1.

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PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS00478; LIM_DOMAIN 1; 2.
PROSITE; PS50023; LIM_DOMAIN_2; 2.
PROSITE; PS50021; HOMEOBOX 2; 1.
HOMEOBOX; DNA-binding; Developmental protein; Nuclear protein;
Repeat; LIM domain; Metal-binding; Zinc; Multigene family.
                                                                                                                                     ProDom; PD000010; Homeobox; 1.
ProDom; PD000094; LIM; 2.
SMART; SM00139; HOX; 1.
SMART; SM00132; LIM; 2.
                                  Pfam; PF00046; homeobox; 1.
Pfam; PF00412; LIM; 2.
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interPro; IPR001781; LIM
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Best Local Similarity
Matches 4; Conserv
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IS2A_ONCTS
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DEVELOPMENTAL STAGE: EXPRESSED IMMEDIATELY AFTER GASTRULATION IN
THE POLSTER, CRANTAL GANGLIA, ROHAN-BEARD NEURONS AND IN
VENTROMEDIAL CELLS OF THE SPINAL CORD. AFTER 16 H, EXPRESSION
IS RESTRICTED TO CELLS SLIGHTLY ANTERIOR TO THE SEGMENT BORDER.
SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.
SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC
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NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND DEVELOPMENTAL EXPRESSION.
MEDLINE=94220748; PubMed=8167375;
Include A., Takahashi M., Hatta Y., Hotta Y., Okamoto H.;
"Developmental regulation of islet-1 mRNA expression during neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dev. Dyn. 1991-11(1994).
-!- FUNCTION: BINDS TO ONE OF THE CIS-ACTING DOMAIN OF THE INSULIN GENE ENHANCER. MAY BE INVOLVED IN SUBTYPE SPECIALIZATION OF PRIMARY MOTONEURONS.
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                                  Pfam; PF00146; homeobox; 1.
Pfam; PF0012; LIM; 2.
ProDom; PD000010; Homeobox; 1.
ProDom; PD000099; LIM; 2.
SMART; SM00189; HOX; 1.
SMART; SM00113; LIM; 2.
SMART; SM00113; LIM; 2.
PROSITE; PS0007; HOMEOROX 1; 1.
PROSITE; PS50073; LIM DOMAIN 1; 2.
PROSITE; PS50071; HOMEOBOX 2; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
PROGENE; LIM domain; Metal-binding; Zinc; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , Match 90.0%; Score 27; DB 1; Length 340; Local Similarity 80.0%; Pred. No. 1.1e+02; hes 4; Conservative 1; Mismatches 0; Indels
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LIM 2.
HOMEOBOX.
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125
111
231 HOI
340 GLI
38262 MW; 1
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         interPro; IPR001781; LIM
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This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gong Z., Hew C.L.;
"Several splicing variants of isl-1 like genes in the chinook salmon
"Several splicing variants of isl-1 like genes in the chinook salmon
(Oncorhynchus techawytscha) encode truncated transcription factors
containing a complete Lil domain.";
Biochim. Biophys. Acta 1260:349-354(1995)
-!- FUNCTION: BINDS TO ONE OF THE CIS-ACTING DOMAIN OF THE INSULIN
GENE ENHANCER. MAY BE INVOLVED IN SUBTYPE SPECIALIZATION OF
PRIMARY MOTONEURONS.
                                                                                                                                                                                                                                                                                                            Gong Z., Hui C.-C., Hew C.L.; "Presence of isl-1-related LIM domain homeobox genes in teleost and their similar patterns of expression in brain and spinal cord."; J. Biol. Chem. 270:3335-3345(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALTERNATIVE PRODUCTS: TWO FORMS OF THIS PROTEIN ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THE SHORTER FORM LACKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.
-!- SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC
                                                                                                                         Oncorhynchus tschawytscha (Chinook salmon) (King salmon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- MISCELLANEOUS: THE N-TERMINAL OF THE SHORT FORM IS INCOMPLETE (MISSING AA 1-24).
                               01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Insulin gene enhancer protein ISL-2A (Islet-2A).
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ALTERNATIVE SPLICING).
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                               TISSUE=Pituitary;
MEDLINE=95155429; PubMed=7852419;
                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Pituitary;
MEDLINE=95178560; PubMed=7873614;
STANDARD;
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                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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P53406;
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ISL2 BRARE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RLFGIKCANCNIGFCSSDLVMRARDNVYHMECF -> SVLG
ARCAAGISCRGMSSLCGTRSCCVELIMVY (IN SHORT
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: BINDS TO ONE OF THE CIS-ACTING DOMAIN OF THE INSULIN GENE ENHANCER. MAY BE INVOLVED IN THE REGIONAL SPECIFICATION OF THE MYOTOWE AND ALSO IN TARGET RECOGNITION BY THE CAUDAL PRIMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Nuclear.
DEVELOPMENTAL STAGE: EXPRESSED 17 H AFTER GASTRULATION MAINLY IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tokumoto M., Gong Z., Tsubokawa T., Hew C., Uyemura K., Hotta Y.,
                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00027; HOMBOBOX 1; 1.
PROSITE; PS00478; LIM_DOMAIN_1; 2.
PROSITE; PS50071; HOMBOBOX 2; 2.
HOMBOBOX; DNA-binding; Developmental protein; Nuclear protein; Repeat; LIM domain; Metal-binding; Zinc; Multigene family;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.0%; Score 27; DB 1; Length 35%; 80.0%; Pred. No. 1.2e+02; tive 1; Mismatches 0; Indels
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MISSING (IN SHORT ISOFORM).
FB726FE5ACFF25F3 CRC64;
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MEDLINE=96005022; PubMed=7556938;
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01-OCT-1996 (Rel. 34, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
11shilin gene enhancer protein ISL-3 (Islet-3)
ISL3 OR ISL-3
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LIM 2.
HOMEOBOX.
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                                                                                                                                     EMBL, X64885; CA446103.1; ALT TERM.
EMBL, X64882; -; NOT_ANNOTATED_CDS.
HSSP; P32965; 1CTL.
                                                                                                                                                                                                                   InterPro; IPR001356; Homeobox.
InterPro; IPR001781; LIM.
                                                                                                                                                                                                                                                            Pfam, PF00046; homeobox; 1.
Pfam, PF00412; LIM, 2.
Probom; PD000010; Homeobox; 1.
Probom; PD000094; LIM; 2.
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40072 MW;
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SMART; SM00132; LIM; 2.
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358 AA;
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tes 4; Conserv
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NCBI_TaxID=7955;
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P53407;
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SEQUENCE
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifised and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
THE VENTRAL MYOTOMES. IN THE HEAD REGION, AFTER 18 H, EXPRESSION IS RESTRICTED TO THE ENTIRE REGION OF THE EYES, THE TECTAL REGION OF THE MIDBRAIN, TRIGEMINAL GANGLIA AND THE GANGLIA ANTERIOR TO THE OTIC VESICLES.
SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.
SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
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Tokumoto M., Gong Z., Tsubokawa T., Hew C.L., Uyemura K., Hotta Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRODOM; PUDUNUST, ..., SMART; SM0389; HOX; 1.
SWART; SM0389; HOX; 1.
SWART; SM00127; LIM; 1.
PROSITE; PS00027; HOMEDBOX 1; 1.
PROSITE; PS00023; LIM DOMAIN 1; 2.
PROSITE; PS50071; HOMEOBOX 2; 1.
HOMEODOX; DNA-binding; Developmental protein; Nuclear protein; Repeat; LIM domain; Metal-binding; Zinc; Multigene family.
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"Molecular heterogeneity among primary motoneurons and within
myotomes revealed by the differential mRNA expression of novel
islet-1 homologs in embryonic zebrafish.";
Dev. Biol. 171:578-589(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 27; DB 1; Length 358;
Pred. No. 1.2e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLN-RICH.
; 3D72568172411D67 CRC64;
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Insulin gene enhancer protein ISL-2 (Islet-2)
ISL2 OR ISL-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
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01-OCT-1996 (Rel. 34, Last seq
15-JUN-2002 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001356; Homeobox.
InterPro; IPR001781; LIM.
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Pfan; PF00412; LIM; 2.
ProDom; PD000010; Homeobox; 1.
ProDom; PD000094; LIM; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191 2
255 3
358 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208 TCYNA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [2]
SEQUENCE FROM N.A.
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DOMAIN
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363 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 TCYNA 212
                                                                                                                                                                            SEQUENCE FROM N.A.
                    SEQUENCE FROM N.A.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                        SUBCELLULAR LOCATION: Nuclear.

DEVELOPMENTAL STAGE: FIRST EXPRESSED AFTER 15 H OF GASTRULATION, SEGMENTALLY IN THE VENTRAL REGION OF THE SPINAL CORD AND THEN LATER IN THE DORSAL REGIONS (ROHAN-BEARD NEURONS).

SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.
SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                               -i- FUNCTION: BINDS TO ONE OF THE CIS-ACTING DOMAIN OF THE INSULIN GENE ENHANCER. MAY BE INVOLVED IN SUBTYPE SPECIALIZATION OF PRIMARY MOTONEURONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oncorhynchus tschawytscha (Chinook salmon) (King salmon).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TaxID=74940;
                                                           "Motoneuron fate specification revealed by patterned LIM homeobox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS00478; LIM DOMAIN 1; 2.
PROSITE; PS50071; HOMEOBOX 2; 1.
Homeobox; DNA-binding; Developmental protein; Nuclear protein;
Repeat; LIM domain; Metal-binding; Zinc; Multigene family.
MEDLINE=96125154; PubMed=8575312;
Appel B., Korzh V., Glasgow E., Thor S., Edlund T., Dawid L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 27; DB 1; Length 359;
Pred. No. 1.2e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AEAD810D2841BB37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update).
15-UTN-2002 (Rel. 41, Last annotation update) insulin gene enhancer protein ISL-3 (Islet-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         363 AA.
                                                                             gene expression in embryonic zebrafish.";
Development 121:4117-4125(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOMEOBOX.
GLN-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D38453; BAA07484.1; -.
EMBL; V09403; AAA80274.1; -.
EMBL; X88805; CAA61283.1; -.
HSSP; P32965; LCTL.
ZFIN; ZDB-GENE-980526-562; is12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40227 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD000010; Homeobox; 1. ProDom; PD000094; LIM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001356; Homeobox
InterPro; IPR001781; LIM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.06;
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Pfam; PF00412; LIM; 2.
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Best Local Similarity 80.v.
4; Conservative
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255
359 AA;
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ISL3 ONCTS
AC P53409;
DT 01-OCT-1996
DT 15-JUN-2002
DE Insulin gene
GN ISL3.
OC Bukaryota; M
OC Actinopteryg
OC Actinopteryg
OC Actinopteryg
OC Actinopteryg
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DOMAIN
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                      Appel B.
Eisen J.
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                                                                                                                                                                                                                                                                                                                                                                  Gong Z., Hew C.L.; "Several splicing variants of isl-1 like genes in the chinook salmon (Oncorhynchus tschawytscha) encode truncated transcription factors
                                                                        Gong Z., Hui C.-C., Hew C.L., "Presence of isl-1-related LIM domain homeobox genes in teleost and their similar patterns of expression in brain and spinal cord.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.
-!- SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 containing a complete LIM domain.";
Biochim. Biophys. Acta 1260:349-354(1995).
-!- FUNCTION: BINDS TO ONE OF THE CIS-ACTING DOMAIN OF THE INSULIN GENE ENHANCER. MAY BE INVOLVED IN SUBTYPE SPECIALIZATION OF PRIMARY MOTONEURONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAP DROME STANDARD; PRT; 398 AA.
016867; P91640; Q9VVF9;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Basic helix-loop-helix neural transcription factor TAP (Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
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SMART; SM00389; HOX; 1.

PROSITE; PS00027; HOMEDBOX 1; 1.

PROSITE; PS000478; LIM DOMAIN 1; 2.

PROSITE; PS50023; LIM DOMAIN 2; 2.

PROSITE; PS50011; HOMEDBOX 2; 1.

HOMEDBOX; DNA-binding; Developmental protein; Nuclear protein; Repeat; LIM domain; Metal-binding; Zinc; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 90.0%; Score 27; DB 1; Length 363; Similarity 80.0%; Pred. No. 1.2e+02; 4; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLN-RICH.
540F676E86ED8C18 CRC64;
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                                                                                                                                                                                  Biol. Chem. 270:3335-3345 (1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X64883; -; NOT_ANNOTATED_CDS
HSSP; P32965; 1CTL.
                                                                                                                                                                                                                                                                                                 IISSUE=Pituitary;
MEDLINE=95178560; PubMed=7873614;
TIŠSUE-Pituitary;
MEDLINE-95155429; PubMed=7852419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40799 MW;
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InterPro; IPR001781; LIM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00046; homeobox; 1.
Pfam; PF00412; LIM; 2.
Probom; PD000010; Homeobox; 1.
Probom; PD000094; LIM; 2.
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REATIN=EarCheley;

RAMINE=COUGNOE; FROM N.A.

RAMAINSEARCH S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Iti P.W., Hoskins R.A., Galle R.F.,

Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson, S.N.,

RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson, S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Blazej R.G., Change M., Pefiffer B.D.,

RA Ballaw R.M., Basu A.M. Baxendal J., Bayraktargoll L., Beasley E.M.,

RA Besson K.Y., Bennos P.V., Berman B.P., Bhandari D., Bolshakov S.,

Borkova D., Botchan M.R., Bouck J., Bayraktargoll L., Beasley E.M.,

RA Berlos B., Delcher A., Deng C., Mays A.D., Dolshakov S.,

Burtis K.C., Busam D.A., Leuler H., Cadieu E., Center A., Chadra I.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chadra I.,

RA Burtis R.C., Busam D.A., Butler H., Cadieu E., Davies P.,

Burtis K.C., Busam D.A., Bay R.D., Davies P.,

RA Burtis K.C., Gabrieliata S.C., Garg N.S., Gelbart W.M., Glasser K.,

RA Harris N.L., Harvey D., Heiman T.J., Wal M.-H., Ibegwan C.,

Adalli M., Kalush F., Karpen G.H., Kez Z., Kennison J.A., Ketchum K.A.,

RA Harris N.L., Harvey D., Heiman T.J., Wal M.-H., Ibegwan C.,

Adalli M., Kalush F., Karpen G.H., Kez Z., Kennison J.A., Ketchum K.A.,

Basko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattere B., Wolyn M., Murphy B., Murph, L.,

Rabko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Briazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

Reinert K., Remington K.A., Sunders R., Wenter E., Wang A.H., Wang X.,

Wang Z.-Y. Wassarman D.A., Weinstock G.M., Weissenbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zhu X., Smith H.O.,

Rance S. B., Wolfer E., Raver S., Rander E., Wang A., Shu H.,

Rance S. B., Woodage T., Worley C., Wu D., Yang S., Zhu X., Smith H.O.,

Rance S. Rance S. R., Rocales E., Rance S. R., Rance S., Scheel L.,

Rance S. R., Rance S., R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Oregon-R; MEDDINE=9821861; MEDLINE=98211866; PubMed=9551861; Ledent V., Gaillard F., Gautier P., Ghysen A., Dambly-Chaudiere C.; Expression and function of tap in the gustatory and olfactory organs of Drosophila.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INT. J. Dev. Biol. 42:163-170(1998).
-!- FUNCTION: MAY PLAY A ROLE IN THE SPECIFICATION OF THE SUGAR-SENSITIVE ADULT GUSTATORY NEURON AND AFFECT THE RESPONSE TO SUGAR
TAP OR BPS OR CG7659.

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Perrygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                  Gautier P., Ledent V., Massaer M., Dambly-Chaudiere C., Ghysen A.;
"tap, a Drosophila bHLH gene expressed in chemosensory organs.";
Gene 191:15-21(1997).
                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=97115720; PubMed=8954743; Bush A.B., Hiromi Y.H., Cole M.D.; "Biparous: a novel bHLH gene expressed in neuronal and glial
                                                                                                                                                                                                                                                                                             STRAIN=Oregon-R;
MEDLINE=97354289; PubMed=9210583;
                                                                                                                                                                                                                   precursors in Drosophila.";
Dev. Biol. 180:759-772(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 287:2185-2195(2000)
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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AND SALT. REGULATED BY POXN.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
             SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF TRANSCRIPTION FACTORS. "ATONAL" SUBPAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Biol. Chem. 276:33512-33517(2001).
-!- FUNCTION: Converts trimethyllysine (TML) into
hydroxytrimethyllysine (HTML).
-!- CATALYTIC ACTIVITY: N(6),N(6), Ltimethyl-L-lysine + 2-
oxoglutarate + O(2) = 3-hydroxy-N(6),N(6),L(6),L(6).N(6)-trimethyl-L-lysine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Trimethyllysine dioxygenase, mitochondrial precursor (EC 1.14.11.8)
[Epsilon-trimethyllysine 2-oxoglutarate dioxygenase) (TML-alpha-
ketoglutarate dioxygenase) (TML hydroxylase) (TMLD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA-binding; Nuclear protein; Transcription regulation; Neurogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; Differentiation.

protein; Differentiation.

166 BASIC DOMAIN (BY SIMILARITY).

7 207 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.0%; Score 27; DB 1; Length 398;
80.0%; Pred. No. 1.3e+02;
.ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 POLY-ASP.
312 POLY-GLN.
44850 MW; 54FF558483B18258 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- COFACTOR: Iron and ascorbate.
-!- PATHWAY: Carnitine biosynthesis; first step.
-!- SUBUNIT: Homodimer.
SUBCELLULAR LOCATION: Nuclear (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  405 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00038; HLH_1; FALSE_NEG.
PROSITE; PS50888; HLH_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21423953; PubMed=11431483;
                                                                                                                                                                                                                                                                                                   EMBL; AE003524; AAF49352.1; -. FlyBase; FBGN0015550; tap.
InterParc, IPRO01092; HLH_basic. Pfam; PF00010; HLH; 1.
                                                                                                                                                                                                                                                          EMBL; AF022883; AAC80572.1; -.
                                                                                                                                                                                                                                                                                 X95845; CAA65103.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         succinate + CO(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      308 3
398 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SCYNA 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 ACYNA 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            biosynthesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Wistar;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OR TMLH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Developmental
DNA BIND 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TMLH RAT
Q91ZW6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TMLH RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -! - FUNCTION: Converts trimethyllysine (TML) into
hydroxytrimethyllysine (HTML).
-!- CATALYTICA ACTIVITY: N(6),N(6),Limethyl-L-lysine + 2-
oxoglutarate + 0(2) = 3-hydroxy-N(6),N(6),N(6)-trimethyl-L-lysine
+ succinate + CO(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-UTN-2002 (Rel. 41, Created)
15-UTN-2002 (Rel. 41, Last sequence update)
15-UTN-2002 (Rel. 41, Last annotation update)
15-UTN-2002 (Rel. 41, Last annotation update)
Trimethyllysine dioxygenase, mitochondrial precursor (EC 1.14.11.8)
(Epsilon-trimethyllysine 2-oxoglutarate dioxygenase) (TML-alpha-
Ketoglutarate dioxygenase) (TML hydroxylase) (TML dioxygenase) (TMLD)
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,

Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara P.

Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.

Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

Wamanoco J., Wakamateu A., Nakamura Y., Nagahari K., Masuho Y.,

Ninomiya K., Iwayanagi T.;

"NEDO human cDNA sequencing project.";

Submitted (FEB-2000) to the EMB/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- COFACTOR: Iron and ascorbate.
-!- PATHWAY: Carnitine biosynthesis; first step.
-!- SUBGELLULAR LOCATION: Mitochondrial matrix (By similarity).
-! SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
-!- SIMILARITY: BELONGS TO THE GAMMA-BBH/TMLD FAMILY.
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Vaz F.M., Offman R., Westinga K., Back J.W., Wanders R.J.A.;
"Molecular and blochemical characterization of rat epsilon-N-trimethyllysine hydroxylase, the first enzyme of carnitine
                                                                                                                                                                       EMBL; AF374406; AAL01252.1; -.
InterPro, IPR004994; Gamma-BBH.
Pfam; PF03322; Gamma-BBH; 1.
Carnitine biosynthesis; Oxidoreductase; Dioxygenase; Iron; Mitochondrion; Transit peptide.
TRANSIT ? MITOCHONDRION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                    90.0%; Score 27; DB 1; Length 405; 80.0%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                             1 ? MITOCHONDRION (POTENTIAL).
? 405 TRIMETHYLLYSINE DIOXYGENASE.
405 AA, 47490 MW; DC4A904309E8DA81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421 AA.
                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biol. Chem. 276:33512-33517(2001).
                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 80.0
nes 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||||:
SCYNS 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SCYNA 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TMLH HUMAN
Q9NVH6;
                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                               TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 19
TMLH_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!-FUNCTION: Converts trimethyllysine (TML) into hydroxytrimethyllysine (HTML).
-!-CATALYTIC ACTIVITY: N(6),N(6).rimethyl-L-lysine + 2-
cxatalytic ACTIVITY: N(6),N(6),N(6),N(6).rimethyl-L-lysine + succinate + CO(2).
-!-COFACTOR: Iron and ascorbate.
-!-COFACTOR: Iron and ascorbate.
-!-PATHWAY: Carnitine biosynthesis; first step.
-!-SUBUNIT: Homodimer (By similarity).
-!-SUBUNIT: Homodimer (By similarity).
-!-SUBURITY: BELONGS TO THE GAMMA-BBH/TMLD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYLL MOUSE STANDARD; PRT; 421 AA.

15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Trimethyllysine dioxygenase, mitochondrial precursor (EC 1.14.11.8)
(Epsilon-trimethyllysine 2-oxoglutarate dioxygenase) (TML-alpha-TMLHE OR TMLH)
                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vaz F.M., Ofman R., Westinga K., Back J.W., Wanders R.J.A., "Molecular and biochemical characterization of rat epsilon-N-trimethyllysine hydroxylase, the first enzyme of carnitine
                                                                                                                                                                        InterPro; IPR004994; Gamma-BBH.
Pfam; PF03322; Gamma-BBH; 1.
Carnitine blosynthesis; Oxidoreductase; Dioxygenase; Iron; Mitochondrion; Transit peptide minorm Mitochondrion; Transit peptide MITOCHONDRION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                  Length 421;
                                                                                                                                                                                                                                                                                                              90.0%; Score 27; DB 1; Length 421
80.0%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                 11 7 MITOCHONDRION (POTENTIAL).
7 421 TRIMETHYLLYSINE DIOXYGENAK.
421 AA; 49517 MW; 4E55DF349B866B43 CRC64;
                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol. Chem. 276:33512-33517(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21423953; PubMed=11431483;
                                                                                                                                       EMBL; AK001589; BAA91775.1; -. Genew; HGNC:18308; TMLHE.
                                                                                                                     EMBL; AF373407; AAL01871.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 13-421 FROM N.A. STRAIN=FVB/N;
                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 80. ت.
اتم 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 SCYNS 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                               1 SCYNA 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rissum=Liver;
                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TMLH MOUSE
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15-JUL-1998 (Rel. 36, Last annotation update)
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094788;
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                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Tokyo 1998;
MEDLINE=20445173; PubMed=10993077;
Shignobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
Shignon sequence of the endocellular bacterial symbiont of aphids
Buchnera sp. APS.";
Mature 407:81-86(2000).
-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!- SIMILARITY: BELONGS TO THE TLDD/PMBA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
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                                                                InterPro, IPR004994, Gamma-BBH,
Pfam, PF03322, Gamma-BBH, 1.
Carnitine biosynthesis; Oxidoreductase; Dioxygenase; Iron;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.0%; Score 27; DB 1; Length 446; 80.0%; Pred. No. 1.4e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                            Length 421;
                                                                                                                                                                                                                      90.0%; Score 27; DB 1; Length 421,
90.0%; Pred. No. 1.4e+02;
90.0%; Pred. Trohes 0; Indels
                                                                                                                                                              MITOCHONDRION (POTENTIAL).
TRIMETHYLLYSINE DIOXYGENASE.
                                                                                                                                                                                                            1474AD5742E88F43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 symbiotic bacterium).
Bacteria; Proteobacteria; gamma subdivision; Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              446 AA; 50401 MW; 4E6027D1C45213B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
PmbA protein homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    446 AA.
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                     EMBL; AY033513; AAK54387.1; ALT_INIT
EMBL; BC010495; AAH10495.1; -.
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                                                                                                                                      Mitochondrion; Transit peptide.
TRANSIT 1
                                                                                                                                                                                                         49609 MW;
                                                                                                                                                                                                                                                                          Best Local Similarity 80.0
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                      421
                                                                                                                                                                                                            421 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=118099;
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                                                                                                                                                                                                                                                                                                                                                                                           SCYNS 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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SEQUENCE 446 AA
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P57191;
                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                       Query Match
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CCRRRRETES
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"TAL1 and LIM-only proteins synergistically induce retinaldehyde
dehydrogenase 2 expression in T-cell acute lymphoblastic leukemia by
acting as cofactors for GATA3.";
Mol. Cell. Biol. 18:6939-6950(1998)
-: FUNCTION: RECOGNIES AS SUBSTRATES FREE RETINAL AND CELLULAR
RETINOL. BINDING PROTEIN-BOUND RETINAL. DOES METABOLIZE OCTANAL AND
DECANAL BUT DOES NOT METABOLIZE CITRAL, BENZALDEHYDE, ACETALDEHYDE
                                                                                                                             SEQUENCE FROM N.A., AND SEQUENCE OF 1-13; 182-215 AND 413-441.
MEDLINE=93209229; PubMed=8458341;
Sumper M., Berg E., Wenzl S., Godl K.;
"How a sex pheromone might act at a concentration below 10(-16) M.";
EMBO J. 12:831-836(1993).
-i- FUNCTION: MAY BE INVOLVED IN CONVERSION OF ASEXUAL MALES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                           Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Volvocaceae; Volvox.
NCBI_TaxID=3067;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
(POTENTIAL)
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Aldehyde dehydrogenase 1A2 (EC 1.2.1.3) (Retinaldehyde-specific dehydrogenase type 2) (RALDH(II)) (RALDH-2).
ALDH1A2 OR RALDH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
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Pred. No. 1.5e+02;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Extracellular matrix; Glycoprotein; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GLCNAC.
                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Extracellular matrix.
                                                                                                                                                                                                                                                                                                              -!- INDUCTION: BY SEXUAL INDUCER GLYCOPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GLCNAC.
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                                                                                                                                                                                                                                                                    FEMALES TO THE SEXUAL PATHWAY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99038200; PubMed=9819382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50860 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.08;
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Perphorin II (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
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Best Local Similaritý
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             484 AA;
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InterPro; IPR002086; Aldehyde dehydr.
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                                                                                                                                                                                                                                499 AA;
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Best Local Similarity
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453 NCYNA 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                · 1 SCYNA 5
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ACT_SITE
SEQUENCE
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                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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Draeger U.C.;
"Molecular identification of a major retinoic-acid-synthesizing
enzyme, a retinaldehyde-specific dehydrogenase.";

Bur. J. Biochem. 240:15-22(1996).
-!- FUNCTION: RECOGNIZES AS SUBSTRATES RREE RETINAL AND CELLULAR
RETINOL-BINDING PROTEIN-BOHND RETINAL. DOES METABOLIZE OCTANAL AND
DECANAL BUT DOES NOT METABOLIZE CITRAL, BENZALDEHYDE
AND PROPANAL EFFICIENTLY (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)0 = an acid + NADH...
-!- PATHWAY: RETINOIC ACID BIOGENESIS.
-!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
AND PROPANAL EFFICIENTLY (BY SIMILARITY).

CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)O = an acid + NADH.

CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)O = an acid + NADH.

BATHWAY: RETINOIC ACID BIOGENESIS.

SUBUNIT: HOMOTETRAMER (BY SIMILARITY).

SUBCELLULAR LOCATION: CYCOPJasmic.

SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Aldehyde dehydrogenase 1A2 (EC 1.2.1.3) (Retinaldehyde-specific dehydrogenase type 2) (RALDH(II)) (RALDH-2).
ALDH1A2 OR ALDH1A7 OR RALDH2.
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-!- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                             NAD (ADP PART) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                            90.0%; Score 27; DB 1; Length 499; 80.0%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
FE0B53A47644246B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              499 AA
                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                     PEGM; PF00171; aldedh; 1.
PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                         InterPro, IPR002086, Aldehyde_dehydr.
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MEDLINE=96390857; PubMed=8797830;
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54780 MW;
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Matches 4; Conservative
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301 3
499 AA;
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                                                                                                                                                                                                                                                                                                             Oxidoreductase; NAD.
NP BIND 244
ACT SITE 267
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453 NCYNA 457
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                                                                                                                                                                                                                                                MIM; 603687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
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ACT_SITE
SEQUENCE
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Aldehydrogenase 1A2 (EC 1.2.1.3) (Retinaldehyde-specific dehydrogenase type 2) (RALDH(II)) (RALDH-2).
ALDH1A2 OR RALDH2.
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                                                                                                                                                                                                                                                                                                                           NAD (ADP PART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 499;
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 27; DB 1; Lengtn 422.
Pred. No. 1.66+02;
                                                                                                                                                                                                                                                                                                                                                                                              54725 MW; E0000596A90B0B7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       499 AA.
                                                                                                                                                                                       MGD; MGI:107928; Aldhla2.
InterPro; IPR002086; Aldehyde_dehydr.
Edem; PF00117; aldedh; J.
PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
POTENTIAL.
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                                                                                                                                             EMBL; X99273; CAA67666.1; -.
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HSSP; P51977; 1BXS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Conservative
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267
301
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Local Similarity
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453 NCYNA 457
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                               1 SCYNA
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                                                                                                                                                                                HUMAN
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ACT SITE
SEQUENCE
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                                                                                                                                     RESULT 27
DHA6_HUMAN
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A Sockanathan S., Jessell T.M.;
Sockanathan S., Jessell T.M.;
Inductor neuron-derived retinoid signaling specifies the subtype
identity of spinal motor neurons.";
Cell 94:503-514(1998).

Cell 94:503-514(1998).

PETINOL-BINDING PROTEIN-BOUND RETINAL. DOES METABOLIZE OCTANAL AND DECANAL BUT DOES NOT METABOLIZE CITRAL, BENZALDEHYDE,
AND PROPANAL EFFICIENTLY (BY SIMILARITY).

CHIPATRY: RETINOIC ACID BIOGENESIS.
CHIPATRY: RETINOIC ACID BIOGENESIS.
CHIPATRY: RETINOIC ACID BIOGENESIS.
CHIPATRY: RETINOIC ACID BIOGENESIS.
CHIPATRY: RELOVER (BY SIMILARITY).
CHIPATRY: RELOVER LOCATION: CYCOPISSMIC.
CHIPATRY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Aldehydrogenase 1A2 (EC 1.2.1.3) (Retinaldehyde-specific dehydrogenase type 2) (RALDH(II)) (RALDH-2).
ALDH1A2 OR RALDH2.
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                                                                                        NAD (ADP PART) (BY SIMILARITY)
                                                                                                                                                                                                90.0%; Score 27; DB 1; Length 499; 80.0%; Pred. No. 1.6e+02; ive 1; Mismatches 0; Indels
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                                                                                                                                POTENTIAL.
E01EF471342267AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
F471F09F3D5645A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             499 AA
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PROSITE; PS00070; ALDEHYDE DEHYDR CYS; 1.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
Pfam; PF00171; aldedh; 1.
PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P51977; 1BXS.
InterPro; IPR002086; Aldehyde_dehydr.
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF064253; AAC34299.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                499 AA; 54774 MW;
                                                                                                                                                     499 AA; 54739 MW;
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                                                                                                                                                                                                                                             4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus (Chicken).
                                                                                        249
267
301
                                                                      Oxidoreductase; NAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oxidoreductase; NAD.
                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                 453 NCYNA 457
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                                                                                                                                                                                                                                                                                                                                                                                                                                             DHAS_CHICK
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-!- TISSUE SPECTRICITY: EXPRESSED AT LOW LEVELS IN MANY TISSUES PAT LOW LEVELS IN MANY TISSUES AND AT HIGHER LEVELS IN SALIVARY GLAND, STOWACH, AND KIDNEY.
-!- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomics 24:333-341(1994).
-!- CATALYTIC ACTIVITY: An aldehyde + NAD(P)(+) + H(2)O = an acid
                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE-Salivary gland;
MEDLINE=95213025; PubMed=7698756;
HSU L.C., Chang W.-C., Hiraoka L., Hsieh C.-L.;
"Molecular cloning, genomic organization, and chromosomal localization of an additional human aldehyde dehydrogenase gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                  01-FEB-1996 (Rel. 33, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) ALDHIA3 OR ALDHE
   512 AA
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BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAIR; OVOTO., IPRO2086; Aldehyde_dehydr. InterPro; IPRO2086; Aldehyde_dehydr. Pfam; PRO0171; aldedh; 1. PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1. PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
                                                      01-FEB-1996 (Rel. 33, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56009 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P51977; 1BXS.
Genew; HGNC:409; ALDH1A3.
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STANDARD;
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280
314
                                                                                                                                                                                                         Homo sapiens (Human)
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280 2
314 3
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                            Oliver K., Harris D., Barrell B.G., Rajandream M.A.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + acetate + CoA = AMP + diphosphate
                                                                                                                                 acetyl-CoA.
-!- SIMILARITY: BELONGS TO THE ATP-DEPENDENT AMP-BINDING ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 27; DB 1; Length 675;
Pred. No. 2.1e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75100 MW; 32CD1F462F789B90 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein C24H6.11c in chromosome
SPAC24H6.11C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           958 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00455; AMP BINDING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AL033502; CAA22000.1; -. InterPro; IRRO0873; AMP-bind. Pfam; PF00501; AMP-binding; 1. PRINTS; PR00154; AMPBINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.0%;
80.0%;
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675 AA;
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                        FAMILY.
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Q09764;
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YA7B_SCHPO
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30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Acetyl-coenzyme A synthetase (EC 6.2.1.1) (Acetate--CoA ligase) (Acyl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY SEQUENCE OF 1-289 FROM N.A. MEDIINE-87004572; PubMed19019678; Valentin-Hansen P., Albrechtsen B., Love-Larsen J.E.; Valentin-Hansen P., Albrechtsen B., Love-Larsen J.E.; EDA-protein recognition: demonstration of three genetically separated operator elements that are required for repression of the
                                                                                                                                                                                                                                                                                                                                                                                                         "Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.8 through 100 minutes."; Nucleic Acids Res. 23:2105-2119(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Valentin-Hansen P., Aiba H., Schuemperli D.;
"The Structure of tandem regulatory regions in the deo operon of
Escherichia coli K12.";
EMBO J. 1:317-322 (1982)
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                                                               Escherichia coli.
Bacteria, Proteobacteria, gamma subdivision, Enterobacteriaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli deoCABD promoters by the DeoR repressor.";
EMBO J. 5:2015-2021(1986).
-!- SIMILARITY: STRONG, TO H.INFLUENZAE H10521.
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                                                                                                                                                                                                                                                                          STRAIN=K12 / MG1655;
MEDLINE=59334362; PubMed=7610040;
Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
Blatener P.R.
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516 AA; 58020 MW; 914D215F4C2B8E6C CRC64;
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EMBL; X04151; -; NOT ANNOTATED CDS.
EXCRETE: EGI2171; YjjI.
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   Hypothetical protein yjjI
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CA38F10.03.
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SCYNS 239
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SEQUENCE 51
                                      OR B4380
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094049;
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multiple domains implicated in protein-protein interactions.";
        with multiple domains im
EMBO J. 16:978-988(1997)
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          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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MEDLINE=97224125; PubMed=9118959;
Peles E., Nativ M., Lustig M., Grumet M., Schilling J., Martinez R.,
Plowman G.D., Schlessinger J.;
"Identification of a novel contactin-associated transmembrane receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Contactin associated protein 1 precursor (Caspr) (Casprl) (Neurexin 1V) (pi90) (Paranodin).
CURINAPI OR CASPR OR NRXN4.
Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Cominquez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Certutti L., Lowe T., McCombie W.R., Paulsen I., Poteshkin J., Shpakovski GV., Ussery D., Barrell B.G., Nurse P., "The genome sequence of Schizosaccharomyces pombe.";
Nature 415:871-880 (2002).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: CONTAINS I STAS DOMAIN.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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POTENTIAL
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InterPro; IPR002645; STAS.
InterPro; IPR001902; Sulfate_transp.
Pfam; PF00027; CNMP binding; 1.
Pfam; PF01916; Sulfate_transp; 1.
SMART; SM00100; CNMP; 1.
PROSITE; PS50801; STAS; 1.
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es 4; Conservative
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958 AA;
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CTA1_RAT
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Arroyo E.J., Xu T., Poliak S., Watson M., Peles E., Scherer S.S.;
"Internodal specializations of myelinated axons in the central nervous
                                                                                                                                                  MEDLINE=97436749; PubMed=9292722;
Menegoz M., Gaspar P., Le Bert M., Galvez T., Burgaya F., Palfrey C.,
Ezan P., Arnos F., Girault J.-A.;
"Paranodin, a glycoprotein of neuronal paranodal membranes.";
Neuron 19:319-331(1997).
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J. Cell Biol. 139:1495-1506(1997).
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-!- FUNCTIONS SERRS TO PLAY A ROLE IN THE FORMATION OF FUNCTIONAL DISTINCT DOMAINS CRITICAL FOR SALTATORY CONDUCTION OF NERVE INFULENCES IN WYELLIANTED NERVE FIBERS. SEENS TO DEMARCATE THE PARANODAL REGION OF THE AXO-GLIAL JUNCTION. IN ASSOCIATION WITH CONTACTIN MAY HAVE A ROLE IN THE SIGNALING BETWEEN AXONS AND WYELINATING GLIAL CELLS.

-!- SUBGUIT: INTERACTS WITH CONTACTIN IN CIS FORM.
-!- SUBGUIT: INTERACTS WITH CONTACTIN IN CIS FORM.
-!- SUBGLIULAR LOCATION: Type I membrane protein (Potential).
-!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN BRAIN. IN WYELINATED NERVE FIBERS OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION OF THE CONTACTION 
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Einheber S., Zanazzi G., Ching W., Scherer S., Milner T.A., Peles
SEQUENCE FROM N.A.
STRAIN=Sprague-Dawley; IISSUE=Brain;
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InterPro; IPR002181; Fibrinogen C.
InterPro; IPR001791; Laminin G.—
InterPro; IPR003585; Neurexin-like.
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Pfam; PF00147; fibrinogen C; 1.
Pfam; PF00754; F5_F8_Lype_C; 1.
SMART; SM00294; 4.Im; 1.
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InterPro; IPR000561; EGF-like.
InterPro; IPR000421; FAS8_C.
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           15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Contactin associated protein 1 precursor (Caspr) (Casprl) (Neurexin IV) (p190).
CNTMAP1 OR CASPR OR NEXN4.
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MEDINE=9724125; PubMed=9118959;
Peles E., Nativ M., Lustig M., Grumet M., Schilling J., Martinez R.,
Plowman G.D., Schlessinger J.;
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SWART; SM00231; FAS86; 1.

SMART; SM00221; LamG; 4.

PROSITE; PS00022; EGF 1; FALSE NEG.

PROSITE; PS01186; EGF 2; FALSE NEG.

PROSITE; PS01286; FAS8C 1; 1.

PROSITE; PS01286; FAS8C 2; 1.

PROSITE; PS00124; PIBRIM AG C DOMAIN; FALSE NEG.

PROSITE; PS50025; LAMG DOWAIN; 4.

Glycoprotein; Cell adhesion; Signal; Transmembrane; SH3-binding;
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1381 AA; 155867 MW; BC1CE83DB57C1BA4 CRC64;
                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL)
F5/8 TYPE C.
LAMININ G-LIKE 1.
LAMININ G-LIKE 2.
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LAMININ G-LIKE 4.
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InterPro; IPR000561; EGF-like.
InterPro; IPR000421; FAS8 C.
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  FINGLE AGE OF THE FORMATION OF FUNCTIONAL DISTINCT DOMAINS CRITICAL FOR SALTATORY CONDUCTION OF NERVE IMPULSES IN MYELINATED NERVE FIBERS. SEEMS TO DEMACRATE THE PRARANOBAL REGION OF THE AXO-GLIAL UNCTION. IN ASSOCIATION WITH CONTACTIN MAY HAVE A ROLE IN THE SIGNALING BETWEEN AXONS AND MYELINATING GLIAL. GELLS. MICE THAT LACK CWITAPL SKHIBLT TREMOR, ATAXIA, AND SIGNIFICANT MOTOR PARESIS. NORMAL PARANOBAL JUNCTIONS FAIL TO FORM, AND THE ORGANIZATION OF THE PARANOBAL LOOPS IS DISKUPTED. CONTACTIN IS UNDETECTABLE IN THE PARANOBAL LOOPS IS POTASSIUM CHANNELS ARE DISPLACED FROM THE JUXTAPARANOBAL INTO THE PARANOBAL DOMAINS. ALSO RESULTS IN A SEVERE DECREASE IN PERIPHERAL NERVE CONDUCTION VELOCITY.
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SUBCELULAR LOCATION: Type I membrane protein (Forential).
TISSUE SPECIFICITY: EXPRESSED IN BRAIN. IN MYELINATED NERVE FIBERS PREDOMINANTLY FOUND IN PARANODAL AXCOLLAL JUNCTIONS. IN THE INTERNODAL REGION OF MYELINATED AXONS IN THE CNS AND THE PNS ALSO SHOUND AS THIN LINE APPOSING THE INNER MESAXON OF THE MYELIN SHEATH. IN PNS NEURONS THIS LINE FORMS A CIRCUMFERRATIAL RING THAT APPOSES THE INNERMOST ASPECT OF SCHMIDT-LANTERMAN INCISURES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY.
MEDLINE=21403569; PubMed=11512672;
Arroyo E.J., Xu T., Poliak S., Matson M., Peles E., Scherer S.S.;
"Internodal specializations of myelinated axons in the central nervous
                                                                                                                                                                                                                                                                                                            15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Contactin associated protein 1 precursor (Caspr) (Casprl) (Neurexin 1V) (Paranodin) (NCPL) (MHDNIV)
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND POSSIBLE FUNCTION.
MEDLINE=21289247; PubMed=11395000;
Bhat M.A., Rios J.C., Lu Y., Garcia-Fresco G.P., Ching W.,
St Martin M., Li J., Einheber S., Chesler M., Rosenbluth J.,
Salzer J.L., Bellen H.J.;
"Axon-glial interactions and the domain organization of myelinated axons requires neurexin IV/Caspr/Paranodin.";
Neuron 30:369-383(2001).
                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Sukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                     (POTENTIAL).
(POTENTIAL).
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(POTENTIAL).
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                                                                                                                                                             90.0%; Score 27; DB 1; Length 1384; 80.0%; Pred. No. 3.9e+02; ive 1; Mismatches 0; Indels
                                                                                                                                         MW; 7727A13DF626DDCA CRC64;
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Cell Tissue Res. 305:53-66(2001)
                                                                                                                                         156265
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SIGNAL

1 20 POTENTIAL.
CHAIN
21 1385 CONTACTIN ASSOCIATED PROTEIN 1.
DOMAIN
21 1284 EXTRACELULAR (POTENTIAL).
TRANSMEM 1285 1305 POTENTIAL
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Pred. No. 3.9e+02;
-:- SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.
-:- SIMILARITY: CONTAINS 1 FIBRINGEN C-TERNINAL DOMAIN.
-:- SIMILARITY: CONTAINS 4 LAMININ G-LIKE DOMAINS.
-:- SIMILARITY: BELONGS TO THE NEUREXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5F4FE33629E25D1D CRC64;
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InterPro; 1PR0012181; FASO.
InterPro; 1PR0012181; Idminin G.
InterPro; 1PR001381; Neurexin-like.
InterPro; 1PR001818; Neurexin-like.
InterPro; 1PR001818; Neurexin-like.
Pfam; PP000054; Idminin G; 4.
Pfam; PP000147; fibrinogen C; 1.
Pfam; PP00174; Fibrinogen C; 1.
SMART; SM00284; FSE Lype C; 1.
SMART; SM00281; EGF; 1.
SMART; SM00281; LamG; 4.
PROSITE; PS00186; EGF 2; FALSE NEG.
PROSITE; PS01186; EGF 2; FALSE NEG.
PROSITE; PS01186; EGF 2; FALSE NEG.
PROSITE; PS00186; FASSC 2; 1.
PROSITE; PS00186; FASSC 2; 1.
PROSITE; PS00186; PASSC 2; 1.
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InterPro; IPR000082; SEA_domain.
InterPro; IPR002350; kazal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- ALTERNATIVE PRODUCTS: AT LEAST 5 ISOFORMS; 1 (SHOWN HERE), 2, 3, 4
AND 5; ARE PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER IN THEIR
ACETYLCHOLINE RECEPTOR CLUSTERING ACTIVITY.
-!- TISSUE SPECIFICITY: EMBRYONIC NERVOUS SYSTEM AND MUSCLE.
-!- DEVELOPMENTAL STAGE: MORE ABUNDANT EARLY IN DEVELOPMENT.
-!- PTM: CONTAINS HEPRANN SULFATE CARINS AS WELL AS N-LINKED AND O-
LINKED OLIGOSACCHARIDES (BY SIMILARITY).
-!- SIMILARITY: CONTAINS 9 KAZAL-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 1 LAMININ GGF-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 1 SEA DOMAIN.
-!- SIMILARITY: CONTAINS 3 LAMININ G-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 3 LAMININ G-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 3 LAMININ G-LIKE DOMAINS.
-!- CAUTION: IT IS UNCERTAIN WHETHER MET-1, MET-18 OR MET-24 IS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92407628; PubMed=1326608;
Rupp F., Oezcalik T., Linial M., Peterson K., Francke U., Scheller R.;
Rupp F., Oezcalik T., Linial M., Peterson K., Francke U., Scheller R.;
J. Neurosci. 12:535-3344 (1992)
-: FUNCTION: COMPONENT OF THE BASAL LAMINA THAT CAUSES THE
AGGREGATION OF ACETYLCHOLINE RECEPTORS AND ACETYLCHOLINE-ESTERASE
ON THE SURFACE OF MUSCLE FIBERS OF THE NEUROMUSCULAR JUNCTION.
-: SUBUNIT: BINDS TO LAMININ.
-: SUBCELLULAR LOCATION: SYNAPTIC BASAL LAMINA AT THE NEUROMUSCULAR
                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-1779 AND 1799-1959 FROM N.A.
TISSUE=Embryonic spinal cord;
MEDLINE=91222570; PubMed=1851019;
Rupp F., Payan D.G., Magill-Solc C., Cowan D.M., Scheller R.H.;
Structure and expression of a rat agrin.";
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01-MMY-1992 (Rel. 22, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
Agrin precursor.
                                                                                                                                                                                                                        PRT; 1959 AA
  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M64780; AAA40703.1; -.
EMBL; M64780; AAA40702.1; ALT_INIT.
EMBL; S44194; AAB23326.1; -.
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Laminin EGF.
Laminin G.
  4; Conservative
                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat)
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InterPro; IPR000561;
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IPR002049;
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                                                                               677 SCYNS 681
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HSSP; P00740; 1EDA
                                                1 SCYNA 5
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  Matches
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R SMART; SM00001; EGF_like; 4.

R SMART; SM00057; FIMAC; 3.

R SMART; SM00274; FOLN; 5.

R SMART; SM00280; KAZAL; 9.

R SMART; SM00280; KAZAL; 9.

R SMART; SM00280; EGF_1: 6.

R SMART; SM0022; EGF_2; 1.

R PROSITE; PS0186; EGF_2; 1.

R PROSITE; PS0186; EGF_2; 1.

R PROSITE; PS0022; EGF_1: 6.

R ROSITE; PS0022; EGF_1: 6.

R ROSITE; PS0024; EGF_1: 6.

R ROSITE; PS0024; EGF_1: 6.

R Glycoprotein; EGF-like domain; Repeat; Alternative splicing; Signal; KW Laminin EGF-like domain; Proteoglycan; Heparan sulfate.
                                                                                                                                                                                                                                                                                                                                                          KAZAL-LIKE 1.
KAZAL-LIKE 2.
KAZAL-LIKE 3.
KAZAL-LIKE 4.
KAZAL-LIKE 6.
KAZAL-LIKE 6.
KAZAL-LIKE 7.
KAZAL-LIKE 7.
KAZAL-LIKE 7.
LAMININ EGF-LIKE 1.
LAMININ EGF-LIKE 2.
KAZAL-LIKE 9.
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EGF-LIKE 4.
LAMININ G-LIKE 3.
SER/THR-RICH.
SER/THR-RICH.
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EGF-LIKE 2.
EGF-LIKE 3.
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POTENTIAL.
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BY SIMILARITY
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EGF-LIKE 1
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Pfam; PF00008; EGF; 4.
Pfam; PF00050; kazal; 9.
Pfam; PF00053; laminin_EGF; 2.
Pfam; PF001390; SEA; 1.
                                                                                 PRINTS; PR00290; KAZALINHBTR.
SMART; SM00180; EGF Lam; 2.
SMART; SM00001; EGF_like; 4.
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1258
1477
1708
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1116
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191
212
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STRAIN-Japanese, and Philippines; TISSUB-Venom;
Tamiya N., Sato A., Kim H.S., Teruuchi T., Takasaki C., Ishikawa Y.,
Tamiya N., McCoy M., Heatwole H., Cogger H.G.;
"Neurotoxins of sea makes genus Laticauda.";
Toxicon 21 Suppl. 3:445-447(1983)
-!- FUNCTION: PRODUCES PERIPHERAL PARALYSIS BY BLOCKING NEUROMUSCULAR
TRANSMISSION AT THE POSTSYNAPTIC SITE. BINDS TO THE NICOTINIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tamiya N., Sato A., Kim H.S., Teruuchi T., Takasaki C., Ishikawa Y., Guinea M.L., McCoy M., Heatwole H., Cogger H.G.;
"Neurotoxina of sea anakes genus Laticauda.";
Toxicon 21 Suppl. 31.445-447(1981)
-!- FUNCTION: PRODUCES PERIPHERAL PARALYSIS BY BLOCKING NEUROMUSCULA
TRANSMISSION AT THE POSTSYNAPTIC SITE. BINDS TO THE NICOTINIC
                                                                                                                                Laticauda colubrina (Yellow-lipped sea krait).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Lapidae; Laticaudinae; Laticauda.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Short neurotoxin A.
Laticauda crockeri (Crocker's sea krait).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Elapidae; Laticaudinae; Laticauda.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venom; Neurotoxin, Postsynaptic neurotoxin; Multigene family.
DISULPID 3 24 BY SIMILARITY.
DISULPID 17 41 BY SIMILARITY.
DISULPID 43 54 BY SIMILARITY.
DISULFID 55 60 BY SIMILARITY.
SEQUENCE 62 AA; 7037 MW; BCBF27EED2D71D4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Venom, Neurotoxin, Postšynaptic neurotoxin, Multigene family.

J. 24 BY SIMILARITY.

DISULFID 17 41 BY SIMILARITY.
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                           01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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01-MAY-1992 (Rel. 22, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
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100.0%; Pred. No. 55.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACETYLCHOLINE RECEPTOR.
PIR, B25866, B25866.
HSSP, P01415, 1QKE.
InterPro, IPR001571; Snake_toxin.
Prom, PP00087; toxin; 1.
Prom, PD000205; SNaKe_toxin; 1.
PROSITE, PS000272; SNAKE_TOXIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00087; toxin; 1. ProDom; PD000206; Snake toxin; 1. PROSITE; PS00272; SNAKE_TOXIN; 1.
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HSSP, P01435, 10KE.
InterPro, IPR003571; Snake_toxin.
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                                                                                                               Short neurotoxin II.
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Best Local Similarity
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NXSA_LATCR
ID NXSA_LATCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eŭkaryota; Metazoa; Arthropoda; Ĉhelicerata; Arachnida; Araneae;
Araneomorphae; Entelegynae; Agelenidae; Agelenopsis.
NCBI_TaxID=6908;
                                                                                                                                                                                                                                                                                              (POTENTIAL).
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TISSUB=Venom;
MEDLINE=94227039; PubMed=8172884;
Ertel E.A., Warren V.A., Adams M.E., Griffin P.R., Cohen C.J.,
Smith M.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1959;
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28;
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7FEFDFDAFF89CC31 CRC64;
                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .)
MISSING (IN ISOFORM 2).
MISSING (IN ISOFORM 3).
MISSING (IN ISOFORM 4).
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                                                                                                                                                                                                                                                                        (GLCNAC. . .)
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Pred. No. 5.4e+02;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Omega-agatoxin IIIC (Omega-Aga-IIIC) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.7%; Scor.
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                                                                                                                                                                                                                                            SIMILARITY
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Best Local Similarity
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NXS2_LATCO
ID _NXS2_LATCO
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P81745;
                                                                           DISULFID
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Matches

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STRAIN=Salomon Island, and Fiji; TISSUE=Venom;
Tamiya N., Sato A., Kim H.S., Teruuchi T., Takasaki C., Ishikawa Y.,
Guinea M.L., McCoy M., Heatwole H., Cogger H.G.;
"Neurotoxins of sea snakes genus Laticauda.";
Toxicon 21 Suppl. 3:445-447(1983)
-!- FUNCTION: PRODUCES PERIPHERAL PARALYSIS BY BLOCKING NEUROMUSCULAR
TRANSMISSION AT THE POSTSYNAPTIC SITE. BINDS TO THE NICOTINIC
ACETYLCHOLINE RECEPTOR.
                                                                                                                Biochemistry 25:395-404(1986).
-!- FUNCTION: PRODUCES PERIPHERAL PARALYSIS BY BLOCKING NEUROMUSCULAR TRANSMISSION AT THE POSTSYNAPTIC SITE. BINDS TO THE NICOTINIC ACETYLCHOLINE RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Short neurotoxin C.
Laticauda colubrina (Yellow-lipped sea krait).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eupldosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Elapidae; Laticaudinae; Laticaudinae; Laticaudinae;
                                                                                                                                                TRANS...

ACETYLCHOLINE...

R PIR; G25866; G25866.

DR HSSP; P01435; 10KE.

DR PRODOM; P0000205; Nake_toxin.

DR PRODOM; P0000205; Snake_toxin; 1.

DR PROSTTE; PS00272; SNAKE TOXIN; 1.

DR PROSTTE; PS00272; SNAKE TOXIN; 1.

RW Venom; Neurotoxin; Postsynaptic neurotoxin; Multigene family.

FT DISULFID 3 24 BY SIMILARITY.

TSULFID 43 54 BY SIMILARITY.

60 BY SIMILARITY.

7 MW; 0571DBF401737C40 CRC64;
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Endo T., Nakanishi M., Furukawa S., Joubert F.J., Tamiya N.,
Hayashi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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100.0%; Pred. No. 39;
ive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 AA.
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MEDLINE=86159724; PubMed=3955004;
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InterPro; IPR003571; Snake_toxin.
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HSSP; P01435; 1QKE.
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NXSC_LATCO
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TISSUE No. 3ato A., Kim H.S., Teruuchi T., Takasaki C., Ishikawa Y.,
Guinea M.L., McCoy M., Heatwole H., Cogger H.G.;
"Neurotoxins of sea snakes genus Laticauda.";
Toxicon 21 Suppl. 3:445-447(1983)
-!- FUNCTION: PRODUCES PERIPHERAL PARALYSIS BY BLOCKING NEUROMUSCULAR
-!- FUNCTION: PRODUCES PERIPHERAL PARALYSIS BY BLOCKING NEUROMUSCULAR
TRANSMISSION AT THE POSTSYNAPTIC SITE. BINDS TO THE NICOTINIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             ualicauda crockeri (Crocker's sea krait).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi;
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea;
Elapidae; Laticaudinae; Laticauda.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Elapidae, Laticaudinae, Laticauda.
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                                                                                               Length 62;
                                                                                                                                           0; Indels
BY SIMILARITY.
BY SIMILARITY.
056C228901737F8F CRC64;
                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Short neurotoxin B.
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01-MAR-1989 (Rel. 10, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Short neurotoxin B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laticauda laticaudata (Blue-ringed sea krait)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 AA
                                                                                                                                                                                                                                                                                                                                                          62 AA.
                                                                                                                                           Mismatches
                                                                                             Score 26;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00087; toxin; 1.
ProDom; PD000206; Snake toxin; 1.
PROSITE; PS00272; SNAKE_TOXIN; 1.
                                                                                                            100.0%; Pre
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InterPro; IPR003571; Snake_toxin.
54
60
7023 MW;
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nes 4; Conservative
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                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                             Query Match
Best Local Similarity
43
55
62 AA;
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P10459;
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DISULFID
SEQUENCE
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Best Loc Matches

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Gaps

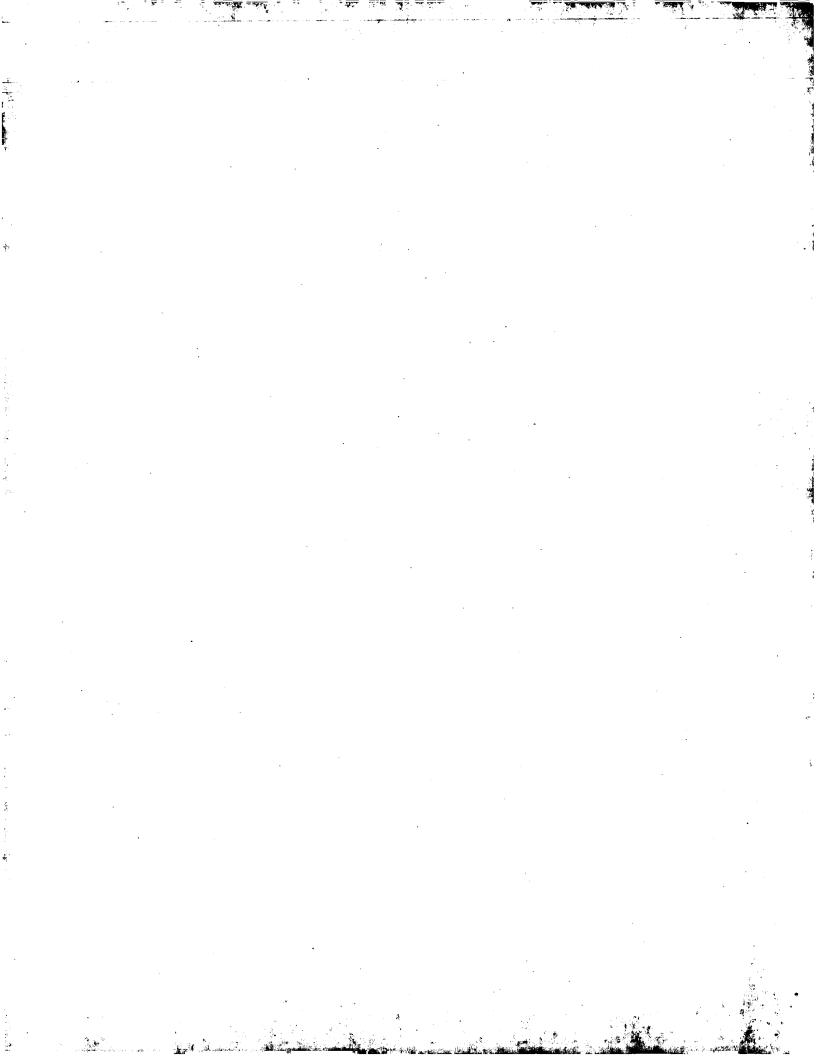
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Gaps

23 SCYN 26

Search completed: July 18, 2003, 15:07:15 Job time: 3.1 secs



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Q9pnms campylobact
Q8zbd6 yersinia pe
Q8z3i4 salmonella
Q8z19 salmonella
Q8za90 escherichia
Q8xa90 escherichia
O13628 schizosacch
O61969 caenorhabdi
O96w1 halocynthia
O55162 rattus norv
Q9scp7 arabidopsis
Q91yk8 mus musculu
Q9x500 uncultured
Q9x505 uncultured
Q9x506 uncultured
Q9x506 uncultured
Q9x506 uncultured
Q9x508 uncultured
                             Q92a84 proteus mir
Q82652 arabidopsis
Q9hwb2 pseudomonas
Q9nul8 homo sapien
Q45844 caenorhabdi
       Q91ex6 cydia pomon
07298 pseudomonas
065097 picea maria
                007298 pseudomonas
Q9bil3 entamoeba h
                                                                                                                                                                                                                      09x511 uncultured
09x516 uncultured
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=21139111; PubMed=11245483;
Smith B.A., Kennedy W.J., Harnden P., Selby P.J., Trejdosiewicz L.K.,
Southbare J.;
"Identification of genes involved in human urothelial cell-matrix
interactions: implications for the progression pathways of malignant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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SEQUENCE 346 AA; 35924 MW; CDFF9948FF493130 CRC64;
                                                                                                                                                                                                                                                                                                            01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 19, Last annotation update)
GPI-anchored metastasis-associated protein homolog.
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100.0%; Pred. No. 87;
iive 0; Mismatches 0.
                                                                                                                                                                                                                                                                                              346 AA.
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                              Q9ZA84
O82652
Q9HWB2
                                                                                                      Q8ZLT9
Q8XA90
O13628
O61969
Q9KVD4
      Q91EX6
O07298
Q9BI13
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Q91YK8
                                                                               Q9PNMS
Q8ZBD6
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                                                       Q9NU18
Q45844
Q17958
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Q9X506
Q9X508
Q9X511
Q9X516
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                                                                                                                                              0966W1
                                                                                                                                                                                                                                                                                                                                                                                                                                    urothelium.";
Cancer Res. 61:1678-1685(2001);
EMBL; AF082889; AAD13751.1; -.
InterPro; IPR001526; LYG UPAR.
 5; Conservative
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                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
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Best Local Similarity
Matches 5; Conserv
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1 SCYNA 5
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Q9UJ74;
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Q9UJ74
ID Q9UJ
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095274
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Q9uj74 homo sapien
Q9fg88 arabidopsis
Q9yvt0 melanoplus
Q9waz6 tt virus. o
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picea abies
picea glauc
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Q9s9a0 viscum albu
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picea abies
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                                                      July 18, 2003, 15:02:40; Search time 12.9 Seconds (without alignments) 79.863 Million cell updates/sec
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Q98px7
Q98px7
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        GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                       protein search, using sw model
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Q9WAZ6
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O65095
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Q9SPW5
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Match Length
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Perfect score:
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Matches 5; Conserv
                                                                 283 SCYNA 287
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                        1 SCYNA
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                                                                                                                                                                                                                       SEQUENCE FROM N.A. Hasedler J., Claas A., Savelyeva L., Schwab M., Hasedl B., Marzku S., Zoeller M.; "Cloning of the human homologue of the metastasis-associated rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          eudicots; Rosidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosid
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=COLUMBIA;
Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Structural analysis of Arabidopsis thaliana chromosome 5. XI."; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB026651; BAB11307.1; -
InterPro; IPR002885; PPR.
InterPro; IPR001585; PPR.
IGREPAMS: TIGREO0756; PPR; 5.
SEQUENCE 460 AA; 51644 MW; B955D35DFE01C3A1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 30; DB 4; Length 346; 100.0%; Pred. No. 87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequence analysis of 19q13.2.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ223603; CAA11469.2; --.
EMBL; AC018758; AAG09062.1; -.
                                                                                                                                                                                                                                                                                                              C4.4A.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 346 AA; 35970 MW; 97FF9B4A554934FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Genomic DNA, chromsome 5, Pl clone MQD19.
Arabidopsis thaliana (Mouse-ear cress).
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Hypothetical 36.0 kDa protein (C4.4A protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  460 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro, IPR001526, LY6_UPAR
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1es 5; Conservative
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                                                                                                               Homo sapiens (Human).
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Best Local Similarity
Local 5; Conserve
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Q9FG85;
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Gaps
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Hijikata M., Takahashi K., Mishiro S.;
"Complete circular DNA genome of a TT virus variant (isolate name
SANBAN) and 44 partial ORF2 sequences implicating a great degree of
diversity and 44 partial ORF2 sequences implicating a great degree of
Virology 260:17-22(1999).
                                                                                                                                                                                                                                                                          Melanoplus sanguinipes entomopoxvirus (MsEPV).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
Entomopoxvirus B.
VCBI_TaxID=83191;
                                                                                                    01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-UTNA-2002 (TrEMBLrel. 21, Last annotation update)
ORF MSV162 putative NAD+ dependent DNA ligase, similar to Thermus thermophilus SW:P26996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Afonso C.L., Tulman E.R., Lu Z., Oma E., Kutish G.F., Rock D.L.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF063866; AAC97679.1; -
InterPro; IPR001679; DNAligase.
InterPro; IPR001680; WDA?
InterPro; IPR001680; WDA?
InterPro; IPR001680; WDA?
InterPro; IPR001680; WDA?
InterPro; IPR001681; WDA.
InterPro; IPR001631; DNAligase_OB.
InterPro; IPR001631; DNAligase_OB.
InterPro; IPR001831; DNAligase_OB; 1.
SMART; SM00532; LiGANC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Afonso C.L., Tulman B.R., Lu Z., Oma E., Kutish G.F., Rock D.L., "The genome of Melanoplus sanguinipes entomopoxvirus."; J. Virol. 73:533-552(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60235 MW; 1B17E513872C33A2 CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; ssDNA viruses; unclassified ssDNA viruses
522 AA
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                                                                  01-MAY-1999 (TrEMBLrel. 10, Created)
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Q9UFY0

RESULT 6 Q9UFY0

Best Loc Matches

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Gaps
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Burgert H.G., Blusch J.H.;
"Immunomodulatory functions encoded by the E3 transcription unit of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum aerophilum.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
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                                                                                                                                                                               Score 27; DB 10; Length 11
Pred. No. 1.4e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pyrobaculum aerophilum.
Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
Thermoproteaceae; Pyrobaculum.
NCBI_TaxID=13773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Virus Genes 21:13-25(2000).
EMBL; AF086570; AAF31748.1; -.
SEQUENCE 129 AA; 14750 MW; B347E50EFFA56DEB CRC64;
                                                                                                                       114 AA; 11981 MW; D30BFC724907CE7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 AA; 13466 MW; BAEA5CDAF26BD132 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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Last annotation update)
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Pred. No. 1.4e+02;
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EMBL; AE009886; AAL64314.1; -
Complete proteome.
SEQUENCE 118 AA; 13466 MW: RAFAGUNAROCENTA
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PubMed=11792869;
                                      Pfam, PF00321; plant_thionins; 1. PF005TF; PS00271; THIONIN; 1. Plant toxin; Thionin. SEQUENCE 114 AA; 11981 MW; D30
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           InterPro; IPR001010; Thionin.
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Query Local Similarity 80.00,
Best Local 4; Conservative
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                                                                                                                                                                                                                                        4; Conservative
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                                                                                                                                                                         Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                              : | | | | 37 NCYNA 41
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                                                                                                                                                                                                                                                                                              1 SCYNA 5
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01-MAR-2002
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Miller J.H.;
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01-DEC-2001
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Q8ZUU2
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Q9JFM1
           S KW DR
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MEDLINE=94122387; PubWed=8292787; Schrader-Fischer G., Apel K.; Apel K.; Apel K.; Apel K.; Apel K.; Apel K.; Apel K.; Apel K.; Apel K.; Apel K.; Apel K.; Apel K.; Apel K.; Apel K.; Apel K.; Apel K.; Apel K.; Apel K.; Apel K.; Apel CellS. THEY SEM TO EXERT THEIR TOXIC EFFECT AT THE LEVEL OF THE CELL MEMBRANE. THE PRECISE FUNCTION, IN PLANTS, OF THESE PROTEINS IS NOT KNOWN (BY SIMILARITY).

-!-- SIMILARITY: BELONGS TO THE PLANT THIONIN FAMILY.
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Wataryota, Viridiplantee, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Santalales; Viscaceae, Viscum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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EMBL; AL110299; CABS3740.1; -.
                                                                                                                                                                      90.0%; Score 27; DB 12; Length 105; 80.0%; Pred. No. 1.3e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 27; DB 4; Length 108;
Pred. No. 1.3e+02;
1; Mismatches 0; Indels
                                                                                                                    4F2949E0F796EA3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
SEQUENCE 108 AA; 11956 MW; 59572E281D3FB01B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY 2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
THIOMIN (TrEMBLrel. 18, Last annotation update)
THIOMIN
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Pfam; PF00171; aldedh; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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                                                                                                                 105 AA; 11792 MW;
EMBL, AB024357; BAA77424.1; -
InterPro; IPR004118; TT ORF2.
Pfam; PF02957; TT_ORF2; 1.
NON_TER 105 105
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                                                                                                                                                                                                                               4; Conservative
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Matches 4; Conservative
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TISSUE=TESTIS;
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| NCYNA 66
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47 ACYNA 51
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                                                                                                                 SEQUENCE
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Q9S9A0

RESULT 7 Q9S9A0

Length 148;

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90.0%;
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                                                            4; Conservative
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Best Local Similarity
Matches 4; Conserv
                   Query Match
Best Local Similarity
Matches 4; Conserv
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13 TCYNA 17
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                                                                                                     1 SCYNA 5
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01-MAY-2000 (
01-MAY-2000 (
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Q9SPX8
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"Specific and distinct expression patterns of two members of the thionin multigene family of barley in transpenic tobacco.";
Submitted (MAR-1996) to the EMBJ/Genbank/DDBJ databases.
-!- FUNCTION: THIONINS ARE SMALL PLANT PROTEINS WHICH ARE TOXIC TO ANIMAL CELLS. THEY SEEM TO EXERT THEIR TOXIC EFFECT AT THE LEVEL.
OF THE CELL MEMBRANE. THE PRECISE FUNCTION, IN PLANTS, OF THESE PROTEINS IS NOT KNOWN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE PLANT THIONIN FAMILY.
                     Gaps
                                                                                                                                                                                                                                                                                                                                                          Hordeum vulgare (Barley).
Bukaryota, Viridiplancae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
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Spermatophyta, Coniferopsida, Coniferales, Pinaceae, Picea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.0%; Score 27; DB 10; Length 13
80.0%; Pred, No. 1.7e+02;
---rohes 0; Indels
                       Indels
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
  Pred. No. 1.6e+02;
1; Mismatches 0;
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                                                                                                                                                                                                             137 AA
                                                                                                                                                                                                           PRT;
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Pfam; PF00321, plant thionins; 1.
PROSITE; PS00271; THTONIN; 1.
Plant toxin; Thionin.
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MEDLINE=98278823; Pubmed=9611216;
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NON TER 1 1 1
SEQÜENCE 148 AA; 16658 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 AA; 14676 MW;
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80.08;
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01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 80.0
nes 4; Conservative
  Best Local Similarity 80.0
Matches 4; Conservative
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33 NCYNA 37
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                                                            1 SCYNA 5
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Q42838
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Perry D.J., Isabel N., Bousquet J.;
"Sequence-tagged-site (STS) markers of arbitrary genes: the amount and nature of variation revealed in norway spruce.";
Heredity 83:239-248(1999).
EMBL; AF127440; AAF02457.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99436016; PubMed=10504420; Perry D.J., Isabel N., Bousquet J.; Perry D.J., Isabel N., Bousquet J.; "Sequence-tagged-site (STS) markers of arbitrary genes: the amount and nature of variation revealed in norway spruce."; Heredity 8:123-248(1999).

EMBL; AF127441; AAF02458.1; -.
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                                                      Gaps
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Coniferopsida, Coniferales, Pinaceae, Picea.
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                                                   0; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAX-2001 (TrEMBLrel. 16, Last annotation update)
ATAF1-like protein (Fragment).
                                                                                                                                                                                                                                                                                                                                          90.0%; Score 27; DB 10; Le 80.0%; Pred. No. 1.8e+02; tive 1; Mismatches 0;
Score 27; DB 10;
Pred. No. 1.8e+02;
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                                                   1; Mismatches
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Q9SPW5

RESULT 14

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Matches

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Perry D.J., Bousquet J.;
"Sequence-tagged-site (STS) markers of arbitrary genes. Development,
characterization and analysis of linkage in black spruce.";
Genetics 149:1089-1098(1988).
EMBL; AF051750; AAC32167.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Vizidiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Coniferopsida, Coniferales, Pinaceae, Picea.
NCBI_TaxID=3335,
                                                                          Picea glauca (White spruce).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Coniferopsida, Coniferales, Pinaceae, Picea.
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                                                                                                                                                                                                                                                                                                                SEQUENCE 154 AA; 17306 MW; 409443B6ED916940 CRC64;
 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
ATAF1-like protein (Fragment).
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DBC-2001 (TrEMBLrel. 19, Last annotation update)
ATAF1-like protein (Fragment).
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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80.0%; Pred. No. 1.8e+02;
tive 1; Mismatches 0
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12 TCYNA 16
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MEDLINE=99436016; PubMed=10504420;

Perry D.J., Isabel N., Bousquet J.;

Sequence-tagged-site (STS) markers of arbitrary genes: the amount and nature of variation revealed in norway spruce.";

Heredity 8:239-248(1999).

EMBL; AP127442; AAF02459.1; -.
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=99436016; PubMed=10504420; Perry D.J., Isabell N., Bousquet J.; Farty D.J., Isabell N., Bousquet J.; Saguence-tagged-site (STS) markers of arbitrary genes: the amount and nature of variation revealed in norway spruce.";
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Spermatophyta, Coniferopsida, Coniferales, Pinaceae, Picea.
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Nakaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Coniferopsida, Coniferales, Pinaceae, Picea.
NCBI_TaxID=3329,
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80.0%; Pred. No. 1.8e+02;
iive 1; Mismatches 0; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence.update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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Last annotation update)
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EMBL; AF127599; AAF02475.1; -.
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                                                                                                                                                                                                            Picea glauca (White spruce)
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32 TCYNA 36
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                      STRAIN=OUS82;
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                                                                                                                                                                               "Characterization of a highly conserved baculovirus structural protein that is specific for occlusion-derived virions."; Virology 218:148-158(1996).
                                                                                                                                                                                                                                       STRAIN=MEXICAN 1;
MEDLINE=97380577; PubMed=9237352;
Kang W., Crook N.E., Winstanley D., O'Reilly D.R.;
"Complete sequence and transposon mutagenesis of the BamHI J fragment of Cydia pomonella granulosis virus.";
Virus Genes 14:131-136(1997).
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STRAIN-MEXICAN I.

Luque T., Finch R., Crook N., O'Reilly D.R., Winstanley D.;

Luque T., Finch R., Crook N., O'Reilly D.R., Winstanley D.;

"The complete sequence of the Cydia pomonella granulovirus genome.";

Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; U53466; AAK70739.1; -

InterPro: IPR0025557; Chitin_bind_PerA.

PÉam; PF01607; CBM 14; 1.

SEQUENCE 156 AA; 17807 MW; ESE0E0107C5554FA CRC64;
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                                                                                                                                                          Theilmann D.A., Chantler J.K., Stweart S., Flipsen H.T., Vlak J.M.,
                                          STRAIN=MEXICAN 1;
MEDLINE=93188168; PubMed=8445726;
MCOOK N.E., Clem R.J., Miller L.K.;
"An apoptosis-inhibiting baculovirus gene with a zinc finger-like motif.";
dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.0%; Score 27; DB 12; Length 156; 80.0%; Pred. No. 1.9e+02;
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MEDLINE-96207404; Pubmed-8615018;
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MEDLINE=98418511; PubMed=9747739;
                                                                                                   J. Virol. 67:2168-2174(1993)
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         NCBI_TaxID=28289;
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Takizawa N.;
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STRAIN=H14320;
MEDINNE=99140151; PubMed=10206698;
Zhao H., Li X., Johnson D.E., Mobley H.L.;
"Identification of protease and rpoN-associated genes of uropathogenic Proteus mirabilis by negative selection in a mouse model of ascending
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Willhoeft U., Campos-Gongora E., Touzni S., Bruchhaus I., Tannich E.;
"Introns of Entamoeba histolytica and Entamoeba dispar.";
Protist 152:149-156(2001).
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Noboru T., Toshiya I., Takashi S., Kazuhiro Y., Masamichi K., Yue-Wu W., Masao F., Hohzoh K.;
"The molecular analysis of NAH7-type cluster located on the chromosomes of Pseudomonas aeruginosa Paxi and Pseudomonas putida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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80.0%; Pred. No. 2.4e+02;
iive 1; Mismatches 0; Indels
                                                                                                                      OUS82.";
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AB004059; BAA20398.1; -.
INTERPTO; IPR004287; HCCA_isomerase.
Pfam; PP03046; HCCA_isomerase; 1.
SEQUENCE 203 AA; 23134 MW; 6779C14A8E862CB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
SEQUENCE 209 AA; 24041 MW; 618A8EC9CD515FCB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 19, Last sequence update)
01-JUEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 24.0 kDa protein.
Entamoeba histolytica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY 1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Entamoebidae, Entamoeba.
NCBI_TaxID=5759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=HM1:IMSS;
MEDLINE=21428166; PubMed=11545438;
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Gaps

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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
[1]
Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen."; Nature 406:959-964(2000).
-:- SIMILARITY: BELONGS TO THE ARAC/XYLS FAMILY OF TRANSCRIPTIONAL REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
0298918.3 (Novel protein similar to putative HIV-1 induced prot HIN-1 and Drosophila ovarian tumor locus protein OTU) (Fragment)
DJ298J18.2.
                                                                                                                                                                                                                                   90.0%; Score 27; DB 16; Length 267; 80.0%; Pred. No. 3e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.0%; Score 27; DB 4; Length 278; 80.0%; Pred. No. 3.1e+02; ive 1; Mismatches 0; Indels
                                                                                           EMBL; AED04845; AAG07676.1; -.
InterPro; IPR000005; HTHARAC.
InterPro; IPR000005; HTH ARAC; 2.
PRINTS; PR00032; HTHARAC.
SMART; SM03342; HTHARAC; 1.
SMART; SM03342; HTHARAC; 1.
DNA-binding; Transcription regulation; Complete proteome. SEQUENCE 267 AA; 30168 WW; IF6FEC2B26ECD266 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL096764; CAB89278.1; -.
InterPro; IPR003323; OTU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    278 AA; 32183 MW; E2266035E8752505 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                            278 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02338; OTU; 1.
PROSITE; PS50802; OTU; 1.
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Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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201 ACYNA 205
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                                                                                                                                                                                                                                                                                                                               76 SCYNS 80
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Q9NU18;
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045844
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       AXX OOC SUPPLIES
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                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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STRAINS-ATCC 15692 / PAO1;
STRAINS-ATCC 15692 / PAO1;
STRAINS-ATCC 15692 / PAO1;
SCOVER C.K., Phan X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.Garckey M.J., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
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                                                                                                         90.0%; Score 27; DB 2; Length 241;
80.0%; Pred. No. 2.7e+02;
Live 1; Mismatches 0; Indels
                                                               241 241 241 241 241 AA; 074A6CE9731E41FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246 AA; 28017 MW; 23107880586D1980 CRC64;
                                                                                                                                                                                                                                                                                                                              01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aubourg S.;
Thesis (1998), Universite Paris, FRANCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE FROM N.A.
STRAIN=CV. COLUMBIA 0; TISSUE=SILIQUES;
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   urinary tract infection.";
Microbiology 145:185-195(1999).
EMBL; AF088981; AAC64578.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AJ011845; CAA09808.1; --
InterPro; IPR004314; DUF239.
Pfam; PF03080, DUF239, 1
NON_TER
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IB1C3-1.
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les 4; Conservative
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186 SCYNS 190
                                                                                                                                                                                                      117 NCYNA 121
                                                                                                                                                                       1 SCYNA 5
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O82652
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Q9HWB2
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SEQUENCE FROM N.A.
STRAIN=NCTC 11168;
MEDIXE=20150912; PubMed=10688204;
MEDIXE=20150912; PubMed=10688204;
Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
"The genome sequence of the food-borne pathogen Campylobacter jejuni
reveals hypervariable sequences.";
                                                                                                                                                                                                                                                                                                                                                                       Nature 403:665-668(2000).
BMBL, AL139077; CAB7324.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 288 AA; 34645 MW; 21EB9C8CF4DC221E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 80.v.
4; Conservative
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117 NCYNA 121
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63 ACYNA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SCYNA 5
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                        NCBI_TaxID=197;
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Campylobacter
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI TaxID=6239;
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Bacteria, Proteobacteria, epsilon subdivision, Campylobacter group,
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                                                                                                                                                                                                                                                                                                                                                                                                                             Score 27; DB 5; Length 284;
Pred. No. 3.1e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                       'Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 287;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                        McMurray A.A.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lloyd C.R.; Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z83116; CAB05562.1; -.
InterPro; IPRO02892; DUF40.
Pfam; PF01838; DUF40; 1.
SEQUENCE 287 AA; 32892 MW; OC627F0AF7E0DEFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                          32288 MW; 62C42A32215A5D74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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Last annotation update)
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80.0%; Pred. No. 3.2e+02;
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                                                                                                      SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
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MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                         investigating biology.";
Science 282:2012-2018(1998).
EMBL; 281132; CABG3439.1; -.
Interpro; IPR002892; DUF40.
Pfam; PF01898; DUF40; 1.
SEQUENCE 284 AA; 32288 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                   90.0%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                  Loury Match
Bust Local Similarity 80.vv.
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Beet Local Similarity 80.v.,
4; Conservative
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FROM N.A.
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   SEQUENCE
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Q9PNM5;
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017958
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RAY REPRESENT OF SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY SORRY S
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SERALISE CO-92 / BIOVAR ORIENTALIS;
MEDLINE-21470413; PubMed=11586360;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Parkhill J., Wren B.W., James K.D., Churcher C., Mungall K.L.,
Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
Prentice M.B., Sebaihia M., Jawes R.M., Davis P., Dougan G.,
Chillingworth T., Cronin A., Davise R.M., Davis P., Dougan G.,
Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.,
"Genome sequence of Yersinia pestis, the causative agent of plague.",
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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   Length 288;
                                                                 0; Indels
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EMBL, AJ414157, CAC92709.1; -
InterPro; IPR001539; Peptidase U32.

Probom; PD004399; Peptidase U32; 1.

Pypothetical protein; Complete proteome.

SEQUENCE 292 Aa; 32714 MW; 3CC6EDD893C7AA9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
90.0%; Score 27; DB 16;
80.0%; Pred. No. 3.2e+02;
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                                                                    1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein YPO3480
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EMBL; AE005544; AAG58295.1; -. EMBL; AP002564; BAB37463.1; -.
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                                                                                                                                                                                                                                                      Orf, hypothetical protein.
YHBV OR Z4520 OR ECS4040.
Escherichia coli 0157:H7.
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                                                                                                    PRELIMINARY;
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NCBI_TaxID=4896;
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Matches 4; Conserv
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123 NCYNA 127
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SEQUENCE 298 AA;
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013628
                                   RESULT 31
Q8XA90
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                                                                                                                                                                                                                                                                                                                                    MEDLINE-21534947; PubMed=11677608; Parkhill J. Dougan G. James K.D. Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M. Baker S., Basham D., Brocks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamin N., Haque A., Hier T.T., Holroyd S., Jägels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Whitehead S., Barrell B.G., Whitehead S., Barrell B.G., Whitehead S., Barrell B.G., Whitehead S., Barrell B.G., Whitehead S., Barrell B.G., Whitehead S., Barrell B.G., Whitehead S., Barry C., Whitehead S., Barry C., Whitehead S., Barry C., Whitehead S., Barry C., Whitehead S., Barry C., Whitehead S., Barry C., Simmonds M., Skelton J., Stevens K., Whitehead S., Barry C., Whitehead S., Barry C., Whitehead S., Barry C., Whitehead S., Barry C., Whitehead S., Barry C., Whitehead S., Barry C., Whitehead S., Barry C., Whitehead S., Barry C., Whitehead S., Barry C., Whitehead S., Barry C., Whitehead S., Barry C., Whitehead S., Barry C., Whitehead S., Barry C., Whitehead S., Barry C., Barry C., Whitehead S., Barry C., Whitehead S., Barry C., Whitehead S., Barry C., Whitehead S., Barry C., Whitehead S., Barry C., Whitehead S., Barry C., Whitehead S., Barry C., Whitehead S., Barry C., Simmonds B., Barry C., Whitehead S., Barry C., Barry C., Whitehead S., Barry C., Barry C., Whitehead S., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry C., Barry
                                                                                                                       Salmonella typhi.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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80.0%; Pred. No. 3.2e+02;
ive 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 413:848-852(2001).
EMBL. AL637278 CADOT797.1; -
Hypothetical protein; Complete proteome,
SEQUENCE 292 AA; 32530 MW; B49857895AF2E6A3 CRC64;
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Last sequence update)
Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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STRAIN-LIZ / SGSC1412 / ATCC 700720;
MEDLINE-21534948; PubMed=11677609;
                                                             Hypothetical protein STY3458.
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Matches 4; Conservative
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Best Local Similarity
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117 NCYNA 121
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123 NCYNA 127
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                     NCBI_TaxID=601;
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                                                                                                                                                                                           Salmonella.
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STRAIN=0157:H7 / RIMD 0509952;
MEDLINB=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiha T., Hattori M., Shinagawa H., Complete genome sequence of enterohemorrhagic Escherichia coli Complete genome sequence of enterohemorrhagic Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Machida M., Yamazaki S., Kunihiro S., Tanaka T., Kushida N., Jinno K., Haikawa Y., Yamazaki J., Yamamoto S., Sekine M., Oguchi A., Nagai Y., Sakai M., Aoki K., Ogura K., Kudoh Y., Kikuchi H., Zhang M.Q., Yanagida M.;
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"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.",
                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.0%; Score 27; DB 16; Length 298; 80.0%; Pred. No. 3.3e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298 AA; 33206 MW; F30AD7D492D62A1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                         Last sequence update)
Last annotation update)
298 AA
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                                                                                                                                                                                                                                                                                                                                        EDL933 / ATCC 700927;
                                                    Created)
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PRT;
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Vibrio cholerae
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ASFCN4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cholerae.
                                                                             Q9KVD4;
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                                                  Q9KVD4
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Q966W1
     RESULT 34
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"A 38 kb segment containing the cdc2 gene from the left arm of fission yeast chromosome II: sequence analysis and characterization of the genomic DNA and cDNAs encoded on the segment."; Yeast 16:71-80(2000) -- I- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
EMBL; AB004537; BAA21416.1; -.
                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI TaxID=6239;
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                                                                                                                                                                                                                                                                                                               90.0%; Score 27; DB 3; Length 304; 80.0%; Pred. No. 3.3e+02; Live 1; Mismatches 0; Indels
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"Direct Submission.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF068717; AAC17763.1;
InterPro; IPR003003; 7TM_nemmatode.
InterPro; IPR00015; Serpin.
Plan; PF0164; 7tm_5.1.
PROSITE; PS00284; SERPIN; UNKNOWN_1.
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"The sequence of C. elegans cosmid H05B21.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                    304 AA; 34283 MW; C87F5F5A24217F23 CRC64;
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SEQUENCE 325 AA; 37998 MW; B0FA2C7390F5619E CRC64;
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
Hypothetical 38.0 kDa protein.
HO5B21.2.
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MEDLINE=99069613; PubMed=9851916;
                                                                                                                                         Interpro; IPR001841; Znf ring.
Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
PROSITE; PS00518; ZF_RING_1; 1.
                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 80.0.
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Best Local Similarity
Matches 4; Conserv
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244 SCYNS 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
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2 NCYNA 6
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06196
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STRAINEL TOW NIG661 / SEROTYPE 01;
MEDLINE=L TOW NIG661 / SEROTYPE 01;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-UTN-2002 (TrEMBLrel. 21, Last annotation update)
Lipid A biosynthesis (kdo)2-(lauroyl)-lipid IVA acyltransferase.
VC0212.
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80.0%; Pred. No. 3.5e+02;
w:emarches 0; Indels
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PROSITE; PS00514; FIBRIN ĀG C DOMAIN; UNKNOWN 1.
SEQUENCE 341 AA; 3885Ī MW; CD0EF8D521781578 CRC64;
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Stolidobranchia, Pyuridae, Halocynthia.
NCBI_TaxID=7729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
  325 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR004960; LipA acyltrans.
Pfam; PF03279; Lip_A acyltrans; 1.
Complete proteome.
SEQUENCE 325 AA; 37215 MW. PERAGE
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PRT;
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MEDLINE=21282877; PubMed=11259430;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 406:477-483(2000).
EMBL; AE004111; AAF93388.1; -.
TIGR; VC0212; -.
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Best Local Similarity 80.v.
Frac 4; Conservative
PRELIMINARY;
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252 SCYNS 256
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Query Match
Best Local Similarity 80...
A; Conservative
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Matches 4; Conserv
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277 NCYNA 281
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Q91YK8;
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09X500
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                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=BD IX; TISSUE=COLON CARCINOMA;
MEDLINE=99002492; PubMed=9788443;
Roesel M., Claas C., Seiter S., Herlevsen M., Zoeller M.;
"Cloning and functional Laracterization of a new phosphatidyl-inositol anchored molecule of a metastasizing rat pancreatic tumor.";
Oncogene 17:1989-2002(1998).
                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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Weichselgartner M., Mewes H.W., Lemcke K., Mayer K.F.X., Quetier F.,
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Shinn P., Chen H., Cheuk R., Kim C.J., Meyers M.C., Banh J.,
Shinn P., Chen H., Chung M.K., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.
Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M.,
Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M.,
Seki M., Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K.,
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80.0%; Pred. No. 3.8e+02;
tive 1; Mismatches 0; Indels
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Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salanoubat M.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            352 AA; 36961 MW; 1894500CFCF9CAF5 CRC64;
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Caffeic acid O-methyltransferase-like protein
(AT393140/T4D2_70).
                                                                                                                                                                                                        01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) Metastasis-associated GPI-anchored protein.
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                                                                                                                                                                                       Created)
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InterPro; IPR001526; LY6_UPAR.
SMART; SM00134; LU; 1.
                                                                                                                                                                                  01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-DEC-2001 (TrEMBLrel. 19,
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Best Local Similarity BU.v.
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                                       SCYNS 298
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162 NCYNA 166
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SCYNA 5
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99203128; PubMed=10103268;
Scala D.J., Kerkhof L.J.;
"Diversity of nitrous oxide reductase (nos2) genes in continental
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80.0%; Pred. No. 3.9e+02;
.ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                         90.0%; Score 27; DB 10; Length 35
80.0%; Pred. No. 3.9e+02;
ive 1; Mismatches 0; Indels
Davis R.W., Theologis A., Ecker J.R.;
"Arabidopsis cDNA clones.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; A1132959; CAB64217.1; -.
EMBL; A7132959; AAK56277.1; -.
InterPro; IPR001601; Methyltransf.
InterPro; IPR001077; O.Metransf2.
InterPro; IPR001077; O.Metransf2.
Fransferase; Transferase.
SEQUENCE 359 AA; 39688 MW; 5847B413BF7563781 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC016549; AAH16549.1; -.
MGD; MGI:1919684; C4.4a.
SROHENCE 363 AA; 37489 MW; D6CE5139A17CC5FA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to metastasis-associated GPI-anchored protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Nitrous oxide reductase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Appl. Environ. Microbiol. 65:1681-1687(1999)
EMBL; AF119936; AAD26832.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      363 AA.
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01-DEC-2001 (TrEMBLrel. 19, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
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MEDLINE=99203128; PubMed=10103268;
Scala D.J., Kerkhof L.J.;
"Diversity of nitrous oxide reductase (nosZ) genes in continental shelf sediments.";
Appl. Baviron. Microbiol. 65:1681-1687(1999).
EMBL: AP119940; AAD26836.1; -.
Query Match
90.0%; Score 27; DB 2; Length 376;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels
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90.0%; Score 27; DB 2; Length 376;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Nitrous oxide reductase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 376 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           uncultured bacterium 696T.
Bacteria, environmental samples.
NCBI_TaxID=92152;
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161 SCYNS 165
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SEQUENCE
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Search completed: July 18, 2003, 15:09:43 Job time : 14.9 secs

||||: 161 SCYNS 165

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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- protein search, using sw model OM protein July 18, 2003, 15:03:05; Search time 14.3 Seconds (without alignments) 73.950 Million cell updates/sec Run on:

1 SGAYYRYGVVY 11 US-10-007-790-7 61 score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

		*			COLUMNIES	
Result No.	Score	Query Match	Length	DB	ΩI	Description
; rd	46	75.4	306	2	G97132	uncharacterized ph
7		63.9	441	7	E72242	•-
м			517	7	T02403	probable beta-qluc
4	39	63.9	1389	0	T41230	hypothetical TPR d
5		62.3	740		D71602	hypothetical prote
9		62.3	1411		T18417	
7	38	62.3	1417		T18418	
æ		60.7	209		H82561	
0		60.7	224		B69657	homoserine O-succi
10	37	60.7	265		A59141	silaffin sillp pre
11	37	60.7	317	7	S61149	probable membrane
12	37	60.7	384		F85439	hypothetical prote
13	37	60.7	558		JC5878	plasma hyaluronan-
14	37	60.7	560	Н	JC4795 .	plasma hyaluronan-
15	37	60.7	574		A69196	cell surface glyco
16	37	ö	695		S37439	transketolase (ĒC
17	37	60.7			870029	probable transmemb
18	36	59.0			A56724	cni protein - frui
19	36	59.0	391	N	T32517	Н
20	36	59.0	4	0	E71869	
21	36	59.0	'n	7	AE1855 .	hypothetical prote
22	36	59.0	ß	Ŕ	B82140	-
23	36	59.0	9	Н	XJBYTK	transketolase (EC
24	36	59.0	965	~	G96586	hypothetical prote
25	36	59.0	56	7	T25444	_
26	35	57.4	Ó	Н	Q1BP2L	_
27	32	57.4	12	0	AE1330	Н
28	35	57.4	7	7	S50638	hypothetical prote
29	35	57.4	147	7	T16672	

hypothetical prote	conserved hypothet	hypothetical prote probable ribosomal	recombination prot	carboxypeptidase G	hypothetical prote	hypothetical prote	homeobox protein -		hypothetical prote	hypothetical prote	hypothetical prote	probable ABC trans	SNQ2 protein - yea
T08321	D86693	T27656 A72780	849464	H83693	T25209	T20439	149754	H84463	D65032	G91055	C85900	F86428	850992
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204	255	338 344	355	374	392	399	399	770	1124	1124	1124	1488	1501
57.4	57.4	57.4	57.4	57.4	57.4	57.4	57.4	57.4	57.4	57.4	57.4	57.4	57.4
35.	3.0	9 20	35	32	35	35	35	35	32	35	32	35	35
30	32	33 54	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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RESULT 1
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uncharacterized phage related protein [imported] - Clostridium acetobutylicum C; Species: Clostridium acetobutylicum

C,Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 14-Sep-2001

C;Accession: G97132
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Daly, M.J.; Bennett, G.J. 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clos A;Reference number: A96900; MUID:21359325; PMID:21359325

A,Accession: G97132 A,Status: preliminary A,Molecule type: DNA A,Residues: 1-306 <KUR> A,Cross-references: GB:AE001437, PIDN:AAX79850.1, PID:gl5024866, GSPDB:GN00168 A,Experimental source: Clostridium acetobutylicum ATCC824

A;Gene: CAC1886

Gaps ; 0 Score 46; DB 2; Length 306; Pred. No. 0.98; 1; Mismatches 0; Indels Query Match
Best Local Similarity 87.5%;
Matches 7; Conservative

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|||||||||| 117 YYRYGVIY 124 4 YYRYGVVY 11 임 ò

## RESULT 2 E72242

Mg-protoporphyrin IX monomethyl ester oxidative cyclase-related protein - Thermotoga mari C;Species: Thermotoga maritima C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 01-Mar-2002

C;Accession: E72242 R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;

Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seque, A;Reference number: A72200; MUID:99287316; PMID:10360571

A;Recession: E7242

A;Status: preliminary

A;Molecule type: DNA...

A;Residues: 1-441 <ARN>
A;Cross-references: GB:AE001800; GB:AE000512; NID:g4982090; PIDN:AAD36604.1; PID:g4982104
A;Experimental source: strain MSB8
C;Genetics:

Genetics: Gene: TM1537

C; Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0865

63.9%; Score 39; DB 2; Length 441; Query Match

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C;Accession: D71602
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.; Fertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.; Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743; PMID:9804551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GB:AE001362; NID:g3845316; PIDN:AAC71978.1; PID:g3845315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                     hypothetical protein PFB0945w - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000|
C;Accession: T18417
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
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Pred. No. 1.3e+02;
4; Mismatches 0;
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A;Molecule type: DNA
A;Residues: 1-1411 <LAW>
A;Cross-references: EMBL:297348; PIDN:CAB10571.2
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68;
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submitted to the EMBL Data Library, July 1997
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submitted to the BMBL Data Library, July 1997
A;Reference number: Z18934
A;Accession: T18418
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Pred. No. 6
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50.0%;
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A, Cross-references: GB: AE001428;
A, Experimental source: clone 3D7
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Best Local Similarity 50.0
Matches 4; Conservative
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188 FYKYGIIY 195
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A;Accession: T18417
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858 FYKYGIIY 865
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Best Local Similarity
Matches 4; Conserva
                                       3 AYYRYGV
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A;Introns: 54/3; 78/1; 97/3; 123/1; 149/1; 178/2; 262/3; 301/2; 374/1; 384/3; 419/1; 455
C;Superfamily: Agrobacterium beta-glucosidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Я
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Bubmitted to the BMBL Data Library, May 1998
A;Description: Arabidopsis thaliana chromosome II BAC F411 genomic sequence.
A;Reference number: 214667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.Resdiudes: 1.517 cROU>
A.GCOSS-references: BMBL:AC004521; NID:g3128166; PIDN:AAC16094.1; PID:g3128190
A.Experimental source: cultivar Columbia
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C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
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C;Superfamily: unassigned tetratricopeptide repeat proteins; tetratricopeptide repeat
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A;Molecule type: DNA
A;Residues: 1-1389 - LYIN>
A;Residues: 1-1389 - LYIN>
A;Cross-references: EMBL:AL035075; PIDN:CAA22636.1; GSPDB:GN00068; SPDB:SPCC1919.05
A;Experimental source: strain 972h-; cosmid c1919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A; Reference number: A84420; MUID: 20083487; PMID: 10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Cross-references: GB:AE002093; NID:g3128190; PIDN:AAC16094.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                    probable beta-glucosidase At2g44480 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 02-Feb-2001 C;Accession: T02403; A8489
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Pred. No. 86;
1; Mismatches 0; Indels
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Pred. No. 31;
1; Mismatches 2; Indels
                                       Indels
   Pred. No. 26;
0; Mismatches
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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Best Local Similarity 85.7%;
Matches 6; Conservative
   70.0%;
Similarity 70.07; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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477 GYKYRYGLVY 486
                                                                                                                 2 GAYYRYGVVY 11
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A;Molecule type: DNA
A;Residues: 1-517 <STO>
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   Best Local
Matches
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Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein XP2400 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: H82561
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Atture 406, 151-157, 2000
A;Title: The genome. sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Status: preliminary
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C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C;Accession: B69657
R;Kunst, F: Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd A.; Entich, S.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
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                                       A; Residues: 1-1417 <LAM>
A; Residues: 1-1417 <LAM>
A; Cross-references: EMBL: 297348; PIDN: CABI0572.2
Genetics: A; Genetics: A; A10trons: 286/1; 478/1; 496/1; 517/1; 554/1; 616/1; 669/1; 924/3
A; Note: C0120w
C; Superfamily: Plasmodium falciparum hypothetical protein C0120w
                                                                                                                                                                                                                Length 1417;
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                                                                                                                                                                                       Score 38; DB 2; Length 131.
Pred; No. 1.36+02;
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A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
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Pred. No. 28;
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50.0%;
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50.0%;
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Matches 4; Conservative
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A.Contents: annotation
C.Genetics:
A.Gene: XF2400
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GAFISYGIIY 37
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861 FYKYGIIY 868
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A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A;Authors: Schleich, S.; Schrocher, R.; Scoffone, B.; Sekiguchi, J.; Sekowska, A.; Scror, Akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpefra, P.; Tognoni, J.; Sekowska, A.; Seror, A;Authors: Voshikawa, H.F.; Zumstein, B.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Uchiyama, A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A;Reference number: A69580; MuID:98044033; PMID:9384377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NyAlternate names: polycationic biosilica-associated protein; silica-precipitating polype NyContains: silaffin 1A; silaffin 1B C;Species: Cylindrotheca fusiformis C;Species: Cylindrotheca fusiformis C;Date: 11.Jan-2000 #sequence revision 11.Jan-2000 #text_change 11.Jan-2000 C;Accession: A59141; B59141; C59141 R;Kroeger, N.; Deutzmann, R.; Sumper, M. Science 25, 1129-1132, 1999 A;Title: Polycationic peptides from diatom biosilica that direct silica nanosphere format A;Reference number: A59141; MUID:20018323; PMID:10550045
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C;Keywords: cell wall; methylated amino acid
C;Keywords: cell wall; methylated amino acid
F;1-19/Domain: signal sequence #status predicted <PRO>
F;0-107/Domain: propeptide #status predicted <PRO>
F;108-265/Product: silaffin sil1p #status predicted <WAT>
F;110,121/Modified site: N6.N6-dimethyllysine (Lys) #status predicted
F;111,122/Modified site: N6-methyl-No-poly(N-methyllysine (Lys) #status prec
F;13,165,184,203,222,241/Modified site: N6-methyl-N6-poly(N-methyl-propylamine)lysine (I)
F;144,166,185,204,223,242/Modified site: N6-methyl-N6-poly(N-methyl-propylamine)lysine (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:Z99115; GB:AL009126; NID:g2634478; PIDN:CAB14109.1; PID:g2634611
A;Experimental source: strain 168
C;Genetics:
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A;Molecule type: DNA
A;Residues: 1-224 <KUN>
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A;Rossidues: 1-265 <-KRO1>
A;Cross-references: GB:ART)91634; NID:g6561486; PIDN:AAF16940.1; PID:g6561487
A;Note: submitted to GenBank, October 1999
A;Notession: B59141
A;Molecule type: protein
A;Rossidues: 141-150 <-KRO2>
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A, Status: not compared with conceptual translation
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C;Superfamily: homoserine succinyltransferase
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Pred. No. 3
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A; Molecule type: protein
A; Residues: 108-120 < KRO3> C; Genetics:
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us-10-007-790-7.rpr

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7-108/Domain: EGF homology <EG1>
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Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity
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plasma hyaluronan-binding protein precursor - mouse
C;Spate: 11-Mar-1998 #sequence_revision 11-Mar-1998 #text_change 16-Jul-1999
C;Accession: JC5878
Fylashinoto, K; Tobe, T; Sumilya, J; Saguchi, K; Sano, Y; Nakano, Y; Choi-Miura, N. Biol. Pharm. Bull. 20, 1127-1130, 1997
A;Title: Cloning of the cDNA for a mouse homologue of human PHBP: A novel hyaluronan-bin A;Reference number: JC5878; MJID:98055239; PMID:9401717
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R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin Nature 402, 769-777, 1999
                                                                                                                                                                                                                                                                                                                 A; Cross-references: EMBL: U28372; NID: 9849170; PID: 9849176; GSPDB: GN00004; MIPS: YDR352w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A,Reference number: A85001; MUID:20083488; PMID:10617198
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                                                       C;Species: Saccharomyces cerevisiae
C;Date: 23-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 19-Apr-2002
C;Accession: S61149
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C;Date: 16-Feb_2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
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    yeast (Saccharomyces cerevisiae)

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C;Superfamily: Saccharomyces probable membrane protein YBR147w
C;Keywords: transmembrane protein
F;64-80/Domain: transmembrane #status predicted <TMM>
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                                                                                                                                                        submitted to the EMBL Data Library, June 1995
A;Description: The sequence of S. cerevisiae cosmid 9476.
A;Reference number: S61148
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85.7%; Pred. No. 52;
ive 1; Mismatches
Joilis.
Probable membrane protein YDR352w - yeast (Sacc)
N;Alternate names: hypothetical protein D9476.6
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Matches 6; Conserv
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Matches 6; Conserv
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A;Residues: 1-317 <DUZ>
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A;Molecule type: mRNA
A;Residues: 1-558 <HAS>
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A,Status: preliminary
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A;Gene: AT4g37210
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Gene: Gubinare, June, June, June, July 1962, J. Chains produced from the same precursor; the jourse-references: disulfide-bonded heterodimer of chains produced from the same precursor; the journally: plasma hyaluronan-binding protein; EGF homology; kringle homology; trypsir; Seywords: chondroitin sulfate proteoglycan; glycoprotein; hyaluronic acid; hydrolase; heavy and sequence #status predicted <210>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;314-516/Product: plasma hyaluronan-binding protein, catalytic chain #status predicted .
;47,207/Binding site: carbohydrate (Asn) (covalent) #status predicted
;77-88,82-97,99-108,115-125,120-136,138-147,154-165,159-176,178-187,194-276,215-257,246-
;362,405,509/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: A69196
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; E
                                                                                                                                                                                                                                               F;192-274/Domain: kringle homology <KRI>
F;312-558/Product: plasma hyaluronan-binding protein small chain #status predicted <MATS:
F;312-548/Domain: trypsin homology <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    te: parts of this sequence, including the amino ends of the mature chains, were deter
EGF homology; kringle homology; trypsir
    Superfamily: plasma hyaluronan-binding protein; EGF homology; kringle homology; trypsir; 1-23/Domain: signal sequence #status predicted <SIG>;1-23/Domain: signal sequence #status predicted <SIG>;24-311/Product: plasma hyaluronan-binding protein large chain #status predicted <MATL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   noi-Miura, N.H.; Tobe, T.; Sumiya, J.; Nakano, Y.; Sano, Y.; Mazda, T.; Tomita, M.
Siochem. 119, 1157-1165, 1996
.tle: Purification and characterization of a novel hyaluronan-binding protein (PHBP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Toomain: signal sequence #status predicted <SIG>
13/Product: plasma hyaluronan-binding protein, 50K chain #status predicted <50K>
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;Date: 15-Oct-1995 #sequence_revision 16-Aug-1996 #text_change 19-Jul-2002
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C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Residues: 1-560 <CHO>
Cross-references: GB:S83182; NID:g1836158; PIDN:AAB46909.1; PID:g1836159
Experimental source: plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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77;
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Pred. No. 77;
1; Mismatches
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Pred. No.
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                                                                                                              F;75-106/Domain: EGF homology <EG1>F;113-145/Domain: EGF homology <EG2>F;152-185/Domain: EGF homology <EG3>
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C;Accession: A56724
Rycht, S.; Newman-Silberberg, F.S.; Barcelo, G.; Schuepbach, T.
Cell 81, 967-978, 1995
A;Title: cornichon and the EGF receptor signaling process are necessary for both anterion
A;Reference number: A56724; MUID:95300228; PMID:7540118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: E71869 F. F. Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Irves, C.C.; Gibson, R.; Marberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; 7 Nature 397, 176-180, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:AF036693; PIDN:AAB88331.1; GSPDB:GN00022; CESP:C49A9.7
A;Experimental source: strain Bristol N2; clone C49A9
                                                                                                                                                                      C;Spēcies: Drosophila melanogaster
C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein C49A9.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 20-Apr-2000
C:Accession: T32517
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C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                          A,Molecule type: mRNA
A,Residues: 1-144 <ROT>
A,Cross-references: GB:U28069; NID:g886768; PIDN:AAA86527.1; PID:g886769
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A;Introns: 21/3; 84/2; 128/2; 159/2; 199/3; 233/2; 263/3; 347/2
C;Superfamily: neurokinin 1 receptor
                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary; not compared with conceptual translation
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Pred. No. 80;
0; Mismatches 2; Indels
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A; Accession: T32517
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A;Molecule type: DNA
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Pred. No. 29;
                                                                                                                                                  cni protein - fruit fly (Drosophila melanogaster)
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C, Superfamily: Drosophila cornichon protein
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Best Local Similarity 77.8%;
Matches 7; Conservative
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132 YYIYGMVY 139
              644 YYRFGOVY 651
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Best Local Similarity
Matches 6; Conserv
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C;Species: Homo. sapiens (man)
C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Apr-1998
C;Accession: 870029
R;Lissy, N.A.; Bellacosa, A.; Sonoda, G.; Miller, P.D.; Jhanwar, S.C.; Testa, J.R.
B;cotim. Biophys. Acta 1306, 1137-141, 1996
A;Title: Isolation, characterization, and mapping to human chromosome 11q24-25 of a cDNA
A;Reference number: 870029; MUID:96221283; PMID:8634329
i Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. A. Bacteriol. 179, 7135-7155, 1997
A; Fitle: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A; Reference number: A69000; MUID: 98037514; PMID: 9371463
A; Accession: A69196
A; Molecule rype: Draininary; nucleic acid sequence not shown; translation not shown A; Residues: 1-574 ATHA
                                                                                                                                                                                                                                                         A;Cross-references: GB:AE000851; GB:AE000666; NID:g2621803; PIDN:AAB85224.1; PID:g262180
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C;Date: 09-bec-1993 #sequence_revision 10-Nov-1995 #text_change 15-Oct-1999
C;Accession: S37439
R;Metzger, M.
submitted to the EMBL Data Library, September 1993
A;Reference number: S37439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:226486; NID:g403308; PIDN:CAA81260.1; PID:g403309 C;Superfamily: transketolase; thiamin pyrophosphate-binding domain homology C;Keywords: transferase F;144-194/Domain: thiamin pyrophosphate-binding domain homology <TPB>
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A;Residues: 1-705 <LIS>
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 574;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
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Pred. No. 79;
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54.5%;
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Best Local Similarity 54.5
Matches 6; Conservative
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les 7; Conservative
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Best Local Similarity 75.0
Matches 6; Conservative
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SGGWYRHGRLY 514
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Best Local Similarity 60.0
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155 GYYYAYPVIY 164
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Residues: 2-36 <NIX>
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Molecule type: DNA
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A, Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A, Reference number: A71800, MUID:99120557, PMID:9923682
A, Accession: E71869
A, Status: prefinnary
A, Molecule type: DNA
A, Residues: 1-421 < ARN>
                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE001523; GB:AE001439; NID:g4155513; PIDN:AAD06515.1; PID:g415551
A;Experimental source: strain J99
C;Genetics:
A;Gene: jhp0937
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A;Experimental source: serogroup O1; strain N16961; biotype El Tor
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A;Gene: all0390
C;Superfamily: Escherichia coli plasmid ColV-K30 aerobactin biosynthesis protein iucC
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A;Experimental source: strain PCC 7120
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Pred. No. 1.2e+02;
1; Mismatches 0; Indels
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235 AFFNYGIIY 243
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YRYGVVF 414
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-597 <HE
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Map position:
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Species: Saccharomyces cerevisiae

Spaces 31. Mar. 1933 #sequence revision 25. Apr. 1997 #text_change 21-Jul-2000

Spaces sion: A9510; S54095; S59062; A42084; S21067; S74183; S7409

Sundstroem, M.; Lindqvist, Y.; Schneider, G.; Hellman, U.; Ronne, H.

Balol. Chem. 268, 24346-24352, 1993

Spaces TKLI gane encodes a transketolage that is required for efficient glycolysisterence number: A49510; MUID:94043273; PMID:8226984
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;Cross-references: EMBL:Z49219; NID:g805025; PIDN:CAA89191.1; PID:g805054; GSPDB:GN00016
;Experimental source: strain AB972
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Residues: 1-680 <COU>; Accession: ALD: 91230676; PIDN:AAB68125.1; PID: 91230682; GSPDB:GNO0(
; Residues: 1-680 <COU>; Residues: 1.680 <COUS;
; Fletcher, T.S.; Kwee, I.L.; Nakada, T.; Largman, C.; Martín, B.M.
iochemistry 31, 1892-1896, 1992
ithle: DNA sequence of the yeast transketolase gene.
; Reference number: A42084; MUID:92144611; PMID:1737042
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Molecule type: DNA
Molecule type: DNA
Molecule type: DNA
Molecule type: J.36, "RS', 39-44, "GESNAHEPNQPKTGSTEIDLSCLTVTRSLCCIY", 78-135, "DMPLTTSRA", 144-2:
WSPOKULKELKRPLHSIRVTS' <FLE>
"SCOSS-references: GB:M63302
MNIXON, P.F.; Duggleby, R.G.
MNIXON, P.F.; Duggleby, R.G.
Title: The N-terminal amino acid sequence of yeast transketolase.
"Title: The N-terminal amino acid sequence of yeast transketolase.
"Reference number: S21067; MUID:92253546; PMID:1812485
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Residues: 181-187;209-213;368-373;104-105 <KOV>
Comment: The active enzyme catalyzes the transfer of a keto group to an aldehyde accept
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transketolase (EC 2.2.1.1) TKL1 - yeast (Saccharomyces cerevisiae)
N;Alternate names: glycolaldehydetransferase; protein YP9499.29c; protein YPR074c
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A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: EMBL:X73224; NID:g404200; PIDN:CAA51693.1; PID:g404201
A;Cross-references: EMBL:X73224; NID:g404200; PIDN:CAA51693.1; PID:g404201
St. Badcock, K.; Churcher, C.M.
Submitted to the EMBL Data Library, May 1995
A;Reference number: S54059
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Score 36; DB 2; Length 597;
Pred. No. 1.2e+02;
1; Mismatches 3; Indels
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FBS Lett. 392, 293-294, 1996
FITTLE: Localization of reactive tyrosine residues of k.
Reference number: S74183; MUID:96371030; PMID:8774865
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A;Cross-references: SGD:S0006278; MIPS:YPR074c
A;Map position: 16R
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Length 2697;

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59.0%; Score 36; DB 2; Ler
                                                100.0%; Pre
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5 GAYYRFRLV 13
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Best Local Similarity
Matches 6; Conserv
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A; Residues: 1-128 <GLA>
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G96586.
hypothetical protein F20D21.30 [imported] - Arabidopsis thaliana
C.Species: Arabidopsis thaliana (mouse-ear crees)
C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C.Accession: 036586
C.Hoclogis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 409, 81-6820, 2000
A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A.Reference number: A86141; MUID:21016719; PMID:11130712
A.Scession: 036586
A.Status preliminary
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A;Introns: 41/3; 75/2; 173/3; 283/3; 354/2; 374/3; 432/2; 470/2; 569/3; 607/3; 667/1;
1/3; 2282/3; 2337/3; 2516/2; 2562/3; 2652/1
C;Superfamily: yeast TOR2 protein
                         A;Pathway: pentose phosphate pathway
C;Superfamily: transketolase; thiamin pyrophosphate-binding domain homology
C;Seywords: homodimer; magnesium; pentose phosphate pathway; thiamin pyrophosphate;
F;2-680/Product: transketolase #status experimental <MAT>
F;146-196/Domain: thiamin pyrophosphate-binding domain homology <TPB>
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A;Cross-references: GB:AE005173; NID:g4585991; PIDN:AAD25627.1; GSPDB:GN00141
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A;Experimental source: strain Bristol N2; clone B0261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein B0261.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;bate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T25440, S.
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                                                                                                                                                                                    Length 680
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Pred. No. 2e+02;
                                                                                                                                                                                                                               2; Indels
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A;Bescription: The sequence of C. elegans cosmid B0261.
A;Reference number: Z20036
A;Recession: T25444
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                            / Match 59.0%; Score 36; DB 1; I
Local Similarity 66.7%; Pred. No. 1.4e+02;
Hes 6; Conservative 1; Mismatches 2,
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Matches 7; Conservative
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A;Gene: F20D21.30
A;Map position: 1
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A;Cross-references: GB:J02459; GB:M17233; GB:M24325; GB:V00636; GB:X00906; NID:g215104; E
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A,Authore: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Matok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A,Reference number: AB1077; MUID:21537279; PMID:11679669
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A;Experimental source: strain EGD-e
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                                                                                                                                                                                                                                                                                                                              hypothetical protein B-64 - phage lambda
C;Species: phage lambda
C;Date: 13-Jun-1983 #sequence revision 13-Jun-1983 #text_change 10-Sep-1999
C;Accession: H43011; D43017; Ā04398
R;Daniels, D.
submitted to the Nucleic Acid Sequence Database, September 1982
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
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A.Reference number: A94614
A.Reference number: A94614
A.Rocession: H43011
A.Rolecule type: DNA
A.Residues: 1-64 -CAN>
A.Residues: 1-64 -CAN>
A.Residues: 1-64 -CAN>
A.Rocession: DNA
A.Residues: 1-64 -CAN>
A.Residues: 1-64 -CAN>
A.Residues: 1-64 -CAN>
A.Residues: 1-64 -CAN>
A.Residues: 1-64 -CAN>
A.Rocession: D43017
A.Residues: 1-64 -CAN>
A.Residues: 1-64 -CAN>
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A,Map position: 92.00-92.39
C,Superfamily: phage lambda hypothetical 7.1K protein (nin region)
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Indels

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conserved hypothetical protein yids (imported) - Lactococcus lactis subsp. lactis (strain C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
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R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlic Benome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis signature and A;Reference number: A86625; WUID:21235186; PMID:11337471
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A;Reaidudes: 1-255 <570-
A;Crosa-references: GB:AE005176; PID:g12723433; PIDN:AAK04646.1; GSPDB:GN00146
A;Experimental source: strain IL1403
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A;Molecule type: DNA
A;Residues: 1-204 - ADDS-
A;Cross-references: EMBL:AF016485; NID:92822278; PID:92822382; HALOSP:H1243
A;Experimental source: strain NRC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical.protein C36B1.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T19775
                                                                                                                                                                                                                                A;Genome: plasmid pNRC100
C;Superfamily: Halobacterium plasmid pNRC100 hypothetical protein H1243
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                                                                                                                                                                                                                                                                                                                                                DB 2; Length 204;
62;
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A;Introns: 33/3; 117/3; 216/3
C;Superfamily: multicatalytic endopeptidase complex chain C9
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A;Molecule type: DNA
A;Residues: 1-253 <WIL>
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Pred. No. 78;
0; Mismatches
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Pred. No. 78;
0; Mismatches
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A.Reference number: 219176
A.Accession: T19775
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Best Local Similarity 85.7%;
Matches 6; Conservative
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Best Local Similarity 85.7%;
Matches 6; Conservative
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Matches 6; Conservative
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                                                                                                                                                    C;Genetics:
A;Gene: HALOSP:H1243
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T08321
hypothetical protein H1243 [imported] - Halobacterium sp. (strain NRC-1) plasmid pNRC100
C;Species: Halobacterium sp.
A;Variety: strain NRC-1
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 03-Nov-2000
C;Accession: T08321
R;Ng, W.V.; Ciufo, S.A.; Smith, T.M.; Bumgarner, R.E.; Baskin, D.; Faust, J.; Hall, B.;
Genome Res. 8, 1131-1141, 1998
A;Titles: Snapshot of a large dynamic replicon in a halophilic Archaeon: megaplasmid or m
A;Reference number: Z16408; WUID:99063795; PMID:9847077
                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, December 1994
A;Description: The sequence of S. cerevisiae cosmids 9781, 8198, 9115, 9981, and lambda
A;Reference number: S50437
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A;Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:U18916; NID:g1384128; PID:g603374; GSPDB:GN00005; MIPS:YER135c
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T16672
R;Wilcox, L.
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                                                                                                                                                    C'Species: Saccharomyces cerevisiae
C'Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 19-Apr-2002
C'Accession: S50638
R'Dietrich, F.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35; DB 2; Length 130;
Pred. No. 39;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57.4%; Score 35; DB 2; Length 147; 55.6%; Pred. No. 44; tive 2; Mismatches 2; Indels

    yeast (Saccharomyces cerevisiae)

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C;Superfamily: Saccharomyces hypothetical protein YER135c
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Best Local Similarity 55.6%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Gene: MIPS:YER135c
A,Cross-references: SGD:S0000937
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                                                                                                                    hypothetical protein YER135c
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117 NGVYYEYGL 125
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GEYYRYSIL 50
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les 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S50638
A; Molecule type: DNA
A; Residues: 1-130 <DIE>
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A;Introns: 36/1; 82/3
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R'Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran Nucleic Acids Ree. 28, 4317-4331, 2000
Affitle: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and c. A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1.374 <STO>
A;Cross-references: GB:AP001508; GB:BA000004; NID:g10172890; PIDN:BAB04071.1; GSPDB:GN001
A;Experimental source: strain C-125
                                                                                                      A)Cross-references: EMBL:X82183; NID:g5S8630; PIDN:CAAS7673.1; PID:g5S8631
C;Genetics:
A;Genetics:
A;Genetics:
C;Genetics:
C;Superfamily: recombination protein rech
C;Superfamily: recombination protein rech
C;Keywords: ATP; DNA binding; DNA recombination; DNA repair; nucleotide binding; P-loop;
F;78-88-85/Region: nucleotide-binding motif B
F;84/Binding site: ATP (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references: EMBL:Z83240; PIDN:CAB05813.1; GSPDB:GN00019; CESP:T23H4.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T25209
R;Matthews, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C,Species: Bacillus halodurans
C,Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               carboxypeptidase G2 BH0352 [imported] - Bacillus halodurans (strain C-125)
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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A;Introns: 26/2; 64/3; 94/1; 115/2; 147/3; 216/3; 275/3; 317/1; 348/1
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                                                                                                                                                                                                                                                                                                                                             Score 35; DB 2; Length 355;
Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
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A;Reference number: 219996
A;Accession: T25209
                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                h 57.4%;
Similarity 75.0%;
6; Conservative
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21 SGSYYKEGV 29
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                                 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-355 <FER>
                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 6; Conserv
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Matches 6; Conserv
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A; Residues: 1-392 <WIL>
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        A:Accession: S49464
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C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: A72780
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; BDNA Res. G. 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: EMBL: AL022288; PIDN: CAA18370.1; GSPDB: GN00019; CESP: ZK1025.3
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A;Residues: 1-344 «KAW»
A;Cross-references: DDBJ:AP000058; NID:g5103388; PIDN:BAA79139.1; PID:g5103618
                                                                                                                                                          C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Jun-2001
C;Accession: T27656
R;Lennard, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Rhodobacter capsulatus
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 02-Feb-2001
C;Accession: S49464
R;Fernandez de Henestrosa, A.R.
submitted to the EMBL Data Library, October 1994
A;Reference number: S49464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Introns: 100/3; 212/1
C;Superfamily: Caenorhabditis elegans hypothetical protein F49C12.2
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60.0%; Pred. No. 1.18+02;
Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                    - Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-338 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 35; DB 2;
Pred. No. 1e+02;
0; Mismatches
                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, March 1998
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A,Gene: APE0227
C,Superfamily: rat ribosomal protein L3
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Experimental source: clone ZK1025 C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57.4%;
75.0%;
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Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                        T27656
hypothetical protein ZK1025.3
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Matches 6; Conservative
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283 AGGFLRYGVV 292
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A;Accession: T27656
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107 AYYEYGV 113
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A;Status: preliminary
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Search completed: July 18, 2003, 15:10:44 Job time : 15.3 secs
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A;Molecule type: DNA
A;Residues: 1-770 <STO>
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A; Residues: 1-399 <RES.
A; Cross-references: GB:LO957; NID:g825647; PIDN:AAA67125.1; PID:g567213
A; Cross-references: GB:LO8757; NID:g825647; PIDN:AAA67125.1; PID:g567213
B; Singh, G; Kaur, S; Stock, J.L.; Jenkins, N.A.; Gilbert, D.J.; Copeland, N.G.; Potter
Proc. Natl. Acad. Sci. U.S.A. 88, 10706-10710, 1991
Proc. Natl. Acad. Sci. U.S.A. 88, 10706-10710, 1991
A; Title: Identification of 10 murine homeobox genes.
A; Reference number: A37290; MUID:92073356; PMID:1683707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Jun-2001
C;Accession: T20439
R;Dobson, R.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19276
A;Accession: T20439
A;Status: preliminary; translated from GB/EMBL/DDBJ
    Gaps
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A;Molecule type: DNA
A;Residues: 346-370 «MUR»
A;Cross-references: GB:M81659; NID:g193973; PIDN:AAA63312.1; PID:g193974
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A;Introns: 165/3; 277/1
C;Superfamily: Caenorhabditis elegans hypothetical protein F49C12.2
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C;Superfamily: unassigned homeobox proteins; homeobox homology
         Indels
              4,
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         Mismatches
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Best Local Similarity 75.0%;
Matches 6; Conservative
         6; Conservative
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                                                                                              1 SGAYYRYGVVY 11
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         Matches
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Rilin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.: Causs, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A;Reference number: A84420; MUID:20083487; PMID:10617197
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C;Genetics:
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C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: H84463
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C;Keywords: DNA binding; homeobox; nucleus; transcription regulation F;326-382/Domain: homeobox homology <HOX>
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C,Superfamily: Arabidopsis thaliana hypothetical protein T21L8.10
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Pred. No. 2.5e+02;
0; Mismatches 3; Indels
                                                                                                        Length 399
                                                                                                    Query Match 57.4%; Score 35; DB 2; I
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 3.
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Best Local Similarity 70.0%;
Matches 7; Conservative
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July 18, 2003, 15:01:44; Search time 37.18 Seconds (without alignments) 39.423 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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/SIDS2/gcgdata/geneseq/geneseqp-embl/
/SIDS2/gcgdata/geneseq/geneseqp-embl/
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/SIDS2/qcgdata/geneseq/geneseqp-emb]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 908470 segs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /SIDS2/gcgdata/geneseg/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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61
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					COLUMNITO	
Result		שים קים גים				
No.	Score	Match	Match Length DB	DB	. QI	Description
1	61	100.0	11	21	AAY87659	Murine PIP3 recogn
8	61	100.0	124	21	AAY87655	Murine PIP3 recogn
e	43	70.5	122	22	AAG80211	Human autoantibody
4	40	9.59	19	20	AAY33030	Carbohydrate antiq
S	40	65.6	398	20	AAY34559	Porphorymonas ging
9	40	65.6	400	20	AAY34558	Porphorymonas ging
7	40	65.6	412	20	AAY34422	Porphorymonas ging
œ	40	65.6	1805	22	ABB65262	Drosophila melanog
6	39	63.9	20	20		Carbohydrate antig
10	38	62.3	.740	21	AAB18330	Plasmodium falcipa

Claim 9; Page 13; 15pp; Japanese

	Plasmodium falcipa			Plasmodium falcipa	Human novel foetal	tat			Human ORFX ORF2248	Human blood coagul	Human blood coagul	Human BLyS binding	Human heavy chain	Human ORFX protein	ě	pk65_4 secreted pr	cornichon	14	ne ne	Human PRO181 (UNQ1				Human polypeptide,	Human lung tumour	Human angiogenesis		Clone #19110 of lu	Human PRO181 prote		secr	human secre	n reco	-
AAW46499	AAY31948	AAY31947			AAU20895	AAB32986		AAG41345	AAB42484	4	AA017145	ABP47134	AAE07014	ABP10506	AAY53622	AAY28813	AAY41306	AAY41732	AAY32925	AAB44288	AAB19524	ABB61865	ABB61866	AAM93330	AAB76851	ABB95423	AAE20143	AAU85506	81			61	AAY85635	
19	20	20	20	20	22	21	21	21	21	23	23	23	22	23	21	20	20	20	20	21	21	22	22	22	22	23	23	23	23	23	20	22	22	23
981	1411	1417	1430	4134	104	158	384	499	260	260	260	19	128	139	142	144	144	144	144	144	144	144	144	144	144	144	144	144	144	144	145	148	241	241
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38	38	38	38	38	37	37	37	37	37	37	37	36	36	36	36	36	36	36	36	36	36		36											
11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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PIP3; phosphatidylinositol-3,4,5-triphosphate; variable region; CDR3; immunogen; antibody; heavy chain; complementarity determining region.
                                                            Murine PIP3 recognizing Mab variable region heavy chain CDR3 region.
                                                                                                                                                                                                                                                                              A monoclonal antibody recognizing phosphatidylinositol-3,4,5-triphosphate
                                                                                                                                                                                                                         (FUKU/) FUKUI Y.
(IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.
AAY87659 standard; Protein; 11 AA.
                                                                                                                                                                                98JP-0252921.
                                                                                                                                                                                                     98JP-0252921
                                         11-AUG-2000 (first entry)
                                                                                                                                                                                                                                                         WPI; 2000-353334/31.
                                                                                                                                      JP2000083664-A.
                                                                                                                                                                                                     07-SEP-1998;
                                                                                                                                                                                07-SEP-1998;
                                                                                                                                                            28-MAR-2000
                    AAY87659;
                                                                                                                   Mus sp.
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This invention describes a novel antibody specifically recognizing phosphatidylinositol-3,4,5-triphosphate (PIP3). The antibody of the invention is used in immunogenic compositions in which a dead salmonella genus microbe is used as an adjuvant and mixed with PIP3. The antibody can be used in an immunoassay containing a step in which the above antibody or its variable region is reacted with PIP3 present in a sample and the bond based on their immunological reaction. The method can determine PIP3 easily in a high sensitivity. This sequence represents the mutine PIP3 recognizing monoclonal antibody variable region heavy chain complementarity determining region, CDR3 described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel antibody specifically recognizing phosphatidylinositol-3,4,5-triphosphate (PIP3). The antibody of the invention is used in immunogenic compositions in which a dead salmonella genus microbe is used as an adjuvant and mixed with PIP3. The antibody can be used in an immunoassay containing a step in which the above antibody or its variable region is reacted with PIP3 present in a sample and the bond based on their immunological reaction. The method can determine PIP3 easily in a high sensitivity. This sequence represents the murine PIP3 recognizing monoclonal antibody variable region heavy
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murine PIP3 recognizing Mab variable region heavy chain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIP3; phosphatidylinositol-3,4,5-triphosphate; variable region; immunogen; antibody; heavy chain.
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                                                                                                                                                                                                                                                    100.0%; Score 61; DB 21; Length 11; 100.0%; Pred. No. 0.00037; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the murine PIP3 recognizing monoclonal antibod
chain described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (FUKU/) FUKUI Y.
(IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A monoclonal antibody recognizing phosphatidylinositol-3,4,5-triphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY87655 standard; Protein; 124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 5; Page 11; 15pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98JP-0252921
                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.v.
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N-PSDB; AAA12202.
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                                                                                                                                                                                                                    11 AA;
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                                                                                                                                                                                   the invention.
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                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
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N-terminus, one or more epitopes that bind specifically to must, one of more epitopes that bind specifically to autoantibodies (Abb) against the islet cell antigen IA2 and, at its C-terminus, one or more epitopes that bind specifically to antibodies (Ab) directed against the glutamate decarboxylase GAD65. (I), also nucleic acid (II) encoding it, vectors containing (II) and transformed cells, are useful for diagnosis and prognosis of diabetes mellitus type I, stiff-man syndrome, polyglandular autoimmune syndrome or other autoimmune conditions associated with Abb against GAD65 or IA2. (I) provides a rapid and simple diagnosis of high specificity and sensitivity, capable of recognizing antibodies against both IA2 and GAD65, simultaneously. Unlike known fusions, where the GAD65 component is at the N-terminus, (I) contains correctly folded conformational epitopes that can react with most MICA autoantibodies. This sequence represents the human autoantibody MICA-3 variable region light chain used in the method of the invention.
                                                                                                                                                                                                                                                       Autoantigen, fusion protein, islet cell antigen, MICA autoantibody, glutamate decarboxylase, diabetes mellitus type I, stiff-man syndrome, polyglandular autoimmune syndrome, autoimmune disorder, IA2; GAD65; variable region, light chain, MICA-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New fusion protein, useful for diagnosis of diabetes type I and other metabolic diseases, is reactive with autoantibodies against both glutamate decarboxylase and islet cell antigen -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes a novel fusion protein (I) that has, at its
                                                                                                                                                                                                                      Human autoantibody MICA-3 variable region light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Xaa encoded by NAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dangel W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 28-29; 68pp; German.
                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                           AAG80211 standard; Protein; 122 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                             /label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LABO-) LABOR KOCH MERK GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-APR-2000; 2000DE-1017782.
25-MAY-2000; 2000DE-1025840.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-MAR-2001; 2001EP-0107702
99 SGAYYRYGVVY 109
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N-PSDB; AAI68760.
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Modified-site
                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP1149914-A2
                                                                                                                                                                                     22-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Richter W,
                                                                                                                                                AAG80211;
                                                                      RESULT 3
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Gaps

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Indels

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Score 43; DB 2 Pred. No. 6.1; 1; Mismatches

Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative

3 AYYRYGVVY 11

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Gaps

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100.0%; Score 61; DB 21; Length 124; 100.0%; Pred. No. 0.0051; ive 0; Mismatches 0; Indels (

Conservative

Query Match Best Local Similarity Matches 11; Conserv

DB 22; Length 122;

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Porphorymonas gingivalis; PG; periodontal disease; gingivitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antigenic Porphorymonas gingivalis peptides for preventing
                                                                                                                                                       Porphorymonas gingivalis protein PG84.
                                  AAY34559 standard; Protein; 398 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hocking DM,
Webb EA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98AU-0003338.
98AU-0003654.
98AU-0004917.
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                                                                                                              (first entry)
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Matches 7; Conservative
                                                                                                                                                                                                                                                     Porphorymonas gingivalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 252 SGAYYSYG 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Agius CT, Barr IG,
Ross BC, Rothel LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SGAYYRYG 8
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N-PSDB; AAX91777.
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22-MAY-1998;
29-JUL-1998;
                                                                                                                                                                                                                                                                                              WO9929870-A1
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                                                                                                                25-AUG-1999
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                                                                           AAY34559;
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                      AAY34559
RESULT
                                                                             This invention describes a novel method for preparing a peptide or recombinant antibody, which mimics an antigenic carbohydrate. The peptides and recombinant antibodies prepared to mimic antigenic carbohydrates can be used to enhance binding of anti-antigenic carbohydrates can be used to enhance binding of alliantigenic carbohydrate antibodies to the antigenic carbohydrate, e.g. as vaccine adjuvants. The peptides can be used to inhibit binding of a ligand to a receptor, which is an antigenic carbohydrate. The methods are used to prepare the peptides and antigenic antibodies, which mimic the antigenic carbohydrates. Carbohydrate-conjugate vaccines could be used in tumour in munity and cancer therapy. The peptides and antibodies can also be used as antibacterials. Peptides that mimic carbohydrate antigens can be formulated to develop a longer lasting immune response. Other advantages of the peptides can be precisely defined, (2) the immunogenicity of the peptides can be significantly enhanced by polymerization or addition or relatively small carrier molecules that reduce the total
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amount of antigen required for immunization, (3) peptide synthesis may be more practical than synthesis of carbohydrate-protein conjugates or the production of anti-idiotypes; (4) peptide mimicking sequences can be engineered into DNA plasmids for DNA vaccination to further manipulate T cell responses. AXY33028-Y33087 represent the carbohydrate antigen peptide mimotopes described in the invention.
                                                                                                                                                                                                                                                                       Mimotope, antigen, carbohydrate, antibody, mimic, vaccine, adjuvant, tumour immunity, cancer therapy, antibacterial, immune response, immunogenicity, anti-idiotype, T cell response manipulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptides and recombinant antibody mimics of carbohydrate antigens, used for, e.g. treatment of cancer and infection
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                                                                                                                                                                                                                                  Carbohydrate antigen peptide mimotope 3.
                                                                                                                AAY33030 standard; peptide; 19 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 21; Page 70; 88pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US02405.
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                                                                                                                                                                                         03-NOV-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYPE-) UNIV PENNSYLVANIA
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                102 AYYRYGYLY 110
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ses 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                     AAY33030;
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Matches
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Margetts MB,

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                                                                                    Porphorymonas gingivalis (PG) polypeptide sequences given in AAY34318 to AAY34583. AAX91802 to AAX91989 represent PCR primers used in the isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease especially gingivitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                 AAX91536 to AAX91801 encode two hundred and sixty six antigenic
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Claim 1; Page 552-553; 588pp; English.
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ID AAY3
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AC AAY3
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DT 25-P
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AAX91536 to AAX91801 encode two hundred and sixty six antigenic Porphorymonas gingivalis (PG) polypeptide sequences given in AAX34318 to AAX34583. AAX91802 to AAX91989 represent PCR primers used in the isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease especially gingivitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                 Antigenic Porphorymonas gingivalis peptides for preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster polypeptide SEQ ID NO 22578.
                                                                                                                                                                                                                                                                                                        Hocking DM, Margetts MB,
Webb EA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB65262 standard; Protein; 1805 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 395; 588pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65.6%;
87.5%;
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                                                                       98WO-AU01023
                                                                                                                                                     98AU-0001546
                                                                                                                                                                                                                98AU-0003338
98AU-0003654
                                                                                                                       97AU-0000839
                                                                                                                                    97AU-0001182
                                                                                                                                                                     98AU-0002264
                                                                                                                                                                                                  98AU-0003128
                                                                                                                                                                                                                                           98AU-0004917
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Best Local Similarity 87.5
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      266 SGAYYSYG 273
                                                                                                                                                                                                                                                                                                        Agius CT, Barr IG,
Ross BC, Rothel LJ,
                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-385613/32
N-PSDB; AAX91640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                412 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SGAYYRYG
                                                                                                                                                                                                                                                                           (CSLC-) CSL LTD.
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              WO9929870-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAR-2002
                                                                          10-DEC-1998;
                                                                                                                                                                                                                                             29-JUL-1998;
                                          17-JUN-1999
                                                                                                                                                       30-JAN-1998
                                                                                                                                                                  10-MAR-1998
09-APR-1998
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05-MAY-1998
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                                                                                                                                     31-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                 gingivitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB65262;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Porphorymonas gingivalis (FG) polypeptide sequences given in AAY34318 to AAY34831. AAX51802 to AAX9189 repersent PCR primers used in the isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX91536 to AAX91801 encode two hundred and sixty six antigenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PG; periodontal disease; gingivitis;
                                          Porphorymonas gingivalis; PG; periodontal disease; gingivitis;
                                                                                                                                                                                                                                                                                                                                                                                                                  Patterson MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40; DB 20; Length 400; Pred. No. 73; 0; Mismatches I; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antigenic Porphorymonas gingivalis peptides for
                                                                                                                                                                                                                                                                                                                                                                                                                  Margetts MB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Porphorymonas gingivalis protein PG84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 551-552; 588pp; English
               Porphorymonas gingivalis protein PG84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY34422 standard; Protein; 412 AA
                                                                                                                                                                                                                                                                                                                                                                                                               Hocking DM,
Webb EA;
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98AU-0004917
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Porphorymonas gingivalis
                                                                                          Porphorymonas gingivalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           especially gingivitis:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGAYYSYG 261
                                                                                                                                                                                                                                                                                                                                                                                                                 Barr IG,
Rothel LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGAYYRYG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-385613/32
                                                            vaccine; antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         400 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccine; antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAX91776
                                                                                                                                                                                                                                                                                                                                                                                    (CSLC-) CSL LTD.
                                                                                                                       WO9929870-A1
                                                                                                                                                                                  10-DEC-1998;
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29-JUL-1998
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09-APR-1998
                                                                                                                                                                                                                                                                                                                         05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gingivitis
                                                                                                                                                                                                                                                                                                                                                                                                                 Agius CT,
                                                                                                                                                                                                                                                                                                                                                                                                                                 ковв ВС,
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BDT 25-
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XX BDE POR
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NAMES OF COLOR OF STREET O

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Gaps

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1; Indels

DB 20; Length 412; 76;

Patterson MA;

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This invention describes a novel method for preparing a peptide or recombinant antibody, which mimics an antigenic carbohydrate. The peptides and recombinant antibodies prepared to mimic antigenic carbohydrates can be used to enhance binding of anti-antigenic carbohydrate antibodies to the antigenic carbohydrate, e.g. as vaccine adjuvants. The peptides can be used to inhibit binding of a ligand to a receptor, which is an antigenic carbohydrate. The methods are used to prepare the peptides and antigenic arribodies, which mimic the antigenic carbohydrates. Carbohydrate-conjugate vaccines could be used in tumour immunity and cancer therapy. The peptides and antibodies can also be used as antibacterials. Peptides that mimic carbohydrate antigens can be formulated to develop a longer lasting immune response. Other advantages of the peptide mimics are; (1) the chemical composition and purity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                    manipulate T cell responses. AAY33028-Y33087 represent the carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                      be more practical than synthesis of carbohydrate-protein conjugates or
the production of anti-idiotypes; (4) peptide mimicking sequences can
be engineered into DNA plasmids for DNA vaccination to further
                                                                                                                                                                                                                                                                                                                                                                  amount of antigen required for immunization; (3) peptide synthesis may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium falciparum, chromosome 2; human malaria parasite; vaccine; antimalarial; malaria; protozoacide; infection; insecticide.
                                                                                                                                                                                                                                                                                                synthesized peptides can be precisely defined; (2) the immunogenicity of the peptides can be significantly enhanced by polymerization or addition or relatively small carrier molecules that reduce the total
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proteins encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of P.falciparum infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmodium falciparum chromosome 2 related protein SEQ ID NO:188.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antigen peptide mimotopes described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 422-424; 577pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gardner M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB18330 standard; Protein; 740 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GAYYRYGVVY 11
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Best Local Similarity
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CARUCCI D.
GARDNER M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VENTER J C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 AA;
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(CARU/)
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                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticidaes, therapeuticis and pharmaceutical fauges. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptides and recombinant antibody mimics of carbohydrate antigens, used for, e.g. treatment of cancer and infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tumour immunity; cancer therapy; antibacterial; immune response; immunogenicity; anti-idiotype; T cell response manipulation.
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                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 22578; 21pp + Sequence Listing; English.
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Pred. No. 3.8e+02;
2; Mismatches 3; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carbohydrate antigen peptide mimotope 41.
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                                                                                                         PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65.6%;
ilarity 54.5%;
Conservative
23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity '
                                                                                                       Adams M,
                                                                                                                                                 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-527317/44
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                                                             (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1805 AA;
                                                                                                                                            WPI; 2001-656860
N-PSDB; ABL09365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kieber-Emmons T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-FEB-1998;
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                                                                                                     Venter JC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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Gaps

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20; Length 20; 3; Indels

(2) the immunogenicity

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     by chromosome 2 of the human malarial parasite, Plasmodium falciparum.

Also described are: (1) nuclectide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II).

(I) and (II) are useful for the development of vaccines against C. f. falciparum infection. (I) and polyclonal antisera or a monoclonal antibody raised to immunogens comprising the sequences of (I), are antibody raised to immunogens comprising the sequences of (I), are antibody raised to immunogens comprising the sequences of (I), are conseful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of infection where the falciparum is sequencing of the Plasmodium chromosome 2 and the infection, or they can be used to identify drug resistance in consection of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the consection and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many contine and drug development. Parasite resistance to drugs and mosquito drugs. AAA70078 to AAA70287 and AAB18144 to AAB18352 represent nucleotide and protein sequences given in the present invention, but which are not securities.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gibberellin signal transduction; spindly phenotype; SPY gene; rescue; psy mutant gene; gibberellin overdose syndrome; paclobutrazol; spy-4 DNA; modulation; plant development; plant height; fruit growth; flower development; leaf size.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid seguence of the spindly (SPY) protein of Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                           62.3%; Score 38; DB 21; Length 740; 50.0%; Pred. No. 3.2e+02; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77..110
/note= "Tetratricopeptide repeat 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..362
:e= "Tetratricopeptide repeat 8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "Tetratricopeptide repeat 7"
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/note= "Tetratricopeptide repeat 4"
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present invention describes proteins and their
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188 FYKYGIIY 195
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AAW46499
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The present sequence represents a protein that is involved in gibberellin signal transduction. Inactivation of the gene produces a spindly be hence the Spy gene). The spindly mutation is characterised by alongated petioles, yellow-green leaves, early flowering, long spindly clongated petioles, yellow-green leaves, early flowering, long spindly bolts, partial male sterility and parthencarpic fruit development. These controls are also observed in wild type plants exhibiting a gibberellin overdose syndrome due to external application of gibberellin. A spy phenotypic mutant was isolated from a library of Agrobacterium-mediated controls are ansient on the genome. Seeds from the library were selected for their ability to germinate in the presence of paclobutrazol.

The sys bull to germinate in the presence of paclobutrazol. Introduction of the SPY gene into plants rescues the spindly phenotype. Introduction of the SPY gene into plants rescues the spindly phenotype. The SPY DNA, vectors and proteins can be used to modulate plant and leaf size.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                     New isolated spindly gene from plants - is involved in gibberellin signal transduction, used to develop products for altering plant development
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 981;
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te= "Tetratricopeptide repeat 10"
"Tetratricopeptide repeat 9"
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77.8%; Pred. No. 4.3e+02;
iive 0; Mismatches 2;
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                                                             /note= "C-terminus"
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                                                                                                                                                      97WO-US08765.
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                                                                                                                                                                                                                                                 Jacobsen SE, Olszewski NE;
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                                 /note=
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255 AYYNLGVVY
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                                                                                                                                                      16-MAY-1997;
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Gaps

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Kemp DJ,

New

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New proteins useful for treatment of Plasmodium infections in humans,
                This sequence represents the Plasmodium falciparum cytoadherence linked asswalal gene 3.1 (ChAG3.1) protein that facilitates flicked asswalal gene 3.1 (ChAG3.1) protein that facilitates cytoadherence of erythrocytes parasitised with Plasmodium spp. to other cells. It is encoded by a gene located on chromosome 3 of P. falciparum. It is a member of a family of ChAG proteins (see also AAY31945-49). The identification of clag genetic species, and the products encoded by them, enables a range of therapeutic agents to be rationally designed and/or identified that are useful for the prophylaxis and treatment of disease conditions caused or exacerbated by infection with Plasmodium spp., e.g. malaria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents the Plasmodium falciparum cytoadherence linked asexual gene 2 (CLAG2) protein that facilitates cytoadherence of erythrocytes parasitised with Plasmodium spp. to other cells. It is encoded by a gene located on chromosome 2 of P. falciparum. It is a member of a family of CLAG proteins (see also AAY31945-48). The identification of clag genetic species, and the products encoded by them, enables a range of therapeutic agents to be rationally designed and/or identified that are useful for the prophylaxis and treatment of disease conditions caused or exacerbated by infection with Plasmodium spp., e.g. malaria,
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                                                                                                                                                                                                                                                                                                       Length 1417;
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                                                                                                                                                                                                                                                                                                  Score 38; DB 20; Length 14
Pred. No. 6.4e+02;
4; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                       62.3%;
50.0%;
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Best Local Similarity 50.0
Lange 4; Conservative
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861 FYKYGIIY 868
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                                                                                                                                                                                                                                     proteins useful for treatment of Plasmodium infections in humans,
                                                                                                                                                                                                                                                                                                                                    This sequence represents the Plasmodium falciparum cytoadherence linked asexual gene 3.2 (CLAG3.2) protein that facilitates cytoadherence of erythrocytes parasitised with Plasmodium spp. to other calciparum. It is encoded by a gene located on chromosome 3 of P. falciparum. It is a member of a family of CLAG proteins (see also AAY31945-49). The identification of clag genetic species, and the products encoded by them, enables a range of therapeutic agents to be rationally designed and/or identified that are useful for the prophylaxis and treatment of disease conditions caused or exacerbated by infection with Plasmodium spp., e.g. malaria,
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                                                                                                                                                                                                                                                                                                Claim 17; Page 126-135; 150pp; English
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                                                                                                                                                            Gardiner DL,
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50.0%;
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FYKYGIIY 865
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                                   25-MAR-1999;
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30-SEP-1999
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Query Match

Matches

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Best

RESULT 13 AAY31947

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Human novel foetal antigen, SEQ ID NO 1139
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                                                                                                                Homo
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           Gaps
                                                                                                                                                                                                                                                                                                                                                  proteins useful for treatment of Plasmodium infections in humans,
                                                                                                                                                                                                                                                                                                                                                                                                                 It is a paralogue of the newly identified cytoadherence linked asexual gene 9 (CLAG9) protein (see AAY11945) encoded by the clagg gene on chromosome 9 gene of P. falciparum. CLAG9 facilitates cytoadherence of erythrocytes parasitised with Plasmodium to other cells. The identification of clag genetic species, and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                               products encoded by them, enables a range of therapeutic agents to be rationally designed and/or identified that are useful for the
                                                                                                                                                                    CLAG9; paralogue; cytoadherence linked asexual gene; CLAG;
erythrocyte; red blood cell; malaria; infection; therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents the protein product of a clag9 paralogue gene (see also AAZ20056) on chromosome 3 of Plasmodium falciparum.
                                                                                                                                                   Plasmodium falciparum cytoadherence gene protein GLAG9 paralogue.
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Pred. No. 2.1e+03;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prophylaxis and treatment of disease conditions caused or exacerbated by infection with Plasmodium spp., e.g. malaria,
                                                                                                                                                                                                                                                                                                               Cowman AF;
          0; Indels
                                                                                                                                                                                                                                                                                                               Holt DC,
 Pred. No. 6.5e+02;
           4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 90-115; 150pp; English.
                                                                                                                                                                                                                                                                                                               Gardiner DL,
                                                                                             AAY31946 standard; Protein; 4134 AA.
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                                                                                                                                                                                                                                                                                           (MENZ-) MENZIES SCHOOL HEALTH RES.
50.0%;
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                                                                                                                                  (first entry)
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           4; Conservative
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879 FYKYGIIY 886
                                                                                                                                                                                                Plasmodium falciparum
                            4 YYRYGVVY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     especially in humans
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                                                                                                                                                                                                                                                                                                                                 WPI; 1999-591099/50
Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                        25-MAR-1999;
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                                                                                                               AAY31946;
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                                                                                   AAY31946
ID AAY3
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immunomodulator; cardiovascular; cytostatic; nephrothropic; cardiovascular; autoimmune disease; rheumatoid arthritis; cardiovascular; autoimmune disease; rheumatoid arthritis; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; cerebral techaemia; angiogenesis; nervous system disorder; wound healing; epithelial cell proliferation; food additive.
Human; foetal tissue antigen; antiinflammatory; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JAN-2001; 2001WO-US01321
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Ruben SM

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New polynucleotides and polypeptides for diagnosing, treating, preventing or prognosing e.g. diseases or disorders of the nervous, musculoskeletal, excretory, gastrointestinal, reproductive, and
                                                                                                                                                                          Claim 11; SEQ ID No 1139; 642pp; English.
05-DEC-2000; 2000US-0251988.
05-DEC-2000; 2000US-0256719.
08-DEC-2000; 2000US-0251479.
08-DEC-2000; 2000US-0251856.
08-DEC-2000; 2000US-0251868.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251989.
11-DEC-2000; 2000US-0251990.
                                                                                  (HUMA-) HUMAN GENOME SCI INC
                                                           11-DEC-2000; 2000US-0254097
05-JAN-2001; 2001US-0259678
                                                                                                 Rosen CA, Barash SC,
                                                                                                              WPI; 2001-488782/53.
N-PSDB; AAS33715.
                                                                                                                                                            respiratory systems
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Matches
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2000US-0234274.
2000US-0234997.
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2000US-0251030
       2000US-0232399
2000US-0232400
                      14-SEP-2000; 2000US-0232401
14-SEP-2000; 2000US-0233063
14-SEP-2000; 2000US-0233064
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2000US-0246475
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2000US-0246524
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13-0CT-2000;
20-0CT-2000;
20-0CT-2000;
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20-0CT-2000;
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08-NOV-2000;
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25-SEP-2000;
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27-SEP-2000;
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02-OCT-2000;
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The invention relates to novel nucleic acids encoding novel human foetal antigens. The nucleic acids and proteins are used to prevent, treat (e.g. by gene therapy) or ameliotrate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. The antibodies to the antigens can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked include autoimmune diseases e.g. rheumatoid arthritis hyperproliferative disorders e.g. rheumatoid arthritis; hyperproliferative disorders e.g. rheumatoid arthritis; cardioxascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac alseade by bacteria, viruses and fungiand coular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to subburn, to maintain organs before ö Plant, transcription factor; gene expression; eucalyptus; pine; acacia; poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor; basic helix-loop-helix zipper; homeocic; homeodomain; homeobox; MADS; homeocicmain zipper; LIM domain; AP2; EREBS; zinc finger domain; examples of diseases and disorders treated by the nucleic acids and regenerate tissues and in chemotaxis. The polypeptides can also be as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. Numerous . 0 proteins are given in the specification. The present sequence DB 22; Length 104; Pinus radiata transcription factor protein sequence #113. 1; Mismatches 60.7%; Score 37; 75.0%; Pred. No. AAB32986 standard; Protein; 158 AA (first entry) 6; Conservative | :||||| 29 SNSYYRYG 36 1 SGAYYRYG 8 Local Similarity

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990S-0139458.
990S-0139459.
990S-0139460.
990S-0139461.
990S-0139462.
99US-0123180.
99US-012548.
99US-012564.
99US-0126264.
99US-012628.
99US-0128234.
99US-0128234.
99US-0128234.
99US-012845.
99US-013047.
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990S-0132863.
990S-0134218.
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99US-0136021.
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99US-0139817.
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99US-0140353.
99US-0140354.
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990S-0142803.
990S-0142920.
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99US-0135124.
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99US-0140823.
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99US-0139119
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                                    25-MAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
08-APR-1999;
16-APR-1999;
13-APR-1999;
23-APR-1999;
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18-JUN-1999;
21-JUN-1999;
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28-APR-1999
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                                                                                                                                                                                                                                                                                                                                                  The present invention relates to novel plant transcription factors from Bucalyptus grandis or Pinus radiata. The present sequence is one such transcription factor and set or may be used to produce a plant having modified gene expression such as a woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or omodify the activity of a polypebide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins: bZIP, bZIP family of G-box binding factors, basic elix, longophelix zipper, homeotic/homeodomain/homeobox/MADS, homeodomain cys2His2, CCAAT box elements and MYB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                              New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide
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 type 2 Cys2His2; CCAAT box element; MYB.
                                                                                                                                                                                                            Wood M, McGrath A, Shenk MA, Glenn M;
                                                                                                                                                                                  (FLET-) FLETCHER CHALLENGE FORESTS LTD.
                                                                                                                                                                       (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGS4380 standard; Protein; 384 AA
                                                                                                                                                                                                                                                                                                                              Claim 8; Page 380; 747pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.7%;
                                                                                                       39-MAR-2000; 2000WO-US06112.
                                                                                                                               99US-0266513.
99US-0149485.
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Best Local Similarity 70.vv,
A; Conservative
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                                                                                                                                                                                                                                    WPI; 2000-579369/54
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                                                     WO200053724-A2.
                           Pinus radiata
                                                                                                                                 11-MAR-1999;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                                                                                                                                       Length 384;
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Pred. No. 2.3e+02;
1; Mismatches 0; Indels
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 9908-0157753.
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9908-0159293.
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Best Local Similarity 85.7%;
Matches 6; Conservative
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AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
                                                                                        Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders,
                                                                                                  useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
                                                                                                                                    Claim 11; Page 3681-3683; 5507pp; English.
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2000DE-1050040.
2000DE-1052319.
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12-APR-2001; 2001DE-1018706
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            (CURA-) CURAGEN CORP.
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Best Local Similarity
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                                                                  N-PSDB; AAC76693
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10-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cholesterol ester storage; systemic lupus erythemicosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive.
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Pred. No. 3e+02;
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85.7%;
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99US-0159331.
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02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
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|24 AYYRYGL 130
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Pred. No. 3.5e+02;
1; Mismatches 2; Indels
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The present invention relates to a mutant of the DNA sequence encoding the protease (FSAP) that activates blood coagulation factor VII (FVII) and single-chain plasminogen activator, where at least one of the base changes G to C at mucleotide 1177 and G to A at mucleotide 1601 is present. The mutant sequences can be used in the treatment and prevention of bleeding disorders associated with inherited or acquired defects of blood coagulation factors V, VIII, IX, X, XI, XII, von Willebrand's factor and/or with antibodies against any of these proteins. The present sequence is the mutant human FSAP protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
prevention of coagulation disorders, also
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                                                             Disclosure; Page 20-22; 27pp; German
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llarity 66.7%;
Conservative
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2001US-276248P.
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25-MAY-2001; 2001US-293499P
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16-MAR-2001; 2
21-MAR-2001; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JAN-2002
                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP47134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ruben SM,
                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP4713
    원
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                   The present invention relates to a mutant of the DNA sequence encoding the protease (FSAP) that activates blood coagulation factor VII (FVII) and single-chain plasminogen activator, where at least one of the base changes G to C at mucleotide 1177 and G to A at nucleotide 1601 is present. The mutant sequences can be used in the treatment and prevention of bleeding disorders associated with inherited or acquired defects of blood coagulation factors V, VIII, IX, X, XI, XII, von Willebrand's factor and/or with antibodies against any of these proteins. The present sequence is the human FSAP protein.
                                                                                                                                                                             New nucleic acid encoding mutant factor 7 activating protease, useful for diagnosis, treatment and prevention of coagulation disorders, also related protein and antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; blood coagulation factor VII activating protease; FSAP; single-chain plasminogen activator; bleeding disorder; haematological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid encoding mutant factor 7 activating protease, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Becker M;
                                                             Becker M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human blood coagulation factor VII activating protease mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37; DB 23; Length 560;
Pred. No. 3.5e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F,
                                                             Ė
                                                               Weimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Weimer
                                                             Lang W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lang W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stoehr H, Feussner A,
Muth-Naumann G;
                                                             Feussner A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA017145 standard; protein; 560 AA
                                                                                                                                                                                                                                                                   Claim 4; Page 17-19; 27pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.7%;
                   (AVET ) AVENTIS BEHRING GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-JUL-2000; 2000DE-1036641.
10-OCT-2000; 2000DE-1050040.
21-OCT-2000; 2000DE-1052319.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AVET ) AVENTIS BEHRING GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2001; 2001EP-0115691.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mutant; mutein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-APR-2001; 2001DE-1018706
                                                             Stoehr H, Feu
Muth-Naumann G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | || || ||:|
GTYYVYGIV 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 GAYYRYGVV 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2002-270939/32.
                                                                                                                        WPI; 2002-270939/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  560 AA
                                                                                                                                               N-PSDB; AAL45696.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-270939,
N-PSDB; AAL45697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens
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Nerlich C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-JUN-2002
                                                             Roemisch J,
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RESULT 22 AAO17145 ID AAO1

Sequence Query Match AA017145;

Homo sapie Synthetic.

useful for

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cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, humanised antibody, CC-chemokine receptor 2, CCR2, nephrotropic, neuroprotective; immunosuppressive; human immunodeficiency virus; HIV infection; cytostatic; vasotropic; lankovyte trafficking; allergy; inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock; multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma; anaphylaxis; malignancy; inflammation; stenosis; allograft rejection; fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS; inflammatory glomerulopathy; vascular intervention; ID9 antibody; neointimal hyperplasia; VH; heavy chain variable region.
                                                                                                                                   diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of the invention.
                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "Complementarity determining region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Complementarity determining region 3"
                                                                                                                                                                                                                                                                    Score 36; DB 23; Length 19;
Pred. No. 13;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O'Brien S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human heavy chain variable (VH) region, 038062.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE07014 standard; Protein; 128 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Unknown
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/label= CDR1
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/label= CDR3
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                                                                                                                                                                                                                                                                       59.0%;
                                                                                                                                                                                                                                                                                     66.78;
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                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note=
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                                                                                                                                                                                                                                                                                                                                                                         SGGYYYYGM 17
                                                                                                                                                                                                                                                                                                                                        1 SGAYYRYGV 9
                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                      19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200157226-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Larosa GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE07014;
                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                       Query Match
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Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                         Matches
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WPI; 2001-488888/53

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The patent discloses a humanised antibody or its antigen-binding fragment, having binding specificity for CC-chemokine receptor 2 (CCR2), comprising an antigen binding region of non-human origin and at least a portion of an immunoglobulin of human origin. The humanised antibodies are useful for inhibiting the interaction of a cell expressing CCR2. They are useful for inhibiting or treating a cell expressing CCR2. They are useful for inhibiting or treating inflammatory disorder, autoimmune disorders such as rheumatoid arthitis and multiple sclerosis, atherogenesis and atherosclerosis, and for inhibiting restenosis. They are useful in therapy or diagnosis, and for inhibiting restenosis. They are useful in therapy or diagnosis, and in the manufacture of a medicament for treating CCR2-mediated and in the manufacture of a medicament for treating allery, anaphylaxis, malignancy, chronic and acute inflammation, histamine and IGE-mediated allery! creating, shock, stenosis, allograft rejection, fibrotic disease, asthma, inflammatory associated with vascular immune deficiency syndrome (AIDS), restenosis associated with vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperporliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyzoidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatodid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 intervention, including angioplasty and/or stent placement in a mammal. Humanised antibodies are also useful for inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a vessel in a mammal, preferally associated with vascular intervention.
The present sequence is human heavy chain variable (VH) region, 038062.
                   Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity for CCR2, and a non-human antigen binding region and human immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36; DB 22; Length 128;
Pred. No. 1e+02;
1; Mismatches 2; Indels
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                                                                                                                          Disclosure; Page 168; 183pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP10506 standard; Protein; 139 AA
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29-AUG-2000; 2000US-228716P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 66.7 ses 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SGAYYRYGV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         myasthenia gravis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200192523-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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1..28 /note= "signal peptide"

Peptide

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(referred to as open reading frame, ORFX, where X is 1-11491 (see Table In the specification). ABN15762 to ABN27252 encode the human ORFX in the specification). ABN15762 to ABN27252 encode the human ORFX proteins given in ABD00101 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX associated disorder. ORFX polynucleotide squences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, insemborrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseorders, disorders related to organ transplantation, cardiovascular diseorders, disorders, infectious lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious disease, autoimmune thyroditis, myaschenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ulcers, for treating osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bone marrow secreted protein; bone marrow stromal cell; cytokine; cell proliferation; cell differentiation, hematopoiesis; anaemia; myeloid cell deficiency; lymphoid cell deficiency; myeloid cell; erythroid progenitor cell; colony stimulating factor; granulocyte; monocyte; macrophage; myelosuppression; megakarycocyte; platelet disorder; thrombocytopenia; hematopoeitic stem cell; stem cell disorder; aplastic anaemia; bone differentiation; paroxysmal nocturnal hemoglobinuria; bone growth; cartilage; tendon; bone fracture; cartilage damage; artificial joint.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes substantially purified human proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bone degenerative disorders, or periodontal disease, and for gut
protection or regeneration and treatment of lung or liver fibrosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             reperfusion injury in various tissues and conditions resulting from
                                                                                                                                                                                                               Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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Pred. No. 1.1e+02;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A bone marrow secreted protein designated hCornichon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID 20994; 1037pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   burns, incisions,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY53622 standard; Protein; 142 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            systemic cytokine damage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 44.4
nes 4; Conservative
                               Shimkets RA, Leach MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59
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                                                                                                         2002-106308/14.
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51 AFYKYNIIY
                                                                                                                                            N-PSDB; ABN26258
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AAY53622
AC AAY53
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DD A bon
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KW Bone
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granulocytes, monocytes or macrophages, to prevent or treat myelo-suppression, to support the growth and proliferation of megakaryocytes and platelets, thereby allowing prevention or treatment of platelet disorders such as thrombocytopenia, to support the growth and proliferation of hematopoeitic stem cells, either in place of or in conjunction with platelet transfusions, to treat stem cell disorders, such as aplastic anaemia and paroxysmal nocturnal hemoglobinuria, or to repopulate the stem cell compartment after irradiation or chemotherapy. They can be used for growth or differentiation of bone, cartilage, tendon, ligament, or nerve tissue, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers, to induce cartilage and/or bone growth in circumstances where bone is not normally formed and thus have an application in healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     be used to support colony forming cells or factor-dependent cell lines, to regulate hematopoiesis, and to treat myeloid or lymphoid cell deficiencies. In addition, they may be used to support the growth and prolliferation of erythroid progenitor cells, and to treat various anaemias. They can have colony stimulating factor (CSF) activity and be used to support the growth and proliferation of myeloid cells such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY53622-43 represent bone marrow secreted proteins of human bone marrow stromal cells. The proteins can exhibit cytokine, cell proliferation, or cell differentiation activity (either inducing or inhibiting). They can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prophylactic use in
                                                                                                                                                                                                                                                                                                                                                                        New isolated human polynucleotide and secreted proteins can induce production of other cytokines in certain cell populations -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oone fractures and cartilage damage or defects, prophylactic use i racture reduction and also in the improved fixation of artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone pk65_4; pk65_4 protein; human foetal kidney cDNA library;
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Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY28813 standard; Protein; 144 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Page 71; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.5%;
                                                                                                                            98WO-US27008
                                                                                                                                                                 97US-0068958
                                                                                                                                                                                 98US-0101603
98US-0102540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 YYLYGMIY 137
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                                                                                                                                                                                                                                                                                                                  WPI; 2000-038344/03.
N-PSDB; AAZ36228.
                                                                                                                                                                                                                                       (CHIR.) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 AA;
                                                                                                                                                                                                                                                                              Cao L;
                                                    WO9933979-A2
                                                                                                                            18-DEC-1998;
                                                                                                                                                                 30-DEC-1997;
                                                                                                                                                                                 24-SEP-1998;
30-SEP-1998;
                                                                                       08-JUL-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY28813;
                                                                                                                                                                                                                                                                             Lin H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 27
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Location/Qualifiers

Homo sapiens

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The present sequence is the pk65 4 secreted protein encoded by the cDNA clone pk65 4. pk66 4 was isolated from a human foetal kidney cDNA library using methods specific for secreted protein cDNAs. The TopPred II computer program predicts three potential transmembrane domains within the protein sequence, centered around amino acids 16, 67, and 133. pk65 4 protein was expressed in a COS cell expression system, and an expressed band of approximately 15kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis. The polynucleotide and protein may effect nutritional activity, cytokine and cell proliferation, immune stimulation or suppression, hematopoiesis regulation, tissue growth, tumour inhibition etc.
                                                                                                                                                                                                                                                                                                   Polynucleotides encoding secreted human proteins, derived from human adult brain, human fetal brain, human fetal brain, blood cDNA libraries
secreted protein; transmembrane domain; cytokine; tissue growth; TopPred II computer program; COS cell expression system; membrane fraction; SD polyacrylamide gel electrophoresis; nutritional activity; cell proliferation; immune stimulation; immune suppression; hematopoiesis regulation; tumour inhibition.
                                                                                                                                                                                                                             Collins-Racie LA, Evans C;
Steininger RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59.0%; Score 36; DB 20; Length 144; 62.5%; Pred. No. 1.2e+02; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                             LaVallie ER,
Agostino MJ,
                                                                                                                                                                                                                                                                                                                                                  Claim 20; Page 105; 122pp; English.
                                                                                                                                            99WO-US06946.
                                                                                                                                                                   98US-0080110.
99US-0280591.
                                                                                                                                                                                                     (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                              Jacobs K, Mccoy JM,
Merberg D, Treacy M,
                                                                                                                                                                                                                                                                WPI; 1999-610849/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 AA;
                                                                                                                                                                                                                                                                           N-PSDB; AAX90853
                                                                                             WO9950405-A1.
                                                                      Homo sapiens
                                                                                                                                            30-MAR-1999;
                                                                                                                                                                   31-MAR-1998;
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                                                                                                                   07-0CT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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Isolated nucleic acids encoding human cornichon molecules, useful in the recombinant production of cornichon proteins and in the prevention, diagnosis and treatment of developmental, reproductive, immunological

Claim 1; Fig 1; 28pp; English.

neoplastic disorders

Corley NC;

Shah P,

Hillman JL,

WPI; 1999-590398/50. N-PSDB; AAZ30544.

(INCY-) INCYTE PHARM INC

97US-0950168 97US-0950168

14-OCT-1997; 14-OCT-1997;

US5968744-A.

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This sequence represents the human cornichon (CORN) protein (I). CORN is involved in the differentiation and determination of body plan in controlling the correct dorsalization of the occyte (i.e. determining the dorsal-ventral axis) and is essential in the correct induction of the dorsal-ventral axis. In this case, CORN is implicated in the correct polarized microtubule cytoskeletons, which are required for proper localization of the anterior and posterior of the anterior and posterior determinant genes (bicoid and oskar) and for the asymmetric positioning of the ocyte nucleus (see Roth et al., Cell (1995)).

(I) may be used for the diagnosis, prevention and treatment of disorders associated with inappropriate expression and/or activity of CORN proteins. These disorders include developmental disorders (e.g. anemia, Cushing's syndrome, epilepsy and achondroplastic dwarfism), hereditary neuropathies (e.g. Charcot-Marie-Tooth disease), reproductive disorders (e.g. infertility, disorders of prolactin production, tumors and disruptions of the menstrual cycle), immunological disorders (e.g. and disruptions of the menstrual cycle), immunological disorders (e.g. acquired immune deficiency syndrome (AIDS), Addison's disease and acquired immune deficiency syndrome (AIDS), Addison's disease and acquired immune deficiency syndrome (AIDS), parasitic, protezoal, complications of cancers, bacterial, viral, parasitic, protezoal, whiffids and fungal infections and other disorders such as spina
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human PRO181 protein sequence.
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hes 5; Conservative
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Matches
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Gaps

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Local Similarity

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Homo sapiens

Human; cornichon; differentiation; body plan; metazoan; oogenesis; embryogenesis; dorsalization; oocyte; dorsal-ventral axis; bicoid; anterior-posterior axis; microtubule; cytoskeleton; oskar; diagnosis; developmental disorder; hereditary neuropathy; seizure disorder; reproductive disorder; immunological disorder; neoplastic disorder; cancer; infection; spina biffida; cataract.

Homo sapiens

AAY41306 standard; Protein; 144 AA.

RESULT 28

Human cornichon protein.

AAY41306
IID AAY4
XX AC AAY4
XXX AAY4
XXX AAY4
XXX XX XXX AAX4
XXX Huma
XXX Huma
XXX Huma
XXX embr
XW embr
XW expr
XW canc
XX COS Homo

18-JAN-2000

AAY41306;

98US-0084643. 98US-0085323. 98US-0085338. 98US-0085573. 98US-0085579. 98US-0085580.

15-MAY-1998; 15-MAY-1998; 15-MAY-1998;

15-MAY-1998; 15-MAY-1998; MAY-1998 15-MAY-1998 15-MAY-1998

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98US-0083500.
98US-0083545.
98US-0083554.
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98US-0084411:
98US-0084598.
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98US-0084639.
98US-0084640.
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                         99WO-US05028
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                                                 11-MAR-1998;
12-MAR-1998;
13-MAR-1998;
17-MAR-1998;
20-MAR-1998;
    WO9946281-A2
                        08-MAR-1999;
                                                                                                         27-MAR-1998;
27-MAR-1998;
                                                                                                                                             31-MAR-1998
               16-SEP-1999
                                             11-MAR-1998
                                                                                 20-MAR-1998
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The present invention describes secreted and transmembrane polypeptides and their polynucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coagulation disorders, cancers and callular adhesion disorders. They may also be used to raise antibodies. AAZ33891 to AAZ34338, and AAY41685 to AA441774 represent polynucleotide and polypeptide sequence given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                New secreted and transmembrane polypeptides and their polynucleotides, useful for treating blood coagulation disorders, cancers and cellular adhesion disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane domain containing protein; human; antibody production; interaction assay; diagnosis; nutritional activity; cytokine; cell proliferation; cell differentiation activity; immune stimulant; immune suppressant; haemactopoiesis regulator; tissue growth activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                Yuan J, Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY32925 standard; Protein; 144 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 12; Fig 129; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                 Gurney A,
                                                                                                                           98US - 0085697
98US - 0085700
98US - 0086023
98US - 00861392
98US - 0086414
98US - 0086414
98US - 0086486
98US - 0087108
98US - 0087108
98US - 0087108
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                                                                                                                                                                                                                                                                                                                                   (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                 Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 YYRYGVVY 11
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Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 AA;
                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAZ34164.
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                                                                                                                                                                                                                                                                                                        11-SEP-1998;
                                                                                                                                                                          18-MAY-1998
                                                                                                                                                                                                  22-MAY-1998
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                                                                                                                                                                                                                                                                              28-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                Wood WI,
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AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polypeptides. The PRO polynucleotides and polypeptides have cytostatic activity. The polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bioactive molecules to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide target cells, e.g. for the treatment of cancers. The polypeptide pairs provide specific targeting of bioactive molecules to cells. AAC78600 to AAC78877 represent PCR primers and probes used in the isolation of the PRO polynucleotide sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel PRO polypeptides and polynucleotides used in detection methods, to target bioactive molecules to specific cells, and to modulate cellular activities -
   Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , Baker KP, Botstein D, Desnoyers L, Eaton DL; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME; Sodowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ; Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA; Stewart TA, Tumas D, Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36; DB 21; Length 14
Pred. No. 1.2e+02;
2; Mismatches 1; Indels
                  expressed sequence tag; detection; cancer.
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99US-0126773
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2000WO-US00219
                                                                                                                                                2000WO-US04341
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Filvaroff E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 59.0
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ferrara N, Filvaroff E,
Goddard A, Godowski PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC.
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                                                                                 WO200053756-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ashkenazi AJ,
                                                                                                                                                  18-FEB-2000;
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Shelton DL,
                                                                                                                                                                                                                 16661
                                                                                                                  14-SEP-2000
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AAB19524
ID AAB19
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                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence is a human transmembrane protein of the invention. The DNAs are useful for expressing recombinant protein for analysis, characterisation or therapeutic use, and are useful as markers for tissues in which the corresponding protein is preferentially expressed. They are also useful as molecular weight markers on Southern gels; as chromosome markers or tags (when labelled) to identify potential genetic disorders, as probes to hybridise and thus discover novel, related DNA sequences, as a source of PCR primers for genetic fingerprinting, as probes to subtract-out known sequences in the process of discovering other novel DNAs, for selecting and making oligomers for attachment to a gene chip or other support, including for examination of expression techniques, and as an anti-protein antibodies using DNA antibodies or elicit another immune response. Where the DNA encodes a protein which binds to be used in interaction trap assays to identify DNAs encoding the other protein with which binding occurs or to identify inhibitors of the brinding interaction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, haematopoiseis regulating activity, tissue growth activity, activity, activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, and tumour
activin; inhibin activity; chemotaxis; chemokinesis; haemostasis;
thrombolysis; anti-inflammatory; cadherin; tumour invasion suppressor;
tumour inhibitor.
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Pred. No. 1.2e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human PRO181 (UNQ155) protein sequence SEQ ID NO:322.
                                                                                                                                                                                                                                                                                                                                                              New proteins and DNA useful for preventing tumours
                                                                                                                                                                                                                                                                                  Sekine S;
                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 72-73; 96pp; English.
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                                                                                                                                                                                                                                                                                Kato S, Kimura T, Nakamura N,
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62.5%;
                                                                                                                                                                                                                             (PROT-) PROTEGENE INC.
(SAGA ) SAGAMI CHEM RES CENT
                                                                                                                                                                 99WO-JP00875.
                                                                                                                                                                                              98JP-0046607
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Query Match
Best Local Similarity 62.50,
Best Local Similarity
5; Conservative
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N-PSDB; AAZ11179, AAZ11186.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inhibition activity
                                                                  Homo sapiens.
                                                                                                                                                              25-FEB-1999;
                                                                                                 WO9943802-A2
                                                                                                                                                                                                27-FEB-1998;
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Gaps

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Length 144;

Hòmo sapiens

Peptide Domain Domain Domain

09-JAN-2001

AAB19524

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Drosophila, developmental biology, cell signalling, insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster polypeptide SEQ ID NO 12387.
                                                                                                                                                                                                                                                ABB61865 standard; Protein; 144 AA.
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11-JUL-2000; 2000US-0614150.
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132 YYLYGMIY 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-656860/75
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4 YYRYGVVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pharmaceutical
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ABB61866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gurney AL, Napier MA, Wood WI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             They are useful for identifying agonists to PRO181 or PRO237 in drug screening and rational drug design.
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0
                                                                                                                                                                                                            PRO181; antitumour; antiproliferative; human; cancer; therapy;
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Pred. No. 1.2e+02;
2; Mismatches 1; Indels
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/note= "Glycosaminoglycan attachment site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1..31
|abel= Type-II_transmembrane_domain
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/label= Transmembrane_domain
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                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1..20
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99US-0144758.
99WO-US20594.
99WO-US30999.
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62.5%;
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                                                                    (first entry)
                                                                                                                                        Antitumour PRO181 protein
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Best Local Similarity 62.5
Matches 5; Conservative
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                                                                                                                                                                                                                                                    drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200053751-A1
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29-MAR-1999; 20-JUL-1999; 08-SEP-1999; 20-DEC-1999;

30-DEC-1999;

38-MAR-1999

14-SEP-2000

Myers EW;

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                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention sequences genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                            Disclosure; SEQ ID NO 12387; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 144;
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Pred. No. 1.2e+02;
1; Mismatches 1; Indels
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Best Local Similarity 75.0%;
Matches 6; Conservative
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Sequence

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us-10-007-790-7.rag

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clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5' and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; lung cancer; lung tumour; lung tumour protein; gene therapy; lung cancer antigen; lung tumour-specific antigen; diagnosis; vaccine; cytostatic; antisense inhibition.
                                                                                                                                                                                                                                          830 Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation -
                                                                                                                                                                                                                                                                                                                                                The invention relates to primers for synthesising full length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human lung tumour protein related protein sequence SEQ ID NO:327
                                                                                                                    Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga
                                                                                                                                                                                                                                                                                                        Claim 8; SEQ ID NO 2859; 1380pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59.0%; Score 36; DB 22; Length 14
62.5%; Pred. No. 1.2e+02;
ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB76851 standard; Protein; 144 AA.
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2000US-0546259.
2000US-0560406.
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99US-0466867.
99US-0476300.
08-JUL-1999; 99JP-0194486.
11-JAN-2000; 2000JP-0118774.
02-MAY-2000; 2000JP-0183765.
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                                                                                (HELI-) HELIX RES INST
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|32 YYLYGMIY 139
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                                                                                                                                                                               WPI; 2001-524255/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 AA;
                                                                                                                                                                                                      N-PSDB; AAK94250
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17-DEC-1999;
30-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention sequences genomic DNA sequences (ABLi6176-ABL30511), expressed DNA (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                           Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; full length cDNA; cDNA synthesis; oligo-capping
                Drosophila melanogaster polypeptide SEQ ID NO 12390
                                                                                                                                                                                                                                                                                                                                                                                    Li PWD, Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM93330 standard; Protein; 144 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human polypeptide, SEQ ID NO: 2859.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUL-2000; 2000EP-0114089.
                                                                                                                                                                                                                                          23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                              23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                      Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             || ||:||
132 YYIYGMVY 139
                                                                                                                                                                                                                                                                                                                                                                                  Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                            (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 AA;
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                                                                                                                                                          WO200171042-A2.
                                                                                pharmaceutical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interactions
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Matches

RESULT 35 AAM93330

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Gaps

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The present invention describes immunogenic portions of lung tumourassociated proteins (I) and the nucleic acids (NAS) that encode them.

(I) have cytostaric activity and can be used in gene therapy, antisense inhibition and in vaccines. The NAs and the lung tumour associated proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with their inappropriate expression, especially lung cancers. For example, the NAs may be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of the protein by expressing inactive proteins or to supplement the patients own production of (I). Additionally, the NAs may be used to produce the lung-tumour associated protein, according to standard recombinant DNA methodology. Conversely, antisense NA molecules may be administered to down regulate protein expression. The NA and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar NA sequences in camples, and hence which patients may be in need of treatment for lung cancer. The (I) may be used as antigens in the production of antibodies and in assays to identify medulators (agonists and antagonists) of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer; atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression and activity of the protein. AAF68083 to AAF6808 and AAB76848 to AAB76878 represent human lung tumour protein related nucleotide and protein sequences which are used in the exemplification of the present invention.
                                                                                                                                      Lung tumor-associated proteins and the nucleic acids that encode them, useful for preventing, diagnosing and treating lung cancer
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                                       Carter D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      r watch 59.0%; Score 36; DB 22; Length 144; Local Similarity 62.5%; Pred. No. 1.2e+02; Length 144; S. Conservative 2. Minnells
                                       Lodes MJ, Fanger GR, Vedvick TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human angiogenesis related protein PRO181 SEQ ID NO: 2.
                                                                                                                                                                                                  Example 1; Page 254; 436pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB95423 standard; Protein; 144 AA
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25-JUL-2000; 2000US-220624P.
25-JUL-2000; 2000US-220664P.
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                                                       Retter MW, Mannion J;
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(CORI-) CORIXA CORP.
                                       Bangur CS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 AA;
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                                       Wang T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophhebitis, lymphangitis, tumour angiona, mas breast carcinoma and liver carcinoma) and wound healing. The present sequence is a PRO protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
JF, Watanabe CK, Williams PM, Wood WI, Ye W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Fig 2; 567pp; English.
                                                                                                                                                                             001US-0796498
                                                                                                                                                                                                                                 2001US-0816744
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GURNEY A L.
HILLAN K J.
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GERRITSEN M E.
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PAONI N F.
STEPHAN J F.
WATANABE C K.
WILLIAMS P M.
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MARSTERS S A.
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FERRARA N.
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                                                                                                                          10-NOV-2000;
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(WOOD/)
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(BAKE/)
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Sequence
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ID AAU8
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                                                                                                                                                                                                                                                                                                                                                                                           Human; cornichon protein; CORN; Cushing's syndrome; muscular dystrophy; developmental disorder; neoplastic; seizure; reproductive; immunological; tubular acidosis, anaemia; polycystic ovary; attoimmune disorder; tumour; breast cancer; prostate; testis; epilepsy; neuropathy; Addison's disease; ulcerative colitis; spermatogenesis; hypothyroidism; cataract; arthritis; infertility; galactorrhea; gynaecomastia; diabetes mellitus; fungicide; dermatitis; acquired immunodeficiency syndrome; AIDS; glomerulonephritis; atherosclerosis; allergy; asthma; bronchitis; Crohn's disease; auditory; gyuaecological; cytostatic; immunosuppressive; gynaecological; antiulcer; ophthalmological; cytostatic; immunosuppressive; gynaecological; antiulcer; osteoporosis; antiparasitic; protozoacide; antibacterial; tranquillizer; osteoporosis; antiparasitic; protozoacide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is useful for diagnosis, prevention and treatment of developmental, reproductive, immunological and neoplastic disorders. Developmental, reproductive, immunological and neoplastic disorders. Developmental, adsorders include renal tubular acidosis, anaemia, Cushing's syndrome, achondroplastic dwarfism, Duchenne and Becker muscular dystrophy, epilepsy, hereditary neuropathies such as Charcot-Marie-Tooth disease, neurofibromatosis, hypothyroidism, seizure disorders such as cerebral palsy, cataract and sensorineural hearing loss and reproductive disorders include disorders of prolactin production, infertility, ownlatory defects, endometriosis, disruptions of the oestrous cycle, disruptions of the menstrual cycle, polycystic ovary syndrome, endometrial and ovarian tumours, autoimmune disorders, ectopic pregnancy, cancer of the breast, galaccorrhea, disruptions of spermatogenesis, cancer of the testis, cancer of the prostate, prostatitis and carcinoma of the male breast and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a purified human cornichon protein (CORN). CORN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human cornichon protein, useful for diagnosis, prevention and treatment of developmental, reproductive, immunological and neoplastic disorders and to screen for molecules that bind the protein -
                                                                                       Gaps
                                                                                       ;
0
                                                 Score 36; DB 23; Length 144;
Pred. No. 1.2e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                    AAE20143 standard; Protein; 144 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shah P;
                                                                                                                                                                                                                                                                                                                                                              Human cornichon protein (CORN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Fig 2; 29pp; English
                                                 59.0%;
62.5%;
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                          Query Match
Best Local Similarity 62.5%,
Thes 5; Conservative
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                                                                                                                                                           YYLYGMIY 139
                                                                                                                         4 YYRYGVVY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-266544/31.
N-PSDB; AAD31079.
               144 AA;
                                                                                                                                                                                                                                                                                                                          18-JUN-2002
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                                                                                                                                                         132
                                                                                                                                                                                                                                                                                        AAE20143;
               Sequence
                                                                                                                                                                                                                  RESULT 38
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gynaecomastia. Immunological disorders include acquired immunodeficiency syndrome (AIDS), diabetes mellitus, arthritis, including rheumatoid arthritis, osteoarthritis, Addison's disease, allergies, astimatitis, osteoarthritis, Crohn's disease, ulcerative collitis, determatitis, bronchitis, Crohn's disease, ulcerative collitis, dermatitis, glomerulonephritis, gout, Graves' disease, multiple sclerosis, osteoporosis, autoimmune thyroiditis, complications of cancer, haemodialysis and extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal and helminthic infections, and trauma CORN, is catalytic or immunogenic fragments is useful for screening libraries of compounds in a variety of drug screening techniques. The present sequence is human CORN. CORN gene is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful for stimulating and/or expanding T cells specific for a tumour protein for determining the presence of a cancer in a patient. A composition containing the polynucleotide and/or polypeptide is useful for treating a lung cancer in a patient. The polypeptide is useful for removing tumour cells from a biological sample. The polynucleotide is
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang T, Watanabe Y, Henderson RA, Johnson JC, Retter MW;
Marnerakis M, Carter D, Fanger GR, Vedvick TS, Bangur CS;
Mcnabb A, Wang A, Fanger N, Switzer A, Mcneill PD, Clapper JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polynucleotide encoding a lung tumour polypeptide useful for stimulating and/or expanding T cells specific for a tumour protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes an isolated polynucleotide and polypeptide
                                                                                                                                                                                                                                                                                                                                                    ..
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                                                                                                                                                                                                                                                                                                     59.0%; Score 36; DB 23; Length 144; 62.5%; Pred. No. 1.2e+02; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tumour; cancer; T cell; immune response stimulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; SEQ ID No 327; 223pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone #19110 of lung tumour protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU85506 standard; Protein; 144 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-SEP-2000; 2000US-0658824.
26-SEP-2000; 2000US-0671325.
06-OCT-2000; 2000US-0677419.
30-CT-2000; 2000US-0702705.
13-DEC-2000; 2000US-070565.
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Matches 5; Conservative
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                                                                                                                                                                                                                                                      . 144 AA;
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also useful as probe or primer to detect the level of mRNA encoding a tumour protein. This is the amino acid sequence of a lung tumour associated protein. described in the method of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                           Gaps
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                                                                                                                               59.0%; Score 36; DB 23; Length 144; 62.5%; Pred. No. 1.2e+02; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     wound healing; chromosome mapping; gene mapping.
                                                                                                                                                                                                                                                                                                                                                     Human PRO181 protein sequence SEQ ID NO:2.
                                                                           ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                         ABB84817 standard; Protein; 144 AA
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2001US-0808689.
2001US-0816744.
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132 YYLYGMIY 139
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                                                                                                        144 AA;
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24-AUG-2000;
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08-NOV-2000;
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                                                                                                                                                                                                                      Gerritsen ME, Goddard A;
J, Marsters SA, Pan J, Paoni NF;
Is PM, Wood WI, Ye W;
                                                                                                                                                                                                                                                                                                                                                                 One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal
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62.5%; Pred. No. 1.2e+02;
ive 2; Mismatches 1; Indels
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, Hillan KJ, Marsters SA,
TK, Williams PM, Wood WI,
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10-MAY-2001; 2001US-0854208.
10-MAY-2001; 2001US-0854280.
25-MAY-2001; 2001US-0866028.
25-MAY-2001; 2001US-0866034.
30-MAY-2001; 2001WO-US17092.
30-MAY-2001; 2001US-0870574.
30-MAY-2001; 2001WO-US17443.
                                                                                                                                                                                                                          Baker KP, Ferrara N, Ger
Godowski PJ, Gurney AL,
Stephan JF, Watanabe CK,
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Best Local Similarity 62.5
Matches 5, Conservative
                                                                                                                                                                                     (GETH ) GENENTECH INC
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N-PSDB; ABL88072.
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Search completed: July 18, 2003, 15:06:42 Job time: 38.18 secs

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; ORGANISM: Mus musculus
US-09-257-069-7
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Best Local Similarity
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Sequence 275, App
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Sequence 78, Appl
Sequence 3, Appli
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Sequence 25,
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Sequence 16,
Sequence 5,
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Sequence 3,
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Sequence 1,
Sequence 3,
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/cgn2 6/ptodatca1/liaa/PCTUS_COMB.pep:*
/cgn2 6/ptodatca1/liaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-257-069-2
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US-08-950-168-1
US-09-365-705-1
US-09-365-705-3
US-09-365-705-3
US-09-365-705-3
US-09-365-705-3
US-09-445-472-4
US-09-445-472-4
US-09-445-472-4
US-09-445-472-16
US-09-445-472-16
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US-08-033-131-78
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US-08-035-131-78
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US-08-758-417A-123
PCT-US92-10983-78
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-08-448-164-3
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Listing first 45 summaries
                                                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length
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Maximum DB
                                                                                                                                                                                                                                                                                                       Sequence:
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; Sequence 2, Application US/09257069
; Patent No. 6448580
; GENERAL INFORMATION:
; APPLICANT: Medical & Biological Laboratories Co.,Ltd.
; TILLE OF INVENTION: Monoclonal Antibody Specific for TILLE OF INVENTION: Monoclonal Antibody Specific for TITLE OF INVENTION: Monoclonal Antibody Specific for TITLE OF INVENTION: MONBER: US/09/257,069
; CURRENT APPLICATION NUMBER: US/09/257,069
; CURRENT APPLICATION NUMBER: US/09/257,069
; PRIOR FILING DATE: 1998-09-07
; RIDER APPLICATION NUMBER: US/09/257,069
; SEQ ID NO 2
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-257-069-2
                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/09257069

Patent No. 6348580

GENERAL INFORMATION:

APPLICANT: Medical & Biological Laboratories Co., Ltd.

TITLE OF INVENTION: Phosphatidylinositol-3,4,5-Triphosphate

TITLE OF INVENTION: Phosphatidylinositol-3,4,5-Triphosphate

FILE REFERENCE: M3-008-US

CURRENT APPLICATION NUMBER: US/09/257,069

CURRENT PILING DATE: 1999-02-24

PRIOR PILING DATE: 1999-00-07

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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Pred. No. 0.00014;
                                      US-08-939-727-8

US-08-442-281-7

US-08-442-281-7

US-08-939-727-7

US-08-938-727-7

US-08-938-442-2

US-08-778-394-4

US-08-778-334-2

US-08-421-822-3

US-08-421-822-3

US-08-421-822-3

US-08-421-822-3

US-08-481-099-115

US-08-38-115-017A-125

US-08-38-115-017A-125

US-08-38-115-017A-125

US-08-38-115-017A-125

US-08-38-115-017A-125

US-08-38-115-017A-125

US-08-38-115-017A-125
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Score 36; DB 2; Length 144;
Pred. No. 34;
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                                                                                                                                                  UPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/950,168
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN CORNICHON PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SUFTURARE: FastESD for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/950,168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/ACENT INFORMATION:
NAME: Billings, Lucy J.,
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-845-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08950168
Patent No. 5968744
: 3174 Porter Drive
Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59.0%;
62.5%;
                                                                                                                                        COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 144 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 62.5
Matches 5; Conservative
                                                                            ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 YYLYGMIY 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIBRARY: BLADN
CLONE: 1318847
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                                                           COUNTRY:
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US-08-950-168-3
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                  100.0%; Score 61; DB 4; Length 124; 100.0%; Pred. No. 0.0017;
                                                                                                                                                                                                                                                                                                                                                                    ANDKESSEE: MUETING, RAASCH, GEBHARDT & SCHWAPPACH, P.A. STREET: 119 NORTH FOURTH STREET, SUITE 203
CITY: MINNEAPOLIS
STATE: MINNESOTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 981;
                                                           0; Indels
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*COMPUTER READABLE FORM:

*MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Plan PC Compatible
OPERATIONG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/649,046
FILING DATE: 16-MAY-1996
FILING DATE: 16-MAY-1996
CLASSIFICATION NUMBER: 35,602
ATORNEY/AGENT INFORMATION:
NAME: MCCORMACK, MYRA H.
REGISTRATION NUMBER: 310.00340101
TELEPHONE: 612-305-1225
TELEFRAME GL2-305-1225
TELEFRAME FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
TENGTH OF SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                Sequence 2, Application US/08649046
Patent No. 5912415
GENERAL INFORMATION:
APPLICANT: OLSZEWSKI, NEIL E.
APPLICANT: JACOBSEN, STEVEN E.
TITLE OF INVENTION: THE SPINDLY GENE, METHODS OF
TITLE OF INVENTION: IDENTIFICATION AND USE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: MUETING, RAASCH, GEBHARDT & SCHWAPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-950-168-1
Sequence 1, Application US/08950168
FERREAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: GOTIEY, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN CORNICHON PROTEIN
NUMBER OF SEQUENCES:
CORNESSPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2e+02;
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Pred. No. 1.2e+02
                                                           0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 981 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                           11; Conservative
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                                                                                                                       99 SGAYYRYGVVY 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-08-649-046-2
                                                                                                  1 SGAYYRYGVVY 11
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Best Local Similarity
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                  Query Match
Best Local Similarity
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US-08-649-046-2
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                                                           Matches
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Pred. No. 34;
1; Mismatches 1; Indels
                                                                                          Score 36; DB 4; Length 144;
Pred. No. 34;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/365,705
FILING DATE: 02-Aug-1999
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09365705
Patent No. 6348576
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
Corley, Neil C.
Shah, Purvi
TITLE OF INVENTION: HUMAN CORNICHON PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/950,168
FILING DATE: 14-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0401 US
TELECOMMUNICATION INFORMATION:
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-365-705-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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US-09-257-179-63
; Sequence 63, Application US/09257179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 144 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS
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                                                                                            Query Match
Best Local Similarity 62.5%;
Matches 5; Conservative
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Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
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132 YYLYGMIY 139
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COMPUTER: IBM Comparible
OPERATING SYSTEM: DOS
SOFTWARE: FascSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/365,705
FILING DATE: 02-Aug-1999
PRIOR APPLICATION NUMBER: US/08/950,168
APPLICATION NUMBER: US/08/950,168
ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, LUCY J.
RECISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 9F-0401 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09365705
Patent No. 6348576
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
Corley, Neil C.
Shah, Purvi
TITLE OF INVENTION: HUMAN CORNICHON PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 144 amino acids
                                                                                    REFERENCE/DOCKET NUMBER: 75
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                       NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                   TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 144 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                59.0%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS
              FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIBRARY: BLADNOT04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 59.0
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   || ||:||
132 YYIYGMVY 139
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                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                    LIBRARY: GenBank
CLONE: 886769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US
ZIP: 94304
                                                                                                                                                                                                                                                                                          TOPOLOGY: line
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
US-09-365-705-1
                                                                                                                                                                                                                                                                                                                                                                       US-08-950-168-3
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GENERAL INFORMATION:
APPLICANT: OSbourn, JK
APPLICANT: Allen, DJ
APPLICANT: McCafferty, JG
TITLE OF INVENTION: Specific binding members, materials and TITLE OF INVENTION: methods.
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                 CUNTRY: United States of America
COUNTRY: United States of America
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PATENT PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,816A
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.8
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 119;
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Pred. No. 61;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 07-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/02240
FILING DATE: 02-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/244,597
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
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FILING DATE: 24-MAR.1>>*
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 23-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9525004.9
APPLICATION NUMBER: GB 9525004.9
Application US/08652816A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
US-08-894-818B-3
; Sequence 3, Application US/08894818B
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: David W. Clough REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 SGAYDNYGI 106
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                                                                                                                                                                                                                                                                                                                                                                                                                Chicago
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APPLICANT: Dignard, Daniel
APPLICANT: Dignard, Daniel
APPLICANT: Bergeron, John J.M.
APPLICANT: Bergeron, John J.M.
APPLICANT: Bergeron, John J.M.
TITLE OF INVENTION: Wethod for screening for
TITLE OF INVENTION: UDP-glucose:glycoprotein glucosyltransferase (UGGT) activity
TITLE OF INVENTION: and nucleic acid encoding for UGGT
FILE REFERENCE: 2139-9"US"
CURRENT APPLICATION NUMBER: US/09/376,330
CURRENT PILING DATE: 1999-08-18
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 35;
2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . LOCATION: (145)
, OTHER INFORMATION: Xaa equals stop translation
US-09-257-179-63
                                   APPLICANT: Ruben et al. TITLE OF INVENTION: 29 Human Secreted Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB 4
Pred. No. 54;
1; Mismatches
                                                                             TITLE OF INVENTION: 2 ILLUMINICATION TITLE OF INVENTION: 2 ILLUMINICATION NUMBER: US/09/257,179 CURRENT APPLICATION NUMBER: US/09/257,179 CARLIER FILING DATE: 1999-02-25 EARLIER FILING DATE: 1998-08-27 EARLIER FILING DATE: 1997-08-29 EARLIER FILING DATE: 1997-08-29 EARLIER FILING DATE: 1997-08-29 EARLIER FILING DATE: 1997-08-29 EARLIER FILING DATE: 1997-08-29 EARLIER FILING DATE: 1997-08-29 EARLIER FILING DATE: 1997-08-29 EARLIER FILING DATE: 1997-08-29 EARLIER FILING DATE: 1997-08-29 INUMBER: FILING DATE: 1997-08-29 INUMBER: FILING DATE: 1997-08-29 INUMBER: FILING DATE: 1997-08-29 INUMBER: FILING DATE: 1997-08-29 INUMBER: FILING DATE: 1997-08-29 INUMBER: FILING DATE: 1997-08-29 INUMBER: PALENTING DATE: 1097-08-29 INUMBER: PALENTING DATE: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; FEATURE:
; OTHER INFORMATION: GLUT-E. col
US-09-376-330-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 25
LENGTH: 106
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.0%;
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60.0%;
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Best Local Similarity 60.0
Matches 6; Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | |: ||||
57 GQYFNSGVVY 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 YYLYGMIY 139
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US-09-376-330-25
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TYPE: PRT

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RESULT 10

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Score 34; DB 4; I
Pred. No. 2.9e+02;
0; Mismatches 3;
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STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
CURRENT FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 151969/1997
PRIOR FILING DATE: 1997-06-10
NUMBER OF SEQ 1D NOS: 33
SOFTWARE: Patentin version 3.0
SEQ 1D NO 4
LENGTH: 522
TYPE: PRT
ORGANISM: Pyrococcus furiosus
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Wasning.c...
STATE: D.C.
COUNTRY: United States of America
TIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 35, Application US/08894818B Patent No. 6261822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (202) 628-5197
TELEFAX: (202) 628-5197
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 654 amino acids
TYPE: amino acid
STRANDENNESS: Sirc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAKAKURA, Hikaru
MORISHITA, Mio
YAMAMOTO, Katsuhiko
MITTA, Masanori
ASADA, Kiyozo
TSUNASAWA, Susumu
KATO, Ikunoshin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: THE TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                        55.7%;
                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 66.7
                                                                                                                                                                                                                                                                                                                                                                                                       504 AYYTYGWAY 512
                                                                                                                                                                                                                                                                                                                                                                  3 AYYRYGVVY 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: /note= Xaa at position 428 is Gly or Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.7%; Score 34; DB 4; Length 522; 66.7%; Pred. No. 2.9e+02; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: SYSTEM FOR EXPRPESSING HYPERTHERMOSTABLE FILE REFERENCE: TAKAKURA=6
CURRENT APPLICATION NUMBER: US/09/445,472
                                                                                                                                                                        HYPERTHERMOSTABLE PROTEASE GENES
                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,818B
FILING DATE: 20-MAX-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03253
FLING APPLICATION DATA:
APPLICATION NUMBER: DCT/JP96/03253
FLING APPLICATION DATA:
APPLICATION NUMBER: JP 323285/1995
FILING DATE: 12-DEC-1995
ATIONEX/AGENT INFORMATION:
                                                                                                                                                                                                                           E: Browdy and Neimark
419 Seventh Street N.W., Ste. 300
                                                                                                                                                                                                                                                                                    D.C.
: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09445472
Patent No. 6358726
                                                                                         APPLICANT: MITTA, Masanori
APPLICANT: ASADA, Kivozo
APPLICANT: TSUNASARA, Susumu
APPLICANT: KATO, Ikunoshin
ITLE OF INVENTION: HYPERTHERM
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                       MORISHITA, Mio
YAMAMOTO, Katsuhiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l: 522 amino acids
amino acid
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Best Local Similarity 66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MORISHITA, Mio
SHIMOJO, Tomoko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASADA, Kiyozo
KATO, Ikunoshin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: TAKAKURA, Hikaru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                      ZIP: 20004
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            504 AYYTYĞWAY 512
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                                                                                                                                                                                                                                                 CITY: Washington STATE: D C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-894-818B-3
                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH:
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APPLICANT:
APPLICANT:
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Gaps
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                                                                                                                                                        Length 522;
                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: YAWAMOTO, Katsuhiko
APPLICANT: MITTA, Masanori
APPLICANT: ASDA, Kiyozo
APPLICANT: TSUNASAWA, Susumu
APPLICANT: KATO, Ikunoshin
TITLE OP INVENTION: HYPERTHERMOSTABLE PROTEASE GENES
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,818B
FILING DATE: 20-MAY-1998
CLASSIFICATION 345
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CT/JP96/03253
FILING DATE: 07-NOV-1996
PRIOR APPLICATION NUMBER: US/08/894,8195
FILING DATE: 12-DEC-1995
ATPLICATION NUMBER: JP 323285/1995
FILING DATE: 12-DEC-1995
ATTONNEY/AGENT INFORMATION:
; NAME/KEY: misc_feature
; LOCATION: (428)
; OTHER INFORMATION: Xaa at position 428 is Gly or Val.
US-09-445-472-4
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Gaps
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APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 200
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 33.5; DB 4; Length 1096;
Pred. No. 7.7e+02;
2; Mismatches 1; Indels 1;
                     Indels
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CURRENT APPLICATION DATE:
DELLING DATE: US/08/053,131
PILING DATE: 26-APR-1993
Pred. No. 7.6e+02;
2; Mismatches 1;
                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Svendsen, Allan
ITILE OF INVENTION: Starch Debranching Enzymes
FILE REFERENCE: 5629.200-US
CURRENT APPLICATION NUMBER: US/09/346,237A
CURRENT FILING DATE: 1999-07-01
EARLIER APPLICATION NUMBER: PA 1998 00868
EARLIER APPLICATION NUMBER: PO/094,353
EARLIER FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                  RESULT 16
US-09-346-237-6
; Sequence 6, Application US/09346237A
; Patent No. 625197.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 78, Application US/08053131
Patent No. 5661016
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: PEPTIDE
LOCATION: (1)..(1096)
. OTHER INSPERMINON: Pullulanase
US-09-346-237-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Klebsiella aerogenes
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63.6%;
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Best Local Similarity 63.6
Matches 7; Conservative
Best Local Similarity 63.6
Matches 7; Conservative
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361 GAFYRYAMTVY 371
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                                                                   2 GAYYRYGV-VY 11
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Sequence 16, Application US/09445472

Patent No. 6358726

GENERAL INFORMATION:

APPLICANT: TAKAKURA, Hikaru

APPLICANT: SHIMOJO, Tomoko

APPLICANT: ASADA, Kiyozo

APPLICANT: ASADA, Kiyozo

APPLICANT: ASADA, Kiyozo

APPLICANT: TAKAKURA EN EN EXPRESSING HYPERTHERMOSTABLE

FILE COF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE

FILE COF TAKAKURAE: 1999-12-06

CURRENT PILING DATE: 1999-12-06

FRIOR PEPLICATION NUMBER: 151969/1997

FRIOR PELING DATE: 1997-06-10

NUMBER OF SEQ ID NOS: 33

SOSTWARE: PATENTIN VERSION 3.0
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                                                                   55.7%; Score 34; DB 4; Length 654; 66.7%; Pred. No. 3.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 34; DB 4; Length 654
Pred. No. 3.7e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/09346237A
Sequence 5, Application US/09346237A
Sequence 5, Application US/09346237A
Setent No. 6265197
GENERAL INFORMATION:
SETENCE 5, Application Henrik
APPLICANT: Stendsen, Allan
TITLE OF INVENTION: Starch Debranching Enzymes
FILE SEPERENCE: 5629, 200-US
CURRENT FILING DATE: 1999-07-01
EARLIER APPLICATION NUMBER: PA 1998 00868
EARLIER PILING DATE: 1998-07-02
EARLIER PILING DATE: 1998-07-02
EARLIER FILING DATE: 1998-07-02
NUMBER: OF SEQ ID NOS: 14
SOFTWARE: FREESO for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (1)..(1090)
OTHER INFORMATION: pullulanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Pyrococcus furiosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                         Best Local Similarity 66.7
Matches 6; Conservative
; MOLECULE TYPE: peptide US-08-894-818B-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 636 AYYTYGWAY 644
                                                                                                                                                                                                          636 AYYTYGWAY 644
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                                                                                                                                                                                                                                                                              RESULT 14
US-09-445-472-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 5
LENGTH: 1090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 16
LENGTH: 654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                        Query Match
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Gaps

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Sequence 78, Application US/07853408B

Sequence 78, Application US/07853408B

SENERAL INFORMATION:

APPLICANT: Lonberg, Nils

APPLICANT: Any Robert M.

TITLE OF INVENTION: Transgenic No. 5789650-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies

TITLE OF SEQUENCES: 150

CORRESPONDENCE ADDRESS:

ADDRESSEE: William M. Smith

STREET: One Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco

STATE: California

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transgenic No. 5814318-Human Animals for
Producing Heterologous Antibodies
                                                                                                                        54.1%; Score 33; DB 1; Length 33; 62.5%; Pred. No. 24; 1; Indels iive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 33; DB 1; Length 33;
Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/853,408B
FILING DATE: 19920318
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
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Patent No. 5814318
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No.
TITLE OF INVENTION: Producing Heter
NUMBER OF SEQUENCES: 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MBDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGIGTRATION NUMBER: 30,223
REFRENCE/DOCKET NUMBER: 146.
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.1%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 33 amino acids
AMINO ACID
                                                                                                                           Query Match 54.1
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 54.1
Best Local Similarity 62.5
Matches 5; Conservative
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                                ; MOLECULE TYPE: peptide US-08-645-641-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                              9 GSYYYYGM 16
                                                                                                                                                                                                                                                    2 GAYYRYGV 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94105
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US-08-645-641-78
Sequence 78, Application US/08645641
Fatent No. 5719032
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Producing Heterologous Antibodies
UNDBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY:
STATE: Call.
COUNTRY: USA
ZIP: 9411-3834

COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/645,641
FILING DATE: 20-MAY-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 20-MAY-1996
CLASSIFICATION NUMBER: MS 07/904,068
FILING DATE: 30-UN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-000913
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
ATTORNEY,AGENT INFORMATION:
NAME: Smith, William M.
BEGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2402
TELEPHONE: 415-326-2422
INFORMATION POR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 GSYYYYGM 16
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Sequence 275, Application US/09042353
Patent No. 6255458
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.1%; Score 33; DB 2; Length 33; 62.5%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: r. LUCKING-LUCK
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,353
FILING DATE: 13-MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
FILING DATE: 18-MAR-1992
                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     14643-9-1-1
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin pales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
                                                                                                                                                             FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/145,707
                                                                                                                                                                                                                                                   FILING DATE:
PILLING DATE:
APPLICATION NUMBER: US 07/904,
FILING DATE: 33-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.:
REGISTRATION NUMBER: 30,233
REFERENCE/DOCKET NUMBER: 14643
TELECOMMUNICATION INFORMATION:
TELEPAX: 415-326-2400
TELEPAX: 415-326-2402
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 33 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |:|| ||:
9 GSYYYYGM 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GAYYRYGV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-042-353-275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-308-865-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Patent No. 5877397
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5877397-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 33;
                            E: Townsend and Townsend Khourie and Crew
One Market Plaza, Steuart Tower, Suite 200
                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/096,762
FILING DATE: 22-JUL-1993
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION NUMBER: US 07/990,660
FILING DATE: 123-JUN-1992
PRIOR APPLICATION NUMBER: US 07/904,068
FILING DATE: 13-JUN-1992
PRIOR APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
ATTONNEY,AGENT INFORMATION:
NAME: SMITCH, WIlliam M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-26-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.1%;
62.5%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
"FWGTH: 33 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 62.5
...nes 5, Conservative
                                        STREET: ONE MALLE CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSYYYYGM 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GAYYRYGV 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 21
US-08-308-865-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Ca
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Gaps
        Producing Heterologous Antibodies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                   ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPETATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic Non-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies
                                                                                   ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/08/758,417A
APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-Dec-1996
CLASSIFICATION: UNMER: US 08/728,463
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
FILING DATE: 07-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MR-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
PILING DATE: 0-DEC-1993
APPLICATION NUMBER: US 08/155,301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-UUL-1993
APPLICATION NUMBER: US 08/053,131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 26 APR-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
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MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 123:
US-08-758-417A-123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 24
PCT-US92-10983-78
Sequence 78, Application PC/TUS9210983
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 123
                              NUMBER OF SEQUENCES: 417
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
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Best Local Similarity
Matches 5; Conserv
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Patent No. 6300129
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 10-0CT-1996

PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-0CT-1996

PRIOR APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996

PRIOR APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
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REFERENCE/DOCKET NUMBER: 36,429
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                                                                                              PRIOR DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-UUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
PRIOR APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
PRIOR APPLICATION NUMBER: US 08/20,741
FILING DATE: 07-DEC-1994
PRIOR APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
PRIOR APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/544,404 FILING DATE: 10-0CT-1995 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463 FILING DATE: 10-0CT-1996
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |:|| ||:
|GSYYYYGM 16
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Best Local Similarity
Matches 5; Conserv
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Gaps

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Length 267;

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Score 33; DB 1;
Pred. No. 2.1e+02;
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; Sequence 3, Application US/08448164
; Patent No. 5925536
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (212)869-8864/9741
      (212)869-8864/9741
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Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                       54.1%;
83.3%;
                                                                                       LENGTH: 267 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                       Query Match 54.1
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                             192 GSYYRY 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                              US-08-015-973-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
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APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
TITLE OF INVENTION: A NOVEL RECEPTOR TITLE OF INVENTION:
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
        NUMBER OF SEQUENCES: 152
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
STREET: New York
CUMTY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/015,973
FILING DATE: 10-FEB-1993
CLASSIFICATION: 435
                                                                                                                                               COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

FILING DATE: 19921217

CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION WINBER: 30,223
RECISTRATION WINBER: 14643-9-2
REFERENCE/DOCKET NUMBER: 14643-9-2
TELEPHONE: 415-326-2400
TELEPHONE: 415-326-2400
TELEPHONE: 415-326-2400
TELEPHONE: 415-326-2400
TELEPHONE: 415-326-2400
TELEPHONE: 415-326-2400
TELEPHONE: 415-326-2400
TELEPHONE: 415-326-2400
TELEPHONE: 415-326-2400
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08015973
Patent No. 5604094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 76
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.1%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 62.5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                          CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |:|| ||:
GSYYYYGM 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GAYYRYGV 9
                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US92-10983-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE
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GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
TITLE OF INVENTION: PHOSPHATASE-BETA
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: Patentin Release #1.0, Version #1.25 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION NUMBER: US/08/448,164 FILING DATE: 24-MAY-1995 CLASSIFICATION NUMBER: US 08/015,973 FILING DATE: 10-FEB-1993 ATTORNEY/AGENT INFORMATION: NAME: Mistorck, S. Lesie REGISTRATION NUMBER: 18,872 REFERENCE/DOMINICATION NUMBER: 7683-021 TELECOMMUNICATION NUMBER: 7683-021 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 33; DB 2; 1
Pred. No. 2.1e+02;
1; Mismatches 0.
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APPLICANT: Takateu, Kiyoshi
APPLICANT: Takateu, Kiyoshi
APPLICANT: Takagi, Astrah
APPLICANT: Takagi, Satoshi
APPLICANT: Murata, Yoshiyuki
TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE PADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 315;
                MEDIUM TYPE: Floppy disk Computible Computer: IBM PC Compatible CORPUTER: IBM PC Compatible CORPUTER: IBM PC COMPASSIONS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,390
FILING DATE: 19910910
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
RESTRENCE/DOCKET VUMBER: 10,705-030
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,282
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33; DB 1;
Pred. No. 2.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/757,390
FILING DATE: 10-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5760204
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
                                                                                                                                                                                                                                                                                                                                  TELEFAX: 212 869864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEO ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 212 8698864/9741
66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 315 amino acids
TYPE: AMINO ACID
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-07-757-390-8
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33; DB 4; Length 267;
                                                   Sequence 3, Application US/08081929
Patent No. 6160090
GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
APPLICANT: Barnea, Gllad
APPLICANT: Martin H.
APPLICANT: Martin H.
APPLICANT: Margolis, Richard U.
TITLE OF INVENTION: STRUCTURAL DOMAINS AND LIGANDS
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/081,929
FILING DATE: 23-UUN-1993
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30742
REFERENCE TOOKET NUMBER: 7683-041-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                          SSEE: PENNIE & EDMONDS
I: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/07757390; Patent No. 5453491; GENERAL INFORMATION: APPLICANT: Takatsu, Kiyoshi APPLICANT: Takatsu, Katra APPLICANT: Takagi, Satoshi APPLICANT: Muzata, Yoshiyuki; TILLE OF INVENTION: Human And Muri; VIMMER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.1%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
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Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                         New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: sin
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                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10036
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STREET: 11
                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                RESULT 27
US-08-081-929-3
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US-07-757-390-8
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Gaps

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MOLECULE TYPE: peptide
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152 YYRFGVL 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                              ADDRESSEE:
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                                        JS-08-939-727-8
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APPLICANT: Takateu, Kiyoshi
APPLICANT: Takagi, Akira
APPLICANT: Takagi, Satoshi
APPLICANT: Murada, Yoshiyuki
TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.1%; Score 33; DB 1; Length 315; 71.4%; Pred. No. 2.5e+02; tive 2; Mismatches 0; Indels
                                                                                                                                                                       DB 1; Length 315;
                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,281
                                                                                                                                                                                        2.5e+02;
                                                                                                                                                                                        Pred. No. 2.5e
2; Mismatches
                                                                                                                                                                     54.1%; Score 33; 71.4%; Pred. No. 3
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/757,390
FILING DATE: 10-SEP-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/08442281 Patent No. 5807991 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 70
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                      LENGTH: 315 amino acida
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 315 amino acids amino acid
                                                                                                                                                                     Query Match 54.1
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 315 amino aci
                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide
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152 YYRFGVL 158
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152 YYRFGVL 158
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Best Local Similarity
Matches 5; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                US-08-442-282-8
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Sequence 8, Application US/08939727
Patent No. 5916767
GENERAL INFORMATION:
APPLICANT: Takatsu, Kiyoshi
APPLICANT: Tominaga, Akira
APPLICANT: Takagi, Satoshi
APPLICANT: Murata, Yoshiyuki
TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Takatsu, Kiyoshi
APPLICANT: Takatsu, Akira
APPLICANT: Takagi, Satoshi
APPLICANT: Takagi, Satoshi
APPLICANT: Murata, Yoshiyuki
TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/939,727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 54.1%; Score 33; DB Best Local Similarity 71.4%; Pred. No. 2.5e Matches 5; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                         STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                           STATE: New York
COUNTRY: U.S.A.
ZIP. 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/757,390
FILING DATE: 10-SEP-1991
ATTORNEY, AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/07757390
Patent No. 5453491
                                                                                                                                                                                                                                                            Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION TELEPHONE: 212 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                315 amino acids
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APPLICANT: Takatsu, Kiyoshi
APPLICANT: Takatsu, Kiyoshi
APPLICANT: Takatsu, Katra
APPLICANT: Takatsu, Akira
APPLICANT: Takatsu, Satchia
APPLICANT: Tominaga, Akira
APPLICANT: Tominaga, Akira
APPLICANT: Murata, Soshiyuki
TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
UNMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STRET: 1155 Avenue of the Americas
CITY: New York
COUNTY: Ne
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                                                                                                                                                                                                                                                                                                                                                                              Length 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,281
                                                                                                                                                                                                                                                                                                                                                                          54.1%; Score 33; DB 1; 71.4%; Pred. No. 2.7e+02; ive 2; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/757,390
FILING DATE: 10-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/08442281
Patent No. 5807991
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18,872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 212 790-9090
TELEFAX: 212 869864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SCO ID NO: 7:
SEQUENCE CHARACTERISTICS:
      212 8698864/9741
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                                                                                                                                           332 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           332 amino acids
                                         TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                          Query Match 54.1
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                          unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
                                                                                                                                                                                                                                      ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-442-282-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |||:||:
169 YYRFGVL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 YYRYGVV 10
                                                                                                                                                                       TYPE: amino acid STRANDEDNESS: unl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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      TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-442-281-7
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Patent No. 5760204

GENERAL INFORMATION:
APPLICANT: Takatsu, Kiyoshi
APPLICANT: Tominaga, Akira
APPLICANT: Takagi, Satoshi
APPLICANT: Marata, Yoshiyuki
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.1%; Score 33; DB 1; Length 332; 71.4%; Pred. No. 2.7e+02; Live 2; Mismatches 0; Indels
                                                                                                            MEDIUM 11FD: R.L.C.P. ALC.

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

SUSTRARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,390

FILING DATE: 19910910

CLASSIFICATION: 50

ATTORNEY AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 7005-030

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
STELEMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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COUNTRY: U.S.A.
ZID: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,282
FILING ATTE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/757,390
FILING DATE: 10-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7005-030
TELEPHONE: 212 790-9090
                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 332 amino acids
TYPE: AMINO ACID
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: peptide US-07-757-390-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | | | | : | | :
169 YYRFGVL 175
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 YYRYGVV 10
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US-08-442-282-7
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COUNTRY:
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TITLE OF INVENTION: NOVEL METHOD FOR TESTING THE
TITLE OF INVENTION: DIFFERENTIATION STATUS IN PANCREATIC CELLS OF A MAMMAL
NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: DatentIn Release #1.0, Version #1.30 (BPO)
APPLICATION NUMBER: US/08/778,394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
TITLE OF INVENTION: NOVEL METHOD FOR TESTING THE
TITLE OF INVENTION: DIFFERENTIATION STATUS IN PANCREATIC CELLS OF A MAMMAL
NUMBER OF SEQUENCES: 16
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.1%; Score 33; DB 3; Length 332; 66.7%; Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54.1%; Score 33; DB 2; 66.7%; Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                             US/08/958,642
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                                                                                       FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/778,423
FILING DATE: December 31, 1996
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08778394
Patent No. 6028184
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 332 amino acids
amino acid
                                                                                                                                                                                                                                                                                  : 332 amino acids
amino acid
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Matches 6; Conservative
                         CURRENT APPLICATION DATA APPLICATION NUMBER: UK
                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-958-642-2
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59 GRYYRTGVL 67
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-778-423A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
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                                                                                                                                                           APPLICANT: Takatsu, Kiyoshi
APPLICANT: Takatsu, Akira
APPLICANT: Takatsu, Akira
APPLICANT: Takati, Satoshi
APPLICANT: Murata, Yoshiyuki
APPLICANT: Murata, Yoshiyuki
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APPLICANT: Murata, Yoshiy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/939,727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NOVEL METHOD FOI
TITLE OF INVENTION: DIFFERENTIATION
NUMBER OF SEQUENCES: 16
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/757,390
FILING DATE: 10-SEP-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                 Sequence 7, Application US/08939727
Patent No. 5916767
GENERAL INFORMATION:
APPLICANT: Takatsu, Kiyoshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFRENCE/DOCKET NUMBER: 7005:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 332 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08958642
Patent No. 5948623
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 71.4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |||:||:
169 YYRFGVL 175
   169 YYRFGVL 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New York
: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: New York
STATE: New Yorl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
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US-08-958-642-2
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Gaps

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0; Indels

71.4%; Pred. No. 2.7e+02; tive 2; Mismatches 0

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5; Conservative
                                                                                                                                                                                  |||:||:
|172 YYRFGVL 178
                                Best Local Similarity
                                                                                                                                   4 YYRYGVV 10
                                                                                                                                                                                                                                                                                                              RESULT 40
US-08-421-822-3
                                                             Matches
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APPLICANT: Devos, Rene
APPLICANT: Fiers, Walter
APPLICANT: Ters, Walter
APPLICANT: Tavernier, Jan
TITLE OF INVENTION: Chimeric Interleukin-5
TITLE OF INVENTION: Receptor/Immunoglobulin Polypeptides
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mr. George M. Gould, Esq.
STREET: 340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54.1%; Score 33; DB 3; Length 332; 66.7%; Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/778,423A
FILING DATE: December 31, 1996
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAPPUTER TEADABLE FORM:

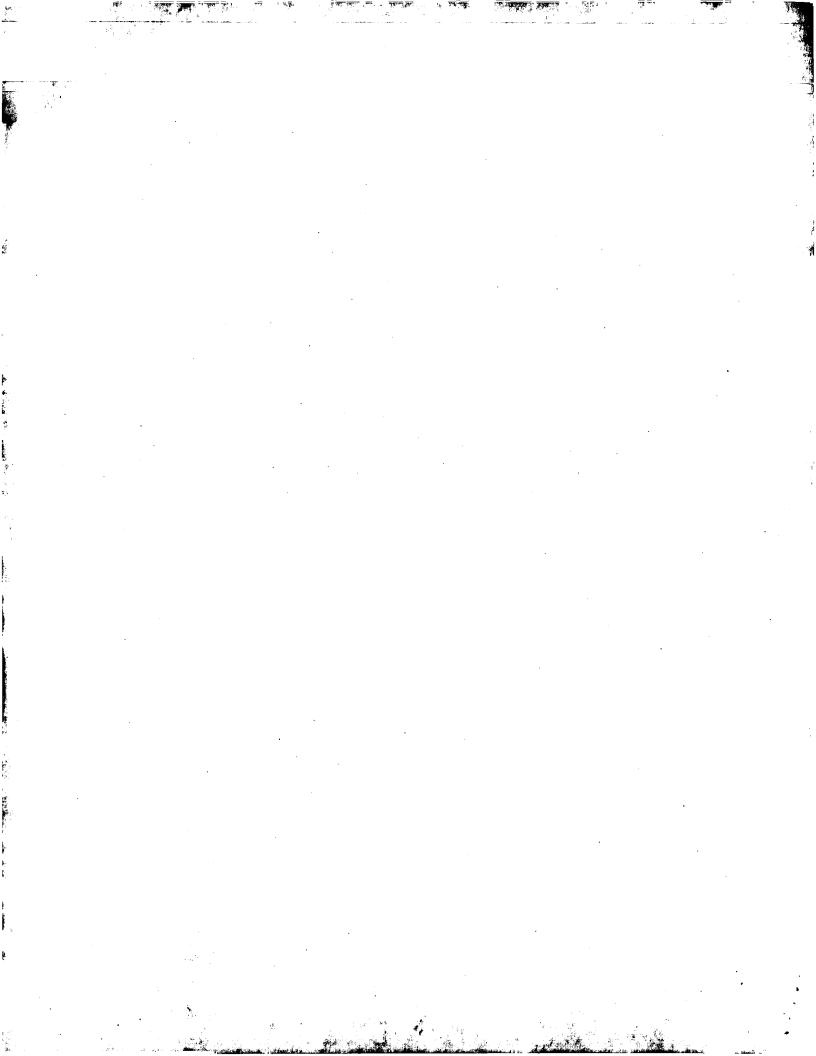
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: RC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/947,130
FLING DATE: 19920916
FLING APPLICATION DATA:
APPLICATION NUMBER: E 91810738.4
FILING DATE: 18-SEP-1991
ATTORNEY/AGENT INPORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 32,655
REFERENCE/OFCT NUMBER: 32,655
REFERENCE/OFCT NUMBER: 31,655
REFERENCE/OFCT NUMBER: 32,655
REFERENCE/OFCT NUMBER: 32,655
REFERENCE/OFCT NUMBER: 31,655
REFERENCE/OFCT NUMBER: 32,655
REGUENCE CHRARATERISTICS:
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REGUENCE CHRARATERISTICS:
REGUENCE CHRARAT
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B13
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amino acid
GY: linear
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TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 66.7
Matches 6; Conservative
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HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
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ADDRESSEE: K. STREET: 340 Kii._
TITY: Nutley
"F: New Jersey
"F: New Jersey
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                                                                                                                                                                                                                                                                                                                                                                                                                US-08-778-423A-2
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US-07-947-130-3
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54.1%; Score 33; DB 1; Length 335;

Query Match

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0
                       GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Fiers, Walter
APPLICANT: Tavernier, Jan
TITLE OF INVENTION: Chimeric Interleukin-5
TITLE OF INVENTION: Chimeric Interleukin-5
TITLE OF INVENTION: Receptor/Immunoglobulin Polypeptides
NUMBER OF SEQUENCES: .22
CORRESPONDENCE ADDRESS:
ADDRESSEB: Mr. George M. Gould, Esq.
STREET: 340 Kingsland Street
CITY: Nutley
STREET: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 335;
                                                                                                                                                                                                                                                                                    COUNTRY:

2IP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/421,822
FILING MATE: 13-APR-1995
FILING TANTON: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 33; DB 1; Pred. No. 2.7e+02; 2; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 13-APR-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/947,130
FILING DATE: 16-SEP-1992
APPLICATION NUMBER: EP 91810738.4
FILING DATE: 18-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: July 18, 2003, 15:11:49
Job time : 13.76 secs
Sequence 3, Application US/08421822 Patent No. 5668256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: mouse
CELL TYPE: B-cell precursor
CELL LINE: B13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-235-6326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.18;
71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 335 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 71.4
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |||:||:
172 YYRFGVL 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
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Sequence 32, Appl
Sequence 3145, Ap
Sequence 77, Appl
Sequence 79, Appl
Sequence 2, Appli
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Sequence 12, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14372, F
Sequence 3, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 322, App
                                                                                                                                           July 18, 2003, 15:09:56; Search time 28.38 Seconds (without alignments) 46.031 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 322,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 322,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 327
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Sequence 32'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published Applications AA:*

1: /cgn2 6/ptodata/1/pubpaa/PCT NEW PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT NEW PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/PCT NEW PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/NSO6 NEW PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/NSO6 PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/NSO8 PUBCOMB.pep:*

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9: /cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/USO9_NEW PUB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/USO9_NEW PUB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/USO9_NEW PUB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/USO9_NEW PUB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/USO0 PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/USO0 NEW PUB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/USO0 NEW PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 .08-10-156-761-14372

1 US-09-912-559-4

1 US-09-912-559-4

1 US-09-912-559-4

2 US-10-172-712-32

2 US-09-880-748-3145

1 US-09-840-459-79

0 US-09-76-275A-322

US-09-978-375A-322
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US-09-736-457-327
US-09-978-697-322
US-09-902-941-327
US-09-978-192A-322
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                                                                                                                                                                                                                                                                                                                                                                                                                          451899 segs, 118759770 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq length: 0
seq length: 200000000
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Match Length DB
                                                                                                                                                                                                                                               US-10-007-790-7
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                                                                                                                                                                                                                                                                                                                                                   Scoring table:
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                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
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App	App	App	App	App	App	App	App	App	App	2, App	App	App	App	App	App	App	App	App	ppli	ppli	App	App	App	App	App	App	App	App
322,	327,	322,	322,	322,	322,	322,	322,	322,	322,	322,	322,	322,	322,	322,	322,	322,	322,	327,	1, A	3, A	120,	120,	120,	120,	322,	120,	327,	322,
Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
	US-09-849-626-327	-09	US-09-978-608A-322	-60	US-09-978-191A-322	-60	US-09-978-564A-322	-666-60-	•	US-09-978-824-322	0	0	US-09-978-193A-322	US-09-999-830A-322	US-09-978-757A-322	US-09-978-187B-322	US-09-978-643A-322	0	US-10-044-477-1	US-10-044-477-3	US-10-227-884-120	US-10-230-163-120	US-10-230-338-120	US-10-218-631-120	US-10-017-081A-322	US-10-230-414-120	10-	US-10-167-749-322
Ţ	11	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	15	15	15	15	15	15	15	15	15	12
144	144	144	144	144	144	144	144	144	144	144	144	144	144	144	144	144	144	144	144	144	144	144	144	144	144	144	144	144
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9.8	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36
1.1	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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Sequence 33, Application US/09828708

Sequence 33, Application US/09828708

Patent No. US20020146753A1

APPLICANT: No. US20020146753A1

APPLICANT: Burton, D. APPLICANT: Schaller, M. APPLICANT: Schaller, M. TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their particit TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their particit TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their particit CURRENT PILICATION NUMBER: US/09/828, 708

CURRENT PILING DATE: 2001-09-24

NUMBER OF SEQ ID NOS: 123

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 33

LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ditzel, H.
APPLICANT: Burton, D.
APPLICANT: Schaller, M.
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their particit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.95;
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Pred. No. 0.95
1; Mismatches
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Patent No. US20020146753A1
GENERAL INFORMATION:
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77.8%;
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 SGAYYYYGM 12
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US-09-828-708-33
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APPLICANT: NERLICH, CLAUDIA
APPLICANT: NERLICH, CLAUDIA
APPLICANT: NUTH-NAUMANN, GUDRUN
TITLE OF INVENTION: MUTANTS OF THE FACTOR VII-ACTIVATING PROTEASE AND
TITLE OF INVENTION: DETECTION METHODS USING SPECIFIC ANTIBODIES
FILE REFERENCE: 06478.1457
CURRENT APPLICATION NUMBER: US/09/912,559
CURRENT APPLICATION NUMBER: DE 100 36 641.4
PRIOR PRICATON NUMBER: DE 100 36 641.4
PRIOR FILING DATE: 2000-07-26
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 4
SOFFWARE: Patentin Ver: 2.1
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Pred. No. 1.5e+02;
.; Mismatches 2
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66.7%; Pred. No. 1.5e+02;
cive 1; Mismatches 2
                                     PRIOR APPLICATION NUMBER: DE 100 30 011.1
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: DE 100 50 040.4
PRIOR PILING DATE: 2000-10-10
PRIOR PLING DATE: 2000-10-10
PRIOR PLING DATE: 2000-10-21
PRIOR FILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 560
  CURRENT APPLICATION NUMBER: US/09/912,559
CURRENT FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: DE 100 36 641.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-912-559-4
; Sequence 4, Application US/09912559
; Patent No. US20020142316Al
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Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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; ORGANISM: Homo sapiens
US-09-912-559-4
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                                                                                                                                                                                                                                                                                                      TYPE: PRT
CORGANISM: Homo sapiens
US-09-912-559-3
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US-10-172-712-32
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85.7%; Pred. No. 1.1e+02;
tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                          Score 40; DB 11; Length 116;
Pred. No. 8.7;
                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
ITLE OE INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT PILING DATE: 2002-05-29
PRIOR PILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-06-02
PRIOR PILING DATE: 2001-06-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 14372
LENGTH: 420
TITLE OF INVENTION: autoimmune disease
FILE REFERENCE: 1361.005US1
CURRENT APPLICATION NUMBER: US/09/828,708
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 116
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Publication No. US20030119018A1
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; ORGANISM: Streptomyces avermitilis
US-10-156-761-14372
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Patent No. US20020142316A1
GENERAL INFORMATION:
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BECKER, MARGRET
NERLICH, CLAUDIA
MUTH-NAUMANN, GUDRUN
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APPLICANT: STOEHR, HANS-ARNOLD
APPLICANT: FEUSSNER, ANNETTE
APPLICANT: MEING, WIEGAND
APPLICANT: WEINER, THOMAS
APPLICANT: BECKER, MARGRET
                                                                                                                                                                                                                                                            Query Match 65.6%;
Best Local Similarity 77.8%;
Matches 7; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SHIBA, TADAYOSHI
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Best Local Similarity 85.7
Matches 6; Conservative
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                                                                                                                                                                         TYPE: PRT
CORGANISM: Homo sapiens
US-09-828-708-12
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APPLICANT:
APPLICANT:
APPLICANT:
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Gaps

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Length 560;

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NAME/KEY: VARIANT

LOCATION: (1)...(128)

COTHER INFORMATION: Xaa = Any Amino Acid

MS-09-840-459-79
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Patent No. US20020150576A1
GENERAL INFORMATION:
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66.7%;
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Best Local Similarity 66.,
6. Conservative
       Newman, Walter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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                                       APPLICANT: GALE, ANDREW J.
APPLICANT: GALE, ANDREW J.
APPLICANT: GALE, ANDREW J.
APPLICANT: GALE, ANDREW J.
APPLICANT: GENEROFF, ELIZABETH D.
APPLICANT: PELEQUER, JEAN-LUC
TITLE OF INVENTION: STABILIZED PROTEINS WITH ENGINEERED DISULFIDE BONDS
FILE REPERENCE: 4198-4001US1
CURRENT APPLICATION NUMBER: US/10/172,712
PRIOR APPLICATION NUMBER: US/10/172,712
PRIOR PAPLICATION NUMBER: 00/298,578
PRIOR FILING DATE: 2001-06-14
NUMBER OF SEQ ID NOS: 32
SOFTWARE PATENTIN VET: 2.1
SEQ ID NO 32
LENGTH: 560
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR PILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PATCHIL VOT: 2.0
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GENERAL INFORMATION: APPLICANT: LARGAS Gregory J.
APPLICANT: Horvath, Christopher
Publication No. US20030125232A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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; ORGANISM: Homo sapiens
US-09-880-748-3145
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ORGANISM: Homo sapiens
US-10-172-712-32
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US-09-880-748-3145
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SOFTWARE: Paten
SEQ ID NO 3145
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Pred. No. 47;
1; Mismatches 2; Indels
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Refee, Thereas
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED OF USE THEREFOR
FILE REFERENCE: 1855.1052-012
CURRENT APPLICATION NUMBER: US/09/840,459
CURRENT APPLICATION NUMBER: DCT/USO1/03537
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1998-07-23
PRIOR FILING DATE: 1998-07-23
PRIOR FILING DATE: 1998-07-23
PRIOR FILING DATE: 1998-07-23
PRIOR FILING DATE: 1998-07-23
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
PRIOR FILING DATE: 1998-07-23
PRIOR FILING DATE: 1998-07-23
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR PRIOR FILING DATE: 1998-07-23
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APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Newman, Walter
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Refe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052-012
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/151,781
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 128
LENGTH: 128
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COCATION: (1)...(128)
COTHER INFORMATION: Xaa = Any Amino Acid
US-09-840-459-77
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                       US-09-978-375A-322
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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                         Gaps
                                                                                                                                                                                                                  Sequence 2, Application US/09765205
| Patent No. US20020034800A1
| GENERAL INFORMATION:
| APPLICANT: Cao, Li
| TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
| FILE REFERENCE: 1458.004/200130.449
| CURRENT APPLICATION NUMBER: US/09/765,205
| CURRENT FILING DATE: 200.10.1.7
| PRIOR APPLICATION NUMBER: US/09/212,440
| PRIOR FILING DATE: 1998-12-16
| NUMBER OF SEQ ID NOS: 46
| SOFTWARE: FastSEQ for Windows Version 3.0
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               59.0%; Score 36; DB 11; Length 128; 66.7%; Pred. No. 47; 2; Indels ive 1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ferrara, Napoleon
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Gerritsen, Mary E.
Goddard, Audrey
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Paoni, Nicholas F.
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Botstein, David
Desnoyers, Luc
Eaton, Dan
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Kuo, Sophia S.
Query Match
Best Local Similarity 66...
6. Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                 107 SGXÝÝÝÝGM 115
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                                                                                              1 SGAYYRYGV 9
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CRGANISM: human
US-09-765-205-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 142
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US-09-765-205-2
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AFTLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REPRENCE: PS508PC11.

FILE REPRENCE: PS508PC11.

CURRENT APPLICATION NUMBER: US/9978,295A

CURRENT FILING DATE: 2001-10-15

PRIOR FILING DATE: 1097-10-17

PRIOR FILING DATE: 1097-11-0-17

PRIOR FILING DATE: 1997-11-13

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PRIOR FILING DATE: 1998-03-10

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PRIOR PRIOR PRIOR NUMBER: 60/077632
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Pred. No. 53;
2; Mismatches 1; Indels
FILE REFERENCE: P2630P1C24
CURRENT APPLICATION WNDBER: US/09/978,375A
CURRENT FILING DATE: 2002-04-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 624
SEO ID NO 322
LENGTH: 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 322, Application US/09978295A Patent No. US20020156006Al GENERAL INFORMATION:
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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APPLICATION NUMBER: 60/077641
FILING DATE: 1998-03-11
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Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 62.5%;
Matches 5; Conservative
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Filvaroff, Ellen
Fong, Sherman
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Goddard, Audrey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Betstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
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Pan, James;
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BER: 60/0776 BER: 30/0777 BER: 03-11 98-03-12 98-03-12 98-03-20 98-03-20 98-03-20 98-03-20 98-03-20 98-03-20 98-03-20	ο σο σο σο σο σο σο σο σο σο σο σο σο σο	. 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 6 10 10 10 10 10 10 10 10 10 10 10 10 10
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PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/08204
PRIOR APPLICATION NUMBER: 60/08204
PRIOR PLILING DATE: 1998-04-22
PRIOR PLILOGATION NUMBER: 60/082700
PRIOR PLILOGATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR PLILOGATION NUMBER: 60/082322
PRIOR PLILOGATION NUMBER: 60/083322
PRIOR PLILOGATION NUMBER: 60/083329
PRIOR PLILOGATION NUMBER: 60/083545
PRIOR PLILOGATION NUMBER: 60/083545
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PRIOR PLILOGATION NUMBER: 60/084546
PRIOR PLILOGATION NUMBER: 60/084549
PRIOR PLILOGATION NUMBER: 60/084549
PRIOR PLILING DATE: 1998-05-07
PRIOR PLILOGATION NUMBER: 60/084549
PRIOR PLILING DATE: 1998-05-07
PRIOR PLILOGATION NUMBER: 60/08459
PRIOR PLILOGATION NUMBER: 60/08459
PRIOR PLILOGATION NUMBER: 60/08459
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PRIOR PLILOGATION NUMBER: 60/08559
PRIOR P

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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC27
CURRENT APPLICATION NUMBER: US/09/978,697
PILIS DATE: 2001-10-16
                                                                                                                                                                                                                                                                                                                         CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/066364
PRIOR APPLICATION NUMBER: 60/066364
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LIOR APPLICATION NUMBER: 60/077649
KIOR FILING DATE: 1998-03-11
RIOR APPLICATION NUMBER: 60/07791
RIOR APPLICATION NUMBER: 60/078004
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APPLICATION NUMBER: 60/078939
FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/079294
FILING DATE: 1998-03-25
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APPLICATION NUMBER: 60/080327
FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/080328
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APPLICATION UNMBER: 60/078886
FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/078936
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RIOR FILING DATE: 1998-03-26
RIOR APPLICATION NUMBER: 60/079664
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APPLICATION NUMBER: 60/079689
FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079663
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APPLICATION NUMBER: 60/079728
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APPLICATION NUMBER: 60/079786
FILING DATE: 1998-03-27
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RIOR FILING DATE: 1998-03-30
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APPLICATION NUMBER: 60/080105
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PRIOR APPLICATION NUMBER: 60/080165
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RIOR FILING DATE: 1998-03-10
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APPLICATION NUMBER: 60/077632
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APPLICATION NUMBER: 60/078910
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PRIOR APPLICATION NUMBER: 60/080107
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APPLICATION NUMBER: 60/080194
                                                                                                    Shelton, David L.
Stewart, Timothy A.
                                                   aoni, Nicholas F.
                                                                               Margaret Ann
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APPLICANT: Mannion, Jane
APPLICANT: Fan, Ligun
APPLICANT: Wang, Aijun
TITLE OF INVENTION: DIAGNOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                 Query Match 59.0%; Score 36; DB 11; Length 144; Best Local Similarity 62.5%; Pred. No. 53; Matches 5; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59.0%; Score 36; DB 11; Length 144; 62.5%; Pred. No. 53; tive 2; Mismatches 1; Indels
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Patent No. US20020169284A1
GENERAL INFORMATION:
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
                                                                                                                                                                                                                                                                                                                                                                            Sequence 327, Application US/09736457
Patent No. US20020168637A1
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
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Bangur, Chaitanya S.
Lodes; Michael A.
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Filvaroff, Ellen
Fong, Sherman
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Vedvick, Tom
Carter, Darrick
Retter, Marc
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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Best Local Similarity 62.5
Matches 5; Conservative
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Kuo, Sophia S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-327
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R FILING DATE: 1998-04-29
R APPLICATION NUMBER: 60/083559
R FILING DATE: 1998-04-29
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R APPLICATION NUMBER: 60/083742
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FILING DATE: 1998-04-28
APPLICATION NUMBER: 60/083392
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APPLICATION UNMBER: 60/083495
FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083496
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FILING DATE: 1998-04-29
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APPLICATION NUMBER: 60/084441
FILING DATE: 1998-05-06
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FILING DATE: 1998-05-07
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FILING DATE: 1998-04-09
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FILLING DATE: 1998-04-15
APPLICATION NUMBER: 60/081817
APPLICATION NUMBER: 60/081819
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FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/082797
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FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083558
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FILING DATE: 1998-05-05
APPLICATION NUMBER: 60/084414
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APPLICATION NUMBER: 60/082568
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APPLICATION NUMBER: 60/083336
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FILING DATE: 1998-04-22
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FILING DATE: 1998-04-09
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APPLICATION NUMBER: 60/
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| PRIOR PAPILICATION DATE 1999-0-5-07
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59.0%; Score 36; DB 11; Length 144;

Query Match

THE THERAPY

APPLICANT: MCNabb, Andria
TITLE OF INVENTION: COMEOSITIONS AND METHODS FOR TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.478C17
CURRENT APPLICATION NUMBER: US/09/902,941
CURRENT FILING DATE: 2001-07-10

NUMBER OF SEQ ID NOS: 2002
SOFTWARE: FastSEQ for Windows Version 4.0
ESQ ID NO 327
LENGTH: 144
TYPE: PRT
ORGANISM: Homo sapiens
US-09-902-941-327

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R APPLICATION NUMBER: 66/079920
R FILING DATE: 1998-03-30
R APPLICATION NUMBER: 66/079923
R APPLICATION NUMBER: 66/080105
R APPLICATION NUMBER: 66/080105
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APPLICATION NUMBER: 60/081838
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/082568
FILING DATE: 1998-04-21
                                                                                                                                                                                      APPLICATION NUMBER: 60/079689
FFILING DATE: 1998-03-27
APPLICATION NUMBER: 60/07963
APPLICATION NUMBER: 60/079728
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APPLICATION NUMBER: 60/080328
FILING DATE: 1998-04-01
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APPLICATION NUMBER: 60/081195
FILING DATE: 1998-04-08
FILING DATE: 1998-04-09
                                                                                            APPLICATION NUMBER: 60/079656
FILING DATE: 1998-03-26
APPLICATION NUMBER: 60/079664
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APPLICATION NUMBER: 60/079786
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APPLICATION NUMBER: 60/080334
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APPLICATION NUMBER: 60/081070
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APPLICATION NUMBER: 60/081049
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APPLICATION NUMBER: 60/081817
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APPLICATION NUMBER: 60/081952
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APPLICATION NUMBER: 60/082704
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APPLICATION NUMBER: 60/082804
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APPLICATION NUMBER: 60/082797
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APPLICATION NUMBER: 60/082796
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APPLICATION NUMBER: 60/083336
                                             PLICATION NUMBER: 60/079294
LING DATE: 1998-03-25
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APPLICATION NUMBER: 60/081955
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MAT: Wood, William I.
OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
OF INVENTION: Acids Encoding the Same
                           Gaps
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                         1; Indels
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CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918685
PRIOR APPLICATION NUMBER: 09/918685
PRIOR APPLICATION NUMBER: 60/06250
PRIOR FILING DATE: 1997-11-0-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-0-17
PRIOR APPLICATION NUMBER: 60/06431
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065314
PRIOR PILING DATE: 1997-11-13
PRIOR PELING DATE: 1999-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR PILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR FILING DATE: 1998-03-11
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PRIOR PILING DATE: 1998-03-13
  Pred. No. 53;
2; Mismatches
                                                                                                                                                                                                                                           Sequence 322, Application US/09978192A
Patent No. US20020177553A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
62.5%;
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Gerritsen, Mary E.
Goddard, Audrey
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Pan, James;
Paoni, Nicholas F.
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T. Baker Kevin P.
T. Botstein, David
T. Desnoyers, Luc
T. Eaton, Dan
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Kuo, Sophia S.
Best Local Similarity 62.5
Matches 5; Conservative
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US-09-978-192A-322
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FILING DATE: 1998-04-27

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APPLICANT: Tunas, Daniel
APPLICANT: Tunas, Daniel
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APPLICANT: Tunas, Daniel
APPLICANT: William I.
APPLICANT: William I.
APPLICANT: William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
AILLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
CURRENT APPLICATION NUMBER: US/09/999,832A
CURRENT APPLICATION NUMBER: US/09/9885
PRIOR PLING DATE: 1097-10-730
PRIOR APPLICATION NUMBER: 60/06250
PRIOR APPLICATION NUMBER: 60/06364
PRIOR PLING DATE: 1997-10-17
PRIOR PLING DATE: 1997-10-17
PRIOR PLING DATE: 1997-10-17
PRIOR PLING DATE: 1998-03-10
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
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PRIOR FILING DATE: 1000
RESULT 17
US-09-99-832A-322
; Sequence 322, Application US/09999
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
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Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Gao, Wei-Qiang
Gerber, Hanspeter
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Desnoyers, Luc
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          R APPLICATION NUMBER: 60/083322

R FILING DATE: 1998-04-28

R FILING DATE: 1998-04-29

R APPLICATION NUMBER: 60/083495

R APPLICATION NUMBER: 60/083495

R FILING DATE: 1998-04-29

R APPLICATION NUMBER: 60/083496

R FILING DATE: 1998-04-29

R APPLICATION NUMBER: 60/083496
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R APPLICATION NUMBER: 60/08358
R APPLICATION NUMBER: 60/08359
R FILING DATE: 1998-04-29
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R APPLICATION NUMBER: 60/084441
R FILING DATE: 1998-05-06
R APPLICATION NUMBER: 60/084637
R FILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/084639
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R APPLICATION NUMBER: 60/084643
R FILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/085339
R FILING DATE: 1998-05-13
R APPLICATION NUMBER: 60/085338
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APPLICATION UNDBER: 60/084640
FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084598
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APPLICATION NUMBER: 60/084600
FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084627
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APPLICATION UNDRER: 60/085579
FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085580
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APPLICATION UNMBER: 60/083545
FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083554
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APPLICATION NUMBER: 60/084414
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APPLICATION NUMBER: 60/085323
FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/085582
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APPLICATION NUMBER: 60/085697
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Best Local Similarity 62.5
Matches 5; Conservative
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APPLICATION NUMBER: 60/079786
FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079920
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APPLICATION NUMBER: 60/081195
                        FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079728
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APPLICATION NUMBER: 60/080327
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APPLICATION NUMBER: 60/080328
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FILING DATE: 1998-04-01
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APPLICATION NUMBER: 60/081203
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APPLICATION NUMBER: 60/079663
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FILING DATE: 1998-03-30
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Query Match
Best Local Similarity 62.5%; Pred. No. 53;
Matches 5; Conservative 2; Mismatches 1;
Qy 4 YYRYGVVX 11
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RESULT 18
US-09-849-626-327
; Sequence 327, Application US/09849626
; Publication No. US20020197669A1
; GENERAL BARGUY. Chaitanya

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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PILC7
CURRENT APPLICATION NUMBER: US/09/978,189
PRIOR APPLICATION ADMEDIATE: 2001-10-15
APPLICANT: MCNeill, Patricia
APPLICANT: Clapper, Jonathan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121 478016
CURRENT APPLICATION NUMBER: US/09/849,626
CURRENT PELING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 1926
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 327
LENGTH: 144

TWIST ID NO 327
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Pred. No. 53;
2; Mismatches
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PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR PLING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR FILING DATE: 1997-11-13
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Publication No: US20030004102A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Grimaldi, J. Christopher
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62.5%;
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Shelton, David L.
Stewart, Timothy A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gerritsen, Mary E.
Goddard, Audrey
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Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
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Paoni, Nicholas F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gurney, Austin L.
Hillan, Kenneth J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Baker Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan
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Kuo, Sophia S.
Napier, Mary A.
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Best Local Similarity 62.5
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mary A.
                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
US-09-849-626-327
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R FILING DATE: 1998-03-20
R APPLICATION NUMBER: 60/078910
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R APPLICATION NUMBER: 60/078939
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R APPLICATION NUMBER: 60/079294
R FILING DATE: 1998-03-25
R APPLICATION NUMBER: 60/079294
FILING DATE: 1998-03-10
APPLICATION NUMBER: 60/077632
FILING DATE: 1998-03-11
APPLICATION NUMBER: 60/077641
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PRIOR PELICATION NUMBER: 60/081070
PRIOR PILING DATE: 1998-04-08
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FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/078936
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APPLICATION NUMBER: 60/078004
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LLING DATE: 1998-03-27
PELICATION NUMBER: 60/079728
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APPLICATION NUMBER: 60/079664
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PELICATION NUMBER: 60/079920
LING DATE: 1998-03-30
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FILLING DATE: 1998-03-30
APPLICATION NUMBER: 60/080105
FILLING DATE: 1998-03-31
APPLICATION NUMBER: 60/080107
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PPLICATION NUMBER: 60/079786
ILING DATE: 1998-03-27
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APPLICATION NUMBER: 60/080165
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FILING DATE: 1998-03-31
APPLICATION NUMBER: 60/080327
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APPLICATION NUMBER: 60/080334
FILING DATE: 1998-04-01
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APPLICATION NUMBER: 60/081049
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APPLICATION NUMBER: 60/080333
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FILING DATE: 1998-04-15
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(CATION NUMBER: 60/085338 IG DATE: 1998-05-13
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PRIOR APPLICATION NUMBER: 60/084643
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339
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FILING DATE: 1998-5-07
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PLICATION NUMBER: 60/084366
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PLICATION NUMBER: 60/084414
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PLICATION NUMBER: 60/083554
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FILE REFERENCE: P2630P1C22
CURRENT APPLICATION NUMBER: US/09/978,608A
CURRENT FILING DATE: 2001-10-16
                                                                                                                                                                                         Query Match 59.0%; Score 36; DB Best Local Similarity 62.5%; Pred. No. 53; Mismatches 5; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 322, Application US/09978608A Sequence 322, Application No. US20030045462A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sodowski, Paul J. Sodowski, Paul J. Christopher
      PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR PELING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR PELING DATE: 1998-05-15
PRIOR PILING DATE: 1998-05-15
PRIOR PILING DATE: 1998-05-15
PRIOR PILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085579
FILING DATE: 1998-05-15
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Shelton, David L.
Stewart, Timothy A.
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APPLICANT: Baker Kevin P.
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ORGANISM: Homo sapiens
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US-09-978-608A-322
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APPLICANT: Kijavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Ruo, Sophia S.
APPLICANT: Naplear, Mary A.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Shelton, David L.
APPLICANT: Tumothy A.
APPLICANT: Williams, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Acides Encoding the Same CURRENT APPLICATION NUMBER: US/09/978,191A CURRENT APPLICATION NUMBER: US/09/978,191A CURRENT FILING DATE: 2001-10-15 PRIOR PELING DATE: 1997-10-17 PRIOR PILING DATE: 1997-10-17 PRIOR PILING DATE: 1997-10-17 PRIOR APPLICATION NUMBER: G0/062250 PRIOR APPLICATION NUMBER: G0/06311 PRIOR APPLICATION NUMBER: G0/06311 PRIOR APPLICATION NUMBER: G0/06311 PRIOR APPLICATION NUMBER: G0/06311 PRIOR APPLICATION NUMBER: G0/077632 PRIOR PILING DATE: 1999-03-10 PRIOR PILING DATE: 1998-03-11 PRIOR PELING DATE: 1998-03-11 PRIOR PILING DATE: 1998-03-12 PRIOR PILING DATE: 1998-03-12 PRIOR PILING DATE: 1998-03-12 PRIOR PILING DATE: 1998-03-12 PRIOR PILING DATE: 1998-03-12 PRIOR PILING DATE: 1998-03-12 PRIOR PILING DATE: 1998-03-12 PRIOR PILING DATE: 1998-03-20 PRIOR PILING DATE: 1998-03-20 PRIOR PILING DATE: 1998-03-20 PRIOR PILING DATE: 1998-03-20 PRIOR PILING DATE: 1998-03-20 PRIOR PILING DATE: 1998-03-20 PRIOR PILING DATE: 1998-03-20 PRIOR PILING DATE: 1998-03-20 PRIOR PILING DATE: 1998-03-20 PRIOR PILING DATE: 1998-03-20 PRIOR PILING DATE: 1998-03-20 PRIOR PILING DATE: 1998-03-20 PRIOR PILING DATE: 1998-03-20 PRIOR PILING DATE: 1998-03-20 PRIOR PILING DATE: 1998-03-20 PRIOR PILING DATE: 1998-03-20 PRIOR PILING DATE: 1998-03-20 PRIOR PILING DATE: 1998-03-20 PRIOR PILING DATE: 1998-03-20 PRIOR PILING DATE: 1998-03-20 PRIOR PILING DATE: 1998-03-20 PRIOR PILING DATE: 1998-03-20 PRIOR PILING DATE: 1998-03-20 PRIOR PILING DATE: 1998-03-20 PRIOR PILING DATE: 1998-03-20 PRIOR PILING DATE: 1998-03-20 PRIOR PILING DATE: 1998-03-20 PRIOR PILING DATE: 1998-03-20 PRIOR PILING DATE: 1998-03-20 PRIOR PILING DATE: 1998-03-20 PRIOR PILING DATE: 1998-03-20 PRIOR PILING DATE: 1998-03-20 PRIOR PILING DATE: 1998-03-20 PRIOR PILING DATE: 1998-03-20 PRIOR PILING DATE: 1998-03-20 PRIOR PILING DATE: 1998-03-20 PRIOR PILING DATE: 1998-03-20 PRIOR PILING DATE: 1998-03-20 PRIOR PILING DATE: 19
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RF FILING DATE: 1998-03-27

RAPELICATION NUMBER: 60/079728

NR FILING DATE: 1998-03-27

NR APPLICATION NUMBER: 60/079786

NR APPLICATION NUMBER: 60/07920

NR APPLICATION NUMBER: 60/07920

NR APPLICATION NUMBER: 60/07920
                          Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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APPLICATION NUMBER: 60/080107
FILING DATE: 1998-03-31
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Godowski, Paul J.
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CURRENT APPLICATION NUMBER: 126/09/978,585A
CURRENT FILING DATE: 2001-10-16
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NUMBER OF SEQ ID NOS: 624
Prior Application removed - See File Wrapper or Palm SEQ ID NO 322
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
                                                                                                     Sequence 322, Application US/09978585A Publication No. US20030049633A1 GENERAL INFORMATION:
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US-09-978-191A-322
Sequence 322, Application US/09978191A
Publication No. US20030050239A1
GENERAL INFORMATION:
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Ferrara, Napoleon
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Shelton, David L.
Stewart, Timothy A.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
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Goddard, Audrey
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Filvaroff, Ellen
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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APPLICANT: Baker Kevin P.
APPLICANT: Betstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan
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Best Local Similarity 62.5
Matches 5; Conservative
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CRGANISM: Homo sapiens
US-09-978-585A-322
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FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081049
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APPLICATION NUMBER: 60/081229
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APPLICATION NUMBER: 60/081817
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APPLICATION NUMBER: 60/083392
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APPLICATION NUMBER: 60/083495
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APPLICATION NUMBER: 60/083558
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                                                                    APPLICATION NUMBER: 60/080328
FILING DATE: 1998-04-01
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APPLICATION NUMBER: 60/082704
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APPLICATION NUMBER: 60/080334
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                                          APPLICATION NUMBER: 60/080327
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PRIOR PELLING DATE: 1998-05-07
PRIOR PELLING DATE: 1998-05-07
PRIOR PELLING DATE: 1998-05-13
PRIOR PAPLICATION NUMBER: 60/085339
PRIOR APPLICATION NUMBER: 60/085323
PRIOR PELLING DATE: 1998-05-13
PRIOR PELLING DATE: 1998-05-13
PRIOR PELLING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085582
PRIOR APPLICATION NUMBER: 60/085582
PRIOR APPLICATION NUMBER: 60/085589
PRIOR PELLING DATE: 1998-05-15
PRIOR PELLING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085599
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                                                                                                                                                                R APPLICATION NUMBER: 60/084598
R FILING DATE: 1998-05-07
R PILING DATE: 1998-05-07
R FILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/084627
R FILING DATE: 1998-05-07
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APPLICATION NUMBER: 60/084640
FILING DATE: 1998-05-07
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Best Local Similarity 62.5%;
Matches 5; Conservative
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ilvaroff, Ellen
90-50-866
                                                FILING DATE: 1998-05-07
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APPLICANT: Baker Kevin P
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132 YYLYGMIY 139
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US-09-978-403A-322
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PRIOR FILLING DATE: 1938-04-09

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R FILING DATE: 1998-04-08
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R APPLICATION NUMBER: 60/081071
R FILING DATE: 1998-04-08
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R FILING DATE: 1998-04-09
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I. APPLICANT: Societed and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                           THILE CF INVENTION: ACIDGE BICCOLLING THE SAME FILE REPRENCE: P2630PLC17

CURRENT APPLICATION NUMBER: 09/918685

PRIOR APPLICATION NUMBER: 06/06220

PRIOR FILING DATE: 1997-11-03

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APPLICATION NUMBER: 60/080328
Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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PRIOR APPLICATION NUMBER: 60/079294
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PRIOR FILING DATE: 1998-03-26
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APPLICATION NUMBER: 60/079920
FILING DATE: 1998-03-30
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APPLICATION NUMBER: 60/080327
FILING DATE: 1998-04-01
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APPLICATION NUMBER: 60/079664
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                                                                                                                                                                                                                                                                                                                                              R APPLICATION NUMBER: 60/085338
R FILING DATE: 1998-05-13
R PAPLICATION NUMBER: 60/085323
R FILING DATE: 1998-05-13
R APPLICATION NUMBER: 60/085582
R FILING DATE: 1998-05-15
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Grimaldi, J. Christopher
Gurney, Austin L.
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APPLICATION UNMBER: 60/085689
FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085579
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FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084643
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FILING DATE: 1998-05-13
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Stewart, Timothy A
Tumas, Daniel
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Goddard, Audrev
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tuo, Sophia S.
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Best Local Similarity 62.5
Matches 5; Conservative
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CURRENT FILING DATE: 2001-10-16
PRIOR PLING DATE: 2001-10-16
PRIOR PLING DATE: 2001-0-30
PRIOR PLING DATE: 2001-07-30
PRIOR PLING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR PLING DATE: 1997-10-30
PRIOR APPLICATION NUMBER: 60/064249
PRIOR APPLICATION NUMBER: 60/064319
PRIOR APPLICATION NUMBER: 60/065311
PRIOR PLING DATE: 1997-11-13
PRIOR PLING DATE: 1997-11-12
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FILING DATE: 1998-04-15
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            60/081071
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APPLICATION NUMBER: 60/083559
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Gaps
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53;
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Pred. No.
PRIOR APPLICATION NUMBER: 60/084643
PRIOR FILING DATE: 1998-05-07
PRIOR FILING DATE: 1998-05-13
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PRIOR FILING DATE: 1998-05-13
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PRIOR FILING DATE: 1998-05-15
PRIOR PRIOR PLING DATE: 1998-05-15
PRIOR PRIOR DATE: 1998-05-15
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PRIOR PLING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/08559
PRIOR PLING DATE: 1998-05-15
PRIOR PLING DATE: 1998-05-15
PRIOR PLING DATE: 1998-05-15
PRIOR PLING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/08559
PRIOR PLING DATE: 1998-05-15
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APPLICANT: Ashkenazi, Avi
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62.5%;
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Goddard, Audrey
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Filvaroff, Ellen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 62.5
Matches 5, Conservative
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Eaton, Dan
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Sao, Wei-Qiang
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Baker Kevin P.
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ITILE OF INVENTION: Acids Encoding the Same

Tumas, Daniel Williams, P. Mickey Wood, William I.

Roy, Margaret Ann Shelton, David L. Stewart, Timothy A.

Pan, James; Paoni, Nicholas F

Mary A

Napier,

Godowski, Paul J. Grimaldi, J. Christopher

Gurney, Austin L. Hillan, Kenneth J Kljavin, Ivar J. Kuo, Sophia S.

FILE REFERENCE: PS/830P1065
CURRENT APPLICATION NUMBER: US/09/999,833A
CURRENT FILING DATE:

CURRENT FILING DATE: 2001-10-24 PRIOR APPLICATION NUMBER: 09/918585

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R FILING DATE: 1997-10-17

R APPLICATION NUMBER: 60/064249

R APPLICATION NUMBER: 60/065311

R FILING DATE: 1997-11-03

R APPLICATION NUMBER: 60/066364

R FILING DATE: 1997-11-21

R APPLICATION NUMBER: 60/077450

R FILING DATE: 1998-03-10

R FILING DATE: 1998-03-11

R APPLICATION NUMBER: 60/077632

R FILING DATE: 1998-03-11 FILING DATE: 2001-07-30 APPLICATION NUMBER: 60/062250 FILING DATE: 1997-10-17 FILING DATE: 1998-03-11 APPLICATION NUMBER: 60/077649 FILING DATE: 1998-03-13 APPLICATION NUMBER: 60/078886 FILING DATE: 1998-03-20 APPLICATION NUMBER: 60/078910 FILING DATE: 1998-03-20 APPLICATION NUMBER: 60/078939 FILING DATE: 1998-03-25 APPLICATION NUMBER: 60/079656 FILING DATE: 1998-03-27 APPLICATION NUMBER: 60/079786 FILING DATE: 1998-03-27 APPLICATION NUMBER: 60/079920 FILING DATE: 1998-03-30 FILING DATE: 1998-03-30 APPLICATION NUMBER: 60/080105 APPLICATION NUMBER: 60/080107 FILING DATE: 1998-03-31 FILING DATE: 1998-04-01 APPLICATION NUMBER: 60/080328 APPLICATION NUMBER: 60/080333 FILING DATE: 1998-04-01 FILING DATE: 1998-04-01 APPLICATION NUMBER: 60/080334 60/081203 FILING DATE: 1998-03-11 APPLICATION NUMBER: 60/077791 FILING DATE: 1998-03-12 APPLICATION NUMBER: 60/078004 APPLICATION NUMBER: 60/078936 FILING DATE: 1998-03-20 APPLICATION NUMBER: 60/079294 FILING DATE: 1998-03-26 APPLICATION NUMBER: 60/079664 APPLICATION NUMBER: 60/079689 APPLICATION NUMBER: 60/079663 CATION NUMBER: 60/079923 APPLICATION NUMBER: 60/080165 APPLICATION NUMBER: 60/080327 ICATION NUMBER: 60/081070 APPLICATION NUMBER: 60/081049 1998-04-08 998-04-08 1998-03-20 1998-03-27 1998-03-27 1998-03-27 1998-03-31 FILING DATE: 1998-03-31 1998-04-01 1998-04-01 1998-03-31 APPLICATION NUMBER: FILING DATE: FILING DATE: PRIOR

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APPLICATION NUMBER: 60/078886
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FILING DATE: 1998-03-25
APPLICATION NUMBER: 60/079656
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APPLICATION NUMBER: 60/079664
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APPLICATION NUMBER: 60/079689
FILING DATE: 1998-03-27
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F FILING DATE: 1998-03-27
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FILING DATE: 1998-03-27
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FILING DATE: 1998-03-27
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FILING DATE: 1998-03-30
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RIOR APPLICATION NUMBER: 60/080105
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PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070
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APPLICATION NUMBER: 60/078910
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FILING DATE: 1998-04-01
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FILING DATE: 1998-04-01
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ING DATE: 1998-04-09
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FILING DATE: 1998-04-15
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                                              LING DATE: 1998-03-10
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Pred. No. 53;
2; Mismatches
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R FILING DATE: 2001-07-30
R APPLICATION NUMBER: 60/062250
R APPLICATION NUMBER: 60/064249
R APPLICATION NUMBER: 60/064249
R FILING DATE: 1997-11-03
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Gurney, Austin L.
Hillan, Kenneth J
APPLICATION NUMBER: 60/085323
FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/085582
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APPLICATION NUMBER: 60/08580
FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085573
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FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085697
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APPLICATION NUMBER: 60/085689
FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085579
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APPLICATION NUMBER: 60/085700
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Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Best Local Similarity 62.5%;
Matches 5; Conservative
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Goddard, Audrey
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
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Napier, Mary A.
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R APPLICATION NUMBER: 60/081952
R FILING DATE: 1998-04-15
A PPLICATION NUMBER: 60/081838
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R FILING DATE: 1998-04-21
R APPLICATION NUMBER: 60/08259
R FILING DATE: 1998-04-21
R APPLICATION NUMBER: 60/082704
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R FILING DATE: 1998-04-23
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FILING DATE: 1998-05-07
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APPLICATION NUMBER: 60/083495
FILING DATE: 1998-04-29
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APPLICATION UNMBER: 60/083558
FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083559
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APPLICATION NUMBER: 60/083500
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APPLICATION NUMBER: 60/084414
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APPLICATION NUMBER: 60/084639
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APPLICATION NUMBER: 60/084598
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APPLICATION NUMBER: 60/0
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Pred. No. 53;
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US-09-978-824-322
; Sequence 322, Application US/09978824
; Publication No. US20030055216A1
; GENERAL INFORMATION:
; APPLICANT: Baker Kevin P.
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PRIOR FILING DATE: 2001-07-30
PRIOR FILING DATE: 1997-10-17
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PRIOR PLING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
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Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William IP
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Best Local Similarity 62.5%;
Matches 5; Conservative
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Goddard, Audrey
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Filvaroff, Ellen
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Gerber, Hanspeter
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Eaton, Dan
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Pan, James;
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R APPLICATION NUMBER: 60/078004
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APPLICATION NUMBER: 60/07886
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R APPLICATION NUMBER: 60/078936
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R AFLING DATE: 1998-03-26
R APPLICATION NUMBER: 60/079664
R FILING DATE: 1998-03-27
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R APPLICATION NUMBER: 60/079663
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R FILING DATE: 1998-03-30
R APPLICATION NUMBER: 60/080105
R FILING DATE: 1998-03-31
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R APPLICATION NUMBER: 60/080165
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R APPLICATION NUMBER: 60/081195
R FILING DATE: 1998-04-08
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R APPLICATION NUMBER: 60/081203
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APPLICATION NUMBER: 60/078910
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APPLICATION NUMBER: 60/080327
FILING DATE: 1998-04-01
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FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/080333
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APPLICATION NUMBER: 60/080334
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APPLICATION NUMBER: 60/081070
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APPLICATION NUMBER: 60/081049
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APPLICATION NUMBER: 60/081071
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APPLICATION UNMBER: 60/081955
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081817
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APPLICATION NUMBER: 60/080194
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R APPLICATION NUMBER: 60/084441

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R APPLICATION NUMBER: 60/083742
R FILING DATE: 1998-04-30
R APPLICATION NUMBER: 60/084366
R FILING DATE: 1998-05-05
R APPLICATION NUMBER: 60/084414 APPLICATION NUMBER: 60/083499 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083545 FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085580
FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085573 FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/082804
FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/082700
FILING DATE: 1998-04-22 FILING DATE: 1998-04-23 APPLICATION NUMBER: 60/083336 FILING DATE: 1998-04-28 APPLICATION NUMBER: 60/083392 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083495 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083496 FILING DATE: 1998-04-29 FILING DATE: 1998-04-29
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APPLICATION NUMBER: 60/083558 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083500 FILING DATE: 1998-05-13 APPLICATION NUMBER: 60/085582 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/082796 FILING DATE: 1998-04-27 APPLICATION NUMBER: 60/083322 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083559 APPLICATION NUMBER: 60/082797 FILING DATE: 1998-04-22 FILING DATE: 1998-05-15 998-04-2 1998-05-1 FILING DATE: PRAILORA PRA PRIOR PRIOR PRIOR

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R FILING DATE: 1998-04-08
R APPLICATION NUMBER: 60/081049
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R APPLICATION NUMBER: 60/081195
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R APPLICATION NUMBER: 60/079728

R PILING DATE: 1998-03-27

R APPLICATION NUMBER: 60/079786

R FILING DATE: 1998-03-27

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R FILING DATE: 1998-03-87

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R APPLICATION NUMBER: 60/079920
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FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079689
APPLICATION UNMBER: 60/079683
APPLICATION NUMBER: 60/079663
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FILING DATE: 1998-03-31
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APPLICATION NUMBER: 60/080334
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APPLICATION NUMBER: 60/081070
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APPLICATION UNMBER: 60/081819
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081952
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APPLICATION NUMBER: 60/082804
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APPLICATION NUMBER: 60/080333
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APPLICATION NUMBER: 60/081229
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APPLICATION NUMBER: 60/081955
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APPLICATION NUMBER: 60/081817
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APPLICATION NUMBER: 60/082568
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APPLICATION NUMBER: 60/082569
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CURRENT APPLICATION NUMBER: US/09/918,585A
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/064311
PRIOR APPLICATION NUMBER: 60/064311
PRIOR APPLICATION NUMBER: 60/064311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
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PRIOR APPLICATION NUMBER: 60/077641
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2; Mismatches
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US-09-918-585A-322
Sequence 322, Application US/09918585A
; Publication No. US20030060406A1
; GENERAL INFORMATION:
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Gurney, Austin L.
Hillan, Kenneth J
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION WUMBER: 60/085704
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Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
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APPLICATION NUMBER: 60/
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Kuo, Sophia S.
Napier, Mary A.
Pan, James;
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
                                                                                                    Query Match
Best Local Similarity 62.5
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Sao, Wei-Qiang
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PRIOR FILING DATE: 1998-04-29
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PRIOR PRILOR PRICE DATE: 1998-04-23
PRIOR FILING DAME: 1998-04-29
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PRIOR PRILOR DAME: 1998-05
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Length 144;

Score 36; DB 12; Pred. No. 53;

59.0%; 62.5%;

Query Match Best Local Similarity

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AFPLICANT: WOOSD, NILISAN I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE OF INVENTION: Acids Encoding the Same FILE OF INVENTION: Acids Encoding the Same CURRENT APPLICATION NUMBER: US/09/978,423A

CURRENT APPLICATION NUMBER: US/09/978,650

PRIOR FILING DATE: 1997-10-730

PRIOR FILING DATE: 1997-10-730

PRIOR FILING DATE: 1997-11-03

PRIOR FILING DATE: 1997-11-03

PRIOR FILING DATE: 1997-11-21

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PRIOR PILING DATE: 1998-03-10

PRIOR FILING DATE: 1998-03-11

PRIOR FILING DATE: 1998-03-11

PRIOR PILING DATE: 1998-03-11
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o. US20030069178A1
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APPLICATION NUMBER: 60/078910
FILING DATE: 1998-03-20
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Williams, P. Mickey
Wood, William I.
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Shelton, David L.
Stewart, Timothy A.
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Paoni, Nicholas F
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
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Hillan, Kenneth
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Grimaldi, J. C
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Sao, Wei-Qiang
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132 YYLYGMIY 139
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                                                                                                                                                                                                                         GENERAL INFORMATION
                                                                                                                                                  -09-978-423A-322
                                                                                                                                                                                                    Publication No.
                                                                                                                                                                            Sequence 322,
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R FILING DATE: 1998-04-22
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R APPLICATION NUMBER: 60/079664

R APPLICATION NUMBER: 60/079669

R FILING DATE: 1998-03-26

R APPLICATION NUMBER: 60/079663

R APPLICATION NUMBER: 60/07963

R APPLICATION NUMBER: 60/07978

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R FILING DATE: 1998-03-30

R APPLICATION NUMBER: 60/080105

R APPLICATION NUMBER: 60/080105

R FILING DATE: 1998-03-31

R APPLICATION NUMBER: 60/080107

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R APPLICATION NUMBER: 60/080165

R FILING DATE: 1998-03-31

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R APPLICATION NUMBER: 60/080333

R FILING DATE: 1998-04-01

R APPLICATION NUMBER: 60/080334

R FILING DATE: 1998-04-01

R APPLICATION NUMBER: 60/081070

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R APPLICATION NUMBER: 60/081952

RR APLICATION NUMBER: 60/081838

R APLICATION NUMBER: 60/08256

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R APPLICATION NUMBER: 60/081203
R FILING DATE: 1998-04-09
A PAPLICATION NUMBER: 60/081229
R FILING DATE: 1998-04-09
R APPLICATION NUMBER: 60/081955
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FILING DATE: 1998-04-15
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DB 12; Length 144; 53; PRIOR APPLICATION NUMBER: 60/081392
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PRIOR PRILING DATE: 1998-04-29
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2; Mismatches

Query Match 59.0%; Score 36; Best Local Similarity 62.5%; Pred. No. 9 Matches 5; Conservative 2; Mismatch

132 YYLYGMIY 139

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FILING DATE: 1998-04-29
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FILE REPRENCE: P3530PLG
CURRENT PAPLICATION NUMBER: US/09/978,193A
CURRENT FILING DATE: 2002-02.21
RRIOR REPLICATION NUMBER: US/09/978,193A
CURRENT FILING DATE: 2001-07-30
PRIOR PELICATION NUMBER: 09/046250
PRIOR PELICATION NUMBER: 09/04249
PRIOR PILING DATE: 1997-10-17
PRIOR PELICATION NUMBER: 60/06250
PRIOR PILING DATE: 1997-10-13
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PRIOR PILING DATE: 1997-11-13
PRIOR PLICATION NUMBER: 60/07360
PRIOR PILING DATE: 1999-03-11
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                                      Sequence 322, Application US/09978193A
Publication No. US20030073624A1
GENERAL INFORMATION:
APPLICANT: Baker Kevin P.
APPLICANT: Betsein, David
APPLICANT: Betsein, David
APPLICANT: Eaton, Dan
                                                                                                                                                                                                                                                                                                                                                                                                   Godowski, Paul'J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Williams, P. Mickey
Wood, William I.
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Kuo, Sophia S.
Napier, Mary A.
Pan, James;
Paoni, Nicholas F.
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Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Gerritsen, Mary E.
Goddard, Audrey
RESULT 30
US-09-978-193A-322
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APPLICANT:
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R FILING DATE: 1998-03-30
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R FILING DATE: 1998-04-15
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R FILING DATE: 1998-04-21
R APPLICATION NUMBER: 60/082569
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APPLICATION NUMBER: 60/080194
APPLICATION NUMBER: 60/080327
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FILING DATE: 1998-04-01
FILING DATE: 1998-04-08
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APPLICATION NUMBER: 60/082796
FILING DATE: 1998-04-23
APPLICATION NUMBER: 60/083336
FILING DATE: 1998-04-27
APPLICATION NUMBER: 60/079689
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APPLICATION NUMBER: 60/080105
FILING DATE: 1998-03-31
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FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/080333
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APPLICATION NUMBER: 60/081071
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APPLICATION NUMBER: 60/081195
FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081203
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APPLICATION NUMBER: 60/081955
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APPLICATION NUMBER: 60/081819
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APPLICATION NUMBER: 60/082804
FILING DATE: 1998-04-22
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APPLICATION NUMBER: 60/083495
                                            APPLICATION NUMBER: 60/079663
FILING DATE: 1998-03-27
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APPLICATION NUMBER: 60/081817
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APPLICATION NUMBER: 60/081952
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ITILE OF INVENTION: Acids Encoding the Same File REPERIOR: P2630P1C70 CURRENT APPLICATION NUMBER: US/09/999,830A CURRENT FILING DATE: 2001-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 09/91618
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William I.
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Goddard, Audrey
                                                                                    Ferrara, Napoleon
Filvaroff, Ellen
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Kuo, Sophia S.
Napier, Mary A.
Pan, James;
Botstein, David
Desnoyers, Luc
Eaton, Dan
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Best Local Similarity 62.5%; Pred. No. 53;
Matches 5; Conservative 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1998-05-15
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US-09-999-830A-322
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Ferrara, Napoleon Filvaroff, Ellen Fong, Sherman Gao, Wei-Qiang

Eaton, Dan

APPLICANT: Ashkenazi, Avi APPLICANT: Baker Kevin P. APPLICANT: Botstein, David APPLICANT: Desnoyers, Luc

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Hillan, Kenneth J
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Williams, P. Mickey
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Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
  1998-03-30
  FILING DATE: 1998-03-31
  Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
Pan, James;
  TLE
   PRIOR
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APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, Williams I.
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TITLE OF INVENTION: Acids Encoding the Same
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  Fong, Sherman
Gao, Wei-Ciang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J.
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Desnoyers, Luc
Eaton, Dan
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  1998-04-21
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Godowski, Paul J. Grimaldi, J. Christopher Gurney, Austin L. Hillan, Kenneth J

Ivar J

Kljavin, Ivar Kuo, Sophia S. Napier, Mary A

Fong, Sherman Gao, Wei-Qiang Gerber, Hanspeter Gerritsen, Mary E.

Goddard, Audrey

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Botstein, David Desnoyers, Luc

Eaton, Dan

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APPLICANT: Ashkenazi, Avi

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OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,477
FILING DATE: 10-Jan-2002
PRIOR APPLICATION NUMBER: US/09/365,705
FILING DATE: 02-Aug-1999
APPLICATION NUMBER: US/09/365,705
FILING DATE: 14-OCT-1997
ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0401 US
TELECOMMUNICATION: INFORMATION:
   Sequence 3, Application US/10044477

Publication No. US20020103342A1

GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
Corley, Neil C.
Shah, Purvi
TITLE OF INVENTION: HUMAN CORNICHON PROTEIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
STREET: 3174 Porter Drive
   MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASLSEQ for Windows Version 2.0
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FILING DATE: 14-OCT-1997
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  ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
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Publication No. US20030125245A1

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Publication No. US20020103342A1
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APPLICANT: Hillman, Jennifer L.
Corley, Neil C.
Shah, Purvi
TITLE OF INVENTION: HUMAN CORNICHON PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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STREET: 3174 Porter Drive
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
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PRIOR FILING DATE: 1999-12-07
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APPLICANT: Smith, Victoria
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APPLICANT: Matanabe, Colin L.
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